

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
21 May 2004 (21.05.2004)

PCT

(10) International Publication Number
WO 2004/041193 A2

(51) International Patent Classification⁷:

A61K

(21) International Application Number:

PCT/US2003/034681

(22) International Filing Date: 31 October 2003 (31.10.2003)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/423,545	1 November 2002 (01.11.2002)	US
60/449,945	25 February 2003 (25.02.2003)	US
60/477,111	9 June 2003 (09.06.2003)	US

(71) Applicant (for all designated States except US): **DECODE GENETICS EHF**, [IS/IS]; Sturlugotu 8, IS-101 Reykjavik (IS).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **REYNISDOTTIR, Inga** [IS/IS]; Gunnarsbraut 26 1R, IS-105 Reykjavik (IS). **GULCHER, Jeffrey, R.** [US/US]; 130 South Canal Street, #9M, Chicago, IL 60606 (US). **GRANT, Struan, F.** [GB/IS]; Sorlajkov 1, IS-107 Reykjavik (IS). **THOR-LEIFSSON, Gudmar** [IS/IS]; Vesturberg 10, IS-111 Reykjavik (IS).

(74) Agents: **CARROLL, Alice, O.** et al.; Hamilton, Brook, Smith & Reynolds, P.C., 530 Virginia Road, P.O. Box 9133, Concord, MA 01742-9133 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KÈ, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN TYPE II DIABETES GENE-Kv CHANNEL-INTERACTING PROTEIN (KChIP1) LOCATED ON CHROMOSOME 5

(57) Abstract: Association of Type II diabetes and a locus on chromosome 5 is disclosed. In particular, the gene KChIP1 within this locus is shown by linkage analysis to be a susceptibility gene for Type II diabetes. Pathway targeting for drug delivery and diagnosis applications in identifying those who have Type II diabetes or are at risk of developing Type II diabetes, in particular those that are non-obese are described.

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HUMAN TYPE II DIABETES GENE – K_v CHANNEL-INTERACTING
PROTEIN (KChIP1) LOCATED ON CHROMOSOME 5

RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application NO.
5 60/477,111 filed June 9, 2003, and to U.S. Provisional Application NO. 60/449,945,
filed on February 25, 2003, and also to U.S. Provisional Application NO. 60/423,545,
filed on November 1, 2002, the entire contents of all applications are incorporated
herein by reference.

10 BACKGROUND OF THE INVENTION

Diabetes mellitus, a metabolic disease in which carbohydrate utilization is
reduced and lipid and protein utilization is enhanced, is caused by an absolute or
relative deficiency of insulin. In the more severe cases, diabetes is characterized by
chronic hyperglycemia, glycosuria, water and electrolyte loss, ketoacidosis and coma.

15 Long term complications include development of neuropathy, retinopathy,
nephropathy, generalized degenerative changes in large and small blood vessels and
increased susceptibility to infection. The most common form of diabetes is Type II,
non-insulin-dependent diabetes that is characterized by hyperglycemia due to
impaired insulin secretion and insulin resistance in target tissues. Both genetic and
20 environmental factors contribute to the disease. For example, obesity plays a major
role in the development of the disease. Type II diabetes is often a mild form of
diabetes mellitus of gradual onset.

The health implications of Type II diabetes are enormous. In 1995, there were
135 million adults with diabetes worldwide. It is estimated that close to 300 million
25 will have diabetes in the year 2025. (King H., *et al.*, *Diabetes Care*, 21(9): 1414-1431
(1998)). The prevalence of Type II diabetes in the adult population in Iceland is 2.5%
(Vilbergsson, S., *et al.*, *Diabet. Med.*, 14(6): 491-498 (1997)), which comprises
approximately 5,000 people over the age of 34 who have the disease. The high
prevalence of the disease and increasing population affected shows an unmet medical
30 need to define the genetic factors involved in Type II diabetes to more precisely
define the associated risk factors. Also needed are therapeutic agents for prevention
of Type II diabetes.

SUMMARY OF THE INVENTION

As described herein, a locus on chromosome 5q35 has been demonstrated which plays a major role in Type II diabetes. The locus, referred to as the Type II diabetes locus, comprises a nucleic acid that encodes, KChIP1.

5 The present invention relates to genes located within the Type II diabetes - related locus, particularly nucleic acids comprising the KChIP1 gene, and the amino acids encoded by these nucleic acids. The invention further relates to pathway targeting for drug delivery and diagnosis in identifying those who have Type II diabetes and those at risk of developing Type II diabetes. Also described are
10 haplotypes and SNPs that can be used to identify individuals with Type II diabetes or at risk of developing Type II diabetes, particularly in those that are non-obese. As a consequence, intervention can be prescribed to these individuals before symptoms of the disease present, *e.g.*, dietary changes, exercise and/or medication. Identification of genes in the Type II diabetes locus can pave the way for a better understanding of
15 the disease process, which in turn can lead to improved diagnostics and therapeutics.

 The present invention pertains to methods of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of a susceptibility to Type II diabetes. The invention additionally pertains
20 to methods of diagnosing Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of Type II diabetes. In one embodiment, in diagnosing Type II diabetes or susceptibility to Type II diabetes by detecting the presence of a polymorphism in a KChIP1 nucleic acid, the presence of the
25 polymorphism in the KChIP1 nucleic acid can be indicated, for example, by the presence of one or more of the polymorphisms indicated in Table 10.

 In other embodiments, the invention relates to methods of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting an alteration in the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid
30 in a test sample, in comparison with the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a control sample, wherein the presence of an

alteration in expression or composition of the polypeptide in the test sample is indicative of a susceptibility to Type II diabetes. The invention additionally relates to a method of diagnosing Type II diabetes in an individual, comprising detecting an alteration in the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a test sample, in comparison with the expression or composition of a polypeptide encoded by KChIP1 nucleic acid in a control sample, wherein the presence of an alteration in expression or composition of the polypeptide in the test sample is indicative of Type II diabetes.

The invention also relates to an isolated nucleic acid molecule comprising a KChIP1 nucleic acid (*e.g.*, SEQ ID NO: 1 or the complement of SEQ ID NO:1). In certain embodiments, the KChIP1 nucleic acid comprises one or more nucleotide sequence(s) selected from the group of nucleic acid sequences as shown in Table 10 (*e.g.*, SEQ ID NOs: 114-258) and the complements of the group of nucleic acid sequences as shown in Table 10. For example, in certain embodiments, the nucleotide sequence contains one or more polymorphism(s), such as those shown in Table 10. In another embodiment, the invention relates to an isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of SEQ ID NO: 1 and the complement of SEQ ID NO: 1. In certain embodiments, the isolated nucleic acid molecule hybridizes under high stringency conditions to a nucleotide sequence comprising one or more nucleotide sequence(s) selected from the group of nucleic acid sequences as shown in Table 10 (*e.g.*, SEQ ID NOs: 114-258) and the complements of the group of nucleic acid sequences as shown in Table 10. For example, in certain embodiments, the nucleotide sequence contains one or more polymorphism(s), such as those shown in Table 10.

Also contemplated by the invention is a method of assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises at least one (or more) nucleic acid sequence(s) selected from the group of SEQ ID NOs: 1 and 114-258, inclusive, wherein the nucleic acid sequence hybridizes to the first nucleic acid under high stringency conditions. In certain embodiments, the second

nucleic acid molecule contains one or more polymorphism(s), such as those shown in Table 10.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention (*e.g.*, SEQ ID NOs: 1 and 114-258; optionally including one or more of the polymorphisms shown in Table 10) operably linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for producing a polypeptide encoded by an isolated nucleic acid molecule having a polymorphism, comprising culturing the recombinant host cell under conditions suitable for expression of the nucleic acid molecule.

Also contemplated by the invention is a method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, the method comprising contacting the sample with an antibody that specifically binds to the encoded polypeptide.

The invention further pertains to a method of identifying an agent that alters expression of a KChIP1 nucleic acid, comprising: contacting a solution containing a nucleic acid comprising the promoter region of the KChIP1 gene operably linked to a reporter gene, with an agent to be tested; assessing the level of expression of the reporter gene in the presence of the agent; and comparing the level of expression of the reporter gene in the presence of the agent with a level of expression of the reporter gene in the absence of the agent; wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the KChIP1 gene or nucleic acid. An agent identified by this method is also contemplated.

The invention additionally comprises a method of identifying an agent that alters expression of a KChIP1 nucleic acid, comprising contacting a solution containing a nucleic acid of the invention or a derivative or fragment thereof, with an agent to be tested; comparing expression of the nucleic acid, derivative or fragment in the presence of the agent with expression of the nucleic acid, derivative or fragment in the absence of the agent; wherein if expression of the nucleic acid, derivative or fragment in the presence of the agent differs, by an amount that is statistically

significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the KChIP1 nucleic acid. In certain embodiments, the expression of the nucleic acid, derivative or fragment in the presence of the agent comprises expression of one or more splicing variants(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent. Agents identified by this method are also contemplated.

Representative agents that alter expression of a KChIP1 nucleic acid contemplated by the invention include, for example, antisense nucleic acids to a KChIP1 gene or nucleic acid; a KChIP1 gene or nucleic acid; a KChIP1 polypeptide; a KChIP1 gene or nucleic acid receptor, or other receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme. A method of altering expression of a KChIP1 nucleic acid, comprising contacting a cell containing a nucleic acid with such an agent is also contemplated.

The invention further pertains to a method of identifying a polypeptide which interacts with a KChIP1 polypeptide (*e.g.*, a KChIP1 polypeptide encoded by a nucleic acid of the invention, such as a nucleic acid comprising one or more polymorphism(s) indicated in Table 10), comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a KChIP1 polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide. If transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide, which interacts with a KChIP1 polypeptide.

In certain methods of the invention, a Type II diabetes therapeutic agent is used. The Type II diabetes therapeutic agent can be an agent that alters (*e.g.*, enhances or inhibits) KChIP1 polypeptide activity and/or KChIP1 nucleic acid expression, as described herein (*e.g.*, a nucleic acid agonist or antagonist).

Type II diabetes therapeutic agents can alter polypeptide activity or nucleic acid expression of a KChIP1 nucleic acid by a variety of means, such as, for example, by providing additional polypeptide or upregulating the transcription or translation of the nucleic acid encoding the KChIP1 polypeptide; by altering posttranslational

processing of the KChIP1 polypeptide; by altering transcription of splicing variants; or by interfering with polypeptide activity (*e.g.*, by binding to the KChIP1 polypeptide, or by binding to another polypeptide that interacts with KChIP1, such as a KChIP1 binding agent as described herein), by altering (*e.g.*, downregulating) the expression, transcription or translation of a nucleic acid encoding KChIP1; or by
5 altering interaction among KChIP1 and a KChIP1 binding agent.

In a further embodiment, the invention relates to Type II diabetes therapeutic agent, such as an agent selected from the group consisting of: a KChIP1 nucleic acid or fragment or derivative thereof; a polypeptide encoded by a KChIP1 nucleic acid
10 (*e.g.*, encoded by a KChIP1 nucleic acid having one or more polymorphism(s) such as those set forth in Table 10); a KChIP1 receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters KChIP1 gene or nucleic acid expression; an agent that alters activity of a polypeptide encoded by a KChIP1 gene or nucleic acid; an agent that alters posttranscriptional processing
15 of a polypeptide encoded by a KChIP1 gene or nucleic acid; an agent that alters interaction of a KChIP1 polypeptide with a KChIP1 binding agent or receptor; an agent that alters transcription of splicing variants encoded by a KChIP1 gene or nucleic acid; and ribozymes. The invention also relates to pharmaceutical compositions comprising at least one Type II diabetes therapeutic agent as described
20 herein.

The invention also pertains to a method of treating a disease or condition associated with a KChIP1 polypeptide (*e.g.*, Type II diabetes) in an individual, comprising administering a Type II diabetes therapeutic agent to the individual, in a therapeutically effective amount. In certain embodiments, the Type II diabetes
25 therapeutic agent is a KChIP1 agonist; in other embodiments, the Type II diabetes therapeutic agent is a KChIP1 antagonist. The invention additionally pertains to use of a Type II diabetes therapeutic agent as described herein, for the manufacture of a medicament for use in the treatment of Type II diabetes, such as by the methods described herein.

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A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous KChIP1 gene or nucleic acid and a nucleic acid encoding a KChIP1 polypeptide, is further contemplated by the invention.

In yet another embodiment, the invention relates to a method for assaying a sample for the presence of a KChIP1 nucleic acid, comprising contacting the sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid under conditions appropriate for hybridization, and assessing whether hybridization has occurred between a KChIP1 nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid; wherein if hybridization has occurred, a KChIP1 nucleic acid is present in sample. In certain embodiments, the contiguous nucleotide sequence is completely complementary to a part of the sequence of said KChIP1 nucleic acid. If desired, amplification of at least part of said KChIP1 nucleic acid can be performed.

In certain other embodiments, the contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or capable of selectively hybridizing to said KChIP1 nucleic acid.

In other embodiments, the invention relates to a reagent for assaying a sample for the presence of a KChIP1 gene or nucleic acid, the reagent comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleic acid sequence of said KChIP1 gene or nucleic acid; or comprising a contiguous nucleotide sequence which is completely complementary to a part of the nucleic acid sequence of said KChIP1 gene or nucleic acid. Also contemplated by the invention is a reagent kit, *e.g.*, for assaying a sample for the presence of a KChIP1 nucleic acid, comprising (*e.g.*, in separate containers) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleic acid sequence of the KChIP1 nucleic acid, and

reagents for detection of said label. In certain embodiments, the labeled nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said KChIP1 gene or nucleic acid. In other embodiments, the labeled nucleic acid can comprise a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 gene or nucleic acid, and which is capable of acting as a primer for said KChIP1 nucleic acid when maintained under conditions for primer extension.

The invention also provides for the use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; b) at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or c) capable of selectively hybridizing to said KChIP1 nucleic acid, for assaying a sample for the presence of a KChIP1 nucleic acid.

In yet another embodiment, the use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; b) at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or c) capable of selectively hybridizing to said KChIP1 nucleic acid; for assaying a sample for the presence of a KChIP1 gene or nucleic acid that has at least one nucleotide difference from the first nucleic acid (*e.g.*, a SNP as set forth in Table 10), such as for diagnosing a susceptibility to a disease or condition associated with a KChIP1.

The invention also relates to a method of diagnosing Type II diabetes or a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of certain "haplotypes" (combinations of genetic markers). In one aspect of the invention of diagnosing a susceptibility of the disease, methods are described comprising screening for one of the at-risk haplotypes in the KChIP1 gene that is more frequently present in an individual susceptible to Type II diabetes, compared to the frequency of its presence in the general population, wherein the presence of an at-risk haplotype is indicative of a susceptibility to Type II

diabetes. An "at-risk haplotype" is intended to embrace one or a combination of haplotypes described herein over the KChIP1 gene that show high correlation to Type II diabetes. In one embodiment, the at-risk haplotype is characterized by the presence of at least one single nucleotide polymorphisms as described in Table 13. In one

5 embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises one or more haplotypes identified in Table 2 (haplotypes identified as A1, A2, A3, A4, A5, A6, B1, B2, B3, B4 and B5) or Table 5 (haplotypes identified as D1, D2, D3, D4 and D5). In certain embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises

10 markers DG5S879, DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S1058 and DG5S37 at the 5q35 locus; or DG5S1058, DG5S37 and DG5S101 at the 5q35 locus; or DG5S881, DG5S1058, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S879, DG5S1058 and DG5S37; or DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; DG5S953, DG5S955, DG5S13

15 and DG5S959 at the 5q35 locus; or DG5S888 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955 and DG5S124 at the 5q35 locus; or DG5S888, DG5S44 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955, DG5S13, DG5S123, and DG5S959 at the 5q35 locus. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. Also described herein is a

20 haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprising markers DG5S13, KCP_1152, and D5S625 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In one particular embodiment, the presence of the -4, 1, 0 haplotype at DG5S13, KCP_1152, and D5S625 is diagnostic of Type II diabetes or of a

25 susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers DG5S124, KCP_1152, KCP_2649, KPC_4976 and KPC-16152 at the 5q35 locus. In one particular embodiment, the presence of the 0, 1, 1, 3 and 0 haplotype at DG5S124, KCP_1152, KCP_2649, KPC_4976 and KPC-16152 is

30 diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type

II diabetes in an individual, comprises markers KCP_173982, KCP_15400, and KCP_18069. In one particular embodiment, the presence of the 0, 1, 1 haplotype at KCP_173982, KCP_15400, and KCP_18069 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

5 In additional embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S124, KCP_1152, KCP_2649, KCP_4976, and KCP_16152 at the 5q35 locus, as well as one of the following 3 markers: KCP_197678, KCP_197775, and KCP_202795 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a
10 susceptibility to Type II diabetes. In particular embodiments, the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP_197679, KCP_1152, KCP_2649, KCP_4976, and KCP_16152; the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP_197775, KCP_1152, KCP_2649, KCP_4976, and KCP_16152; or the presence of the 0, 1, 1, 1, 3, 0 haplotype at DG5S124, KCP_202795, KCP_1152, KCP_2649,
15 KCP_4976, and KCP_16152; is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

The presence or absence of the haplotype can be determined by various methods, including, for example, using enzymatic amplification of nucleic acid from the individual, electrophoretic analysis, restriction fragment length polymorphism
20 analysis and/or sequence analysis.

Also described herein is a method of diagnosing Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 10, Table 2, Table 5 and/or Table 13 in the locus on chromosome
25 5q35, wherein the presence of the haplotype is diagnostic of Type II diabetes. Also contemplated is a method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 10 and/or Table 13 in the locus on chromosome 5q35, wherein the
30 presence of the haplotype is diagnostic of a susceptibility to Type II diabetes.

A method for the diagnosis and identification of a susceptibility to Type II diabetes in an individual is also described, comprising: screening for an at-risk haplotype in the KChIP1 nucleic acid that is more frequently present in an individual susceptible to Type II diabetes compared to an individual who is not susceptible to Type II diabetes, wherein the at-risk haplotype increases the risk significantly. In certain embodiments, the significant increase is at least about 20% or the significant increase is identified as an odds ratio of at least about 1.2.

A major application of the current invention involves prediction of those at higher risk of developing a Type II diabetes. Diagnostic tests that define genetic factors contributing to Type II diabetes might be used together with or independent of the known clinical risk factors to define an individual's risk relative to the general population. Better means for identifying those individuals at risk for Type II diabetes should lead to better prophylactic and treatment regimens, including more aggressive management of the current clinical risk factors.

Another application of the current invention is the specific identification of a rate-limiting pathway involved in Type II diabetes. A disease gene with genetic variation that is significantly more common in diabetic patients as compared to controls represents a specifically validated causative step in the pathogenesis of Type II diabetes. That is, the uncertainty about whether a gene is causative or simply reactive to the disease process is eliminated. The protein encoded by the disease gene defines a rate-limiting molecular pathway involved in the biological process of Type II diabetes predisposition. The proteins encoded by such Type II genes or its interacting proteins in its molecular pathway may represent drug targets that may be selectively modulated by small molecule, protein, antibody, or nucleic acid therapies. Such specific information is greatly needed since the population affected with Type II diabetes is growing.

A third application of the current invention is its use to predict an individual's response to a particular drug, even drugs that do not act on KChIP1 or its pathway. It is a well-known phenomenon that in general, patients do not respond equally to the same drug. Much of the differences in drug response to a given drug is thought to be based on genetic and protein differences among individuals in certain genes and their

corresponding pathways. Our invention defines the association of KChIP1 with Type II diabetes. Some current or future therapeutic agents may be able to affect this gene directly or indirectly and therefore, be effective in those patients whose Type II diabetes risk is in part determined by the KChIP1 genetic variation. On the other hand, those same drugs may be less effective or ineffective in those patients who do not have at risk variation in the KChIP1 gene. Therefore, KChIP1 variation or haplotypes may be used as a pharmacogenomic diagnostic to predict drug response and guide choice of therapeutic agent in a given individual.

10 BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other objects, features and advantages of the invention will be apparent from the following more particular description of preferred embodiments of the invention, as illustrated in the accompanying drawings.

FIG. 1.1 through 1.148 show the KChIP1 genomic DNA (SEQ ID NO: 1).

15 This sequence is taken from NCBI Build 33. The numbering in FIG. 1, as well as the "start" and "end" numbers in all Tables refer to the location in Chromosome 5 in NCBI Build 33. The numbering in FIG. 1 refers to the last base in the line immediately preceding the number; the numbers are in decreasing order because of the "reverse orientation" of the gene.

20 FIG. 2 shows the amino acid sequence of KChIP1 as published by An *et al.* *Nature*, 403(6768): 553-6 (2000) (SEQ ID NO: 2).

FIG. 3 shows the nucleic acid sequence (SEQ ID NO: 3) encoding the amino acid sequence of KChIP1 as published by An *et al.*, *Nature*, 403(6768): 553-6 (2000) (SEQ ID NO: 2).

25 FIG. 4 is a series of graphs showing the results of a genome-wide scan using 906 microsatellite markers. Results are shown for three phenotypes: all Type II diabetics (solid lines), obese Type II diabetics (dotted lines) and non-obese Type II diabetics (dashed lines). The multipoint allele-sharing LOD-score is on the vertical axis, and the centimorgan distance from the P-terminus of the chromosome is on the horizontal axis.

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FIG. 5 graphically depicts the multipoint allele-sharing LOD-score of the locus on chromosome 5 after 38 microsatellite markers have been added to the framework set in a 40-cM interval, from 160 cM to 200 cM. Results are shown for the same three phenotypes as in FIG. 4; all Type II diabetics (solid line), non-obese Type II diabetics (dashed line) and obese Type II diabetics (dotted line). the results of a genome-wide scan using 906 microsatellite markers.

FIG. 6 graphically depicts the single-marker and haplotype association within the 1-LOD-drop for 590 non-obese diabetics vs 477 unrelated population controls. The location of the markers and haplotypes is on the horizontal axis and the corresponding two-sided P-value on the vertical axis. All haplotypes with a P-value less than 0.01 are shown. The horizontal bars indicate the span of the corresponding haplotypes and the marker density is shown at the bottom of the figure. All locations refer to NCBI Build 33 and the 1-LOD-drop spans from 167.64 to 171.28 Mb.

FIG. 7 schematically shows the location of genes and markers in region B. The microsatellites used in the locus-wide association study are shown as filled circles at the top. The filled boxes indicate the locations of exons, or clusters of exons, for KCHIP1. The shaded boxes indicated the location and size of the neighboring genes, LCP2, KCNMB1, GABRP and RANBP17, and the grey horizontal lines indicate the span of the five most significant microsatellite haplotypes in the region.

DETAILED DESCRIPTION OF THE INVENTION

Extensive genealogical information for a population with population-based lists of patients with Type II diabetes has been combined with powerful gene sharing methods to map a locus on chromosome 5q35. Diabetics and their relatives were genotyped with a genome-wide marker set including 906 microsatellite markers, with an average marker density of 4cM. Due to the role obesity plays in the development of diabetes, the material was fractionated according to body mass index (BMI). Presented herein are results of a genome wide search of genes that cause Type II diabetes in Iceland.

Loci Associated with Diabetes

Evidence for genes causing the early onset monogenic form of diabetes have been previously identified. Mutations in six genes have been discovered that cause MODY, or maturity onset diabetes of the young. MODY1 – MODY6 are due to mutations in HNF4a, glucokinase, HNF1a, IPF1, HNF1b and NEUROD1 (MODY1: Yamagata K, *et al.*, *Nature* 384:458-460 (1996); MODY2: Froguel P, F *et al.*, *Nature* 356: 162-164(1992); MODY3: Yamagata, K., *et al.*, *Nature* 384: 455-458 (1996); MODY4: Yoshioka M., *et al.*, *Diabetes* May;46(5):887-94 (1997) MODY5: Horikawa, Y., *et al.*, *Nat. Genet.* 17: 384-385 (1997) MODY6: Kristinsson S.Y., *et al.*, *Diabetologia* Nov;44(11):2098-103 (2001)).

One gene has been identified as a disease gene that contributes to the late-onset form of diabetes, the calpain 10 gene (CAPN10). CAPN10, was identified though a genome-wide screen of Mexican American sibpairs with diabetes (Horikawa, Y., *et al.*, *Nat. Genet.* 26(2) 163-175(2000)). The risk allele has been shown to be associated with impaired regulation of glucose-induced secretion and decreased rate of insulin-stimulated glucose disposal (Lynn, S., *et al.*, *Diabetes*, 51(1): 247-250 (2002); Sreenan, S.K., *et al.*, *Diabetes* 50(9) 2013-2020 (2001) and Baier, L. J., *et al.*, *J. Clin. Invest.* 106(7) R69-73 (2000)).

Many genome-wide screens in a variety of populations have been performed that have resulted in major loci for Diabetes. Loci are reported on chromosome 2q37 (Hanis, C.L., *et al.*, *Nat. Genet.*, 13(2):161-166 (1996)), chromosome 15q21 (Cox, *et al.*, *Nat. Genet.* 21(2):213-215 (1999)), chromosome 10q26 (Duggirala, R., *et al.*, *Am. J. Hum. Genet.*, 68(5):1149-1164 (2001)), chromosome 3p (Ehm, M.G., *et al.*, *Am. J. Hum. Genet.*, 66(6):1871-1881 (2000)) in Mexican Americans, and chromosomes 1q21-23 and 11q23-q25 (Hanson R. L. *et al.*, *Am J. Hum Genet.*, 63(4):1130-1138 (1998)) in PIMA Indians. In the Caucasian population, linkages have been observed to chromosome 12q24 in Finns (Mahtani, *et al.*, *Nat. Genet.*, 14(1):90-4 (1994)), chromosome 1q21-q23 in Americans in Utah (Elbein, S.C., *et al.*, *Diabetes*, 48(5):1175-1182 (1999)), chromosome 3q27-pter in French families (Vionnet, N., *et al.*, *Am. J. Hum. Genet.* 67(6):1470-80 (2000) and chromosome 18p11 in Scandinavians (Parker, A., *et al.*, *Diabetes*, 50(3) 675-680 (2001)). A recent study

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reported a major locus in indigenous Australians on chromosome 2q24.3 (Busfield, F., *et al.*, *Am. J. Hum. Genet.*, 70(2): 349-357 (2002)). Many other studies have resulted in suggestive loci or have replicated these loci.

Association studies have been reported for Type II diabetes. Most of these studies show modest association to the disease in a group of people but do not account for the disease. Altshuler *et al.*, reviewed the association work that has been done and concluded that association to only one of 16 genes revealed held up to scrutiny. Altshuler *et al.*, confirmed that the Pro12Ala polymorphism in PPAR γ is associated with Type II diabetes. Until now, there have been no linkage studies in Type II diabetes linking the disease to chromosome 5q35

KChIP1

The invention described herein has linked Type II diabetes to a gene encoding Kv channel-interacting protein 1 (KChIP1; also known as KCNIP1). In the brain and heart, rapidly inactivating (A-type) voltage-gated potassium (Kv) currents operate at subthreshold membrane potentials to control the excitability of neurons and cardiac myocytes. Although pore-forming α -subunits of the Kv4, or Shal-related, channel family form A-Type currents in heterologous cells, these differ significantly from native A-Type currents. To identify proteins that interacted with the Kv4 subunit, An *et al.*, ("Modulation of A-Type potassium channels by a family of calcium sensors" *Nature* 403:553-6 (2000)) used the yeast two-hybrid system with the intracellular amino terminus of the rat Kv4.3 subunit to screen rat midbrain cDNA libraries. Two Kv channel-interacting proteins were identified and called KChIPs (KChIP-1 and KChIP2). Library screening and database mining identified mouse and human orthologs of these genes. The KChIP1 cDNA encodes a 216-amino acid protein. The KChIPs have 4 EF-hand-like domains and bind calcium ions. Both KChIPs have distinct N termini but share approximately 70% amino acid identity throughout a carboxy-terminal 185-amino acid core domain that contains the 4 EF-hand-like motifs. Although the KChIPs have around 40% amino acid similarity to neuronal calcium sensor-1 and are members of the recoverin /NCS subfamily of calcium-binding proteins, other members of this subfamily, such as hippocalcin, did not

interact with Kv4 channels in the yeast 2-hybrid assay. An *et al.*, (*supra*) additionally found that expression of KChIPs and Kv4 together reconstitutes several features of native A-Type currents by modulating the density, inactivation kinetics, and rate of recovery from inactivation of Kv4 channels in heterologous cells. Both KChIPs
5 colocalize and coimmunoprecipitate with brain Kv4 alpha-subunits, and are thus integral components of native Kv4 channel complexes. As the activity and density of neuronal A-Type currents tightly control responses to excitatory synaptic inputs, these KChIPs may regulate A-Type currents, and hence neuronal excitability, in response to changes in intracellular calcium.

10 The glycosphingolipid sulfatide is present in secretory granules and at the surface of pancreatic β -cells (Buschard K, Fredman P. "Sulphatide as an antigen in diabetes mellitus". *Diabetes Nutr Metab* 4:221-228 (1996)), and antisulfatide antibodies (ASA; IgG1) are found in serum from the majority of patients with newly diagnosed Type I diabetes. Buschard *et al.*, ("Sulfatide controls insulin secretion by
15 modulation of ATP-sensitive K(+)-channel activity and Ca(2+)-dependent exocytosis in rat pancreatic beta-cells" *Diabetes* 51:2514-21 (2002)) demonstrated that sulfatide produced a glucose- and concentration-dependent inhibition of insulin release from isolated rat pancreatic islets. This inhibition of insulin secretion was due to activation of ATP-sensitive K⁺-(K_{ATP}) channels in single rat β -cells. No effect of sulfatide was
20 observed on whole-cell Ca²⁺-channel activity or glucose-induced elevation of cytoplasmic Ca²⁺ concentration. A key observation was that sulfatide stimulated Ca²⁺-dependent exocytosis determined by capacitance measurements and depolarized-induced insulin secretion from islets exposed to diazoxide and high external KCl. The monoclonal sulfatide antibody Sulph I as well as ASA-positive serum reduced
25 glucose-induced insulin secretion by inhibition of Ca²⁺-dependent exocytosis. This suggests that sulfatide is important for the control of glucose-induced insulin secretion and that both an increase and a decrease in the sulfatide content have an impact on the secretory capacity of the individual β -cells.

ASSESSMENT FOR AT-RISK HAPLOTYPES

A "haplotype," as described herein, refers to a combination of genetic markers ("alleles"), such as those set forth in Table 2 and Table 5. In a certain embodiment, the haplotype can comprise one or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular "alleles" at "polymorphic sites" associated with KChPI1. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules) is referred to herein as a "polymorphic site". Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism ("SNP"). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP. Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an "allele" of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are referred to as "variant" alleles. For example, the reference KChPI1 sequence is described herein by SEQ ID NO: 1. The term, "variant KChPI1", as used herein, refers to a sequence that differs from SEQ ID NO: 1 but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are KChPI1 variants. Additional variants can include changes that affect a polypeptide, *e.g.*, the KChPI1 polypeptide. These sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an

interruption of the coding sequence of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such sequence changes alter the polypeptide encoded by a KChPI1 nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with Type II diabetes or a susceptibility to Type II diabetes can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 6, Table 7, Table 9, Table 11, Table 12 and Table 13 are found more frequently in individuals with Type II diabetes than in individuals without Type II diabetes. Therefore, these haplotypes have predictive value for detecting Type II diabetes or a susceptibility to Type II diabetes in an individual. The haplotypes described herein are a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites, such as the methods described above.

In certain methods described herein, an individual who is at risk for Type II diabetes is an individual in whom an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one that confers a significant risk of Type II diabetes. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at

least about 1.2, including but not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8 and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

An at-risk haplotype in, or comprising portions of, the KChPI1 gene, is one where the haplotype is more frequently present in an individual at risk for Type II diabetes (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of Type II diabetes or susceptibility to Type II diabetes.

Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent-based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In one embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the KChIP1 gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual has Type II diabetes, or is susceptible to Type II diabetes. See, for example, Table 6, Table 7, Table 9, Table 11, Table 12 and 13 (below) for SNPs and markers that can form haplotypes that can be used as screening tools. These markers and SNPs can be identified in at-risk haplotypes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 2 and Table 5. The presence of the haplotype is indicative a susceptibility to Type II diabetes, and therefore is indicative of an individual who falls within a target population for the treatment methods described herein.

NUCLEIC ACID THERAPEUTIC AGENTS

In another embodiment, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below); or a nucleic acid encoding a KChIP1 polypeptide, can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a nucleic acid is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the polypeptide encoded by that mRNA and/or DNA, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA that encodes a KChIP1 polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patent Nos. 5,176,996, 5,264,564 and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*BioTechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the polypeptide. The antisense oligonucleotides bind to mRNA transcripts and prevent translation. Absolute

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complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA
5 may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree
10 of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule,
15 hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication NO: WO 88/09810) or the blood-brain barrier (see,
20 *e.g.*, PCT International Publication NO: WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm.Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

25 The antisense molecules are delivered to cells that express a KChIP1 polypeptide *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed
30 on the target cell surface) can be administered systematically. Alternatively, in a another embodiment, a recombinant DNA construct is utilized in which the antisense

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oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above.

For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically). In another embodiment of the invention, small double-stranded interfering RNA (RNA interference (RNAi)) can be used. RNAi is a post-transcription process, in which double-stranded RNA is introduced, and sequence-specific gene silencing results, though catalytic degradation of the targeted mRNA. See, *e.g.*, Elbashir, S.M. *et al.*, *Nature* 411:494-498 (2001); Lee, N.S., *Nature Biotech.* 19:500-505 (2002); Lee, S-K. *et al.*, *Nature Medicine* 8(7):681-686 (2002); the entire teachings of these references are incorporated herein by reference.

Endogenous expression of a gene product can also be reduced by inactivating or "knocking out" the gene or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the gene. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above.

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Alternatively, expression of non-altered genes can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene, or the complement thereof, or a portion thereof, in place of an gene in the cell, as described above. In another embodiment, 5 targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a polypeptide variant that differs from that present in the cell.

Alternatively, endogenous expression of a gene product can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region (*i.e.*, 10 the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity 15 of the gene product, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the antisense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a nucleic acid RNA or nucleic acid sequence) can be used to investigate the role of one or more members of 20 the KChIP1 pathway in the development of disease-related conditions. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

The therapeutic agents as described herein can be delivered in a composition, as described above, or alone. They can be administered systemically, or can be 25 targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Patent NO: 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein. In addition, a combination of any of the above methods of treatment (*e.g.*, administration 30 of non-altered polypeptide in conjunction with antisense therapy targeting altered

mRNA; administration of a first splicing variant in conjunction with antisense therapy targeting a second splicing variant) can also be used.

The invention additionally pertains to use of such therapeutic agents, as described herein, for the manufacture of a medicament for the treatment of Type II diabetes e.g., using the methods described herein.

MONITORING PROGRESS OF TREATMENT

The current invention also pertains to methods of monitoring the effectiveness of treatment on the regulation of expression (*e.g.*, relative or absolute expression) of one or more KChIP1 isoforms at the RNA or protein level or its enzymatic activity. KChIP1 message or protein or enzymatic activity can be measured in a sample of peripheral blood or cells derived therefrom. An assessment of the levels of expression or activity can be made before and during treatment with KChIP1 therapeutic agents. For example, in one embodiment of the invention, an individual who is a member of the target population can be assessed for response to treatment with a KChIP1 inhibitor, by examining calcium levels or Kv channel-interacting proteins activity or absolute and/or relative levels of KChIP1 protein or mRNA isoforms in peripheral blood in general or specific cell subfractions or combination of cell subfractions. In addition, variation such as haplotypes or mutations within or near (within 100 to 200kb) of the KChIP1 gene may be used to identify individuals who are at higher risk for Type II diabetes to increase the power and efficiency of clinical trials for pharmaceutical agents to prevent or treat Type II diabetes. The haplotypes and other variations may be used to exclude or fractionate patients in a clinical trial who are likely to have non- KChIP1 involvement in their Type II diabetes risk in order to enrich patients who have other genes or pathways involved and boost the power and sensitivity of the clinical trial. Such variation may be used as a pharmacogenomic test to guide selection of pharmaceutical agents for individuals.

Described herein is the first known linkage study of Type II diabetes showing a connection to chromosome 5q35. Based on the linkage studies conducted, a direct relationship between Type II diabetes and the locus on chromosome 5q35, in particular the KChIP1 gene, has been discovered.

NUCLEIC ACIDS OF THE INVENTION

KChIP1 Nucleic Acids, Portions and Variants

5 Accordingly, the invention pertains to isolated nucleic acid molecules comprising human KChIP1 nucleic acid. The term, "KChIP1 nucleic acid," as used herein, refers to an isolated nucleic acid molecule encoding a KChIP1 polypeptide (e.g., a KChIP1 gene, such as shown in SEQ ID NO:1). The KChIP1 nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-
10 stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including
15 regulatory sequences, for example).

For example, the KChIP1 nucleic acid can be the genomic sequence shown in FIG. 1, or a portion or fragment of the isolated nucleic acid molecule (e.g., cDNA or the gene) that encodes KChIP1 polypeptide. In certain embodiments, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group
20 consisting of SEQ ID NOs: 1 and 114-258 (e.g., in Table 10) or the complement of such a nucleic acid molecule.

Additionally, nucleic acid molecules of the invention can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those
25 that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed
30 sequences (e.g., as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in

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which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other
5 circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the
10 chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb but not limited to 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory
15 sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the
20 DNA molecules of the present invention. An isolated nucleic acid molecule can include a nucleic acid molecule or nucleic acid sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous organisms, as
25 well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleic acid sequences. Such isolated nucleic acid molecules are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (e.g., from other mammalian species), for gene
30 mapping (e.g., by *in situ* hybridization with chromosomes), or for detecting

expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a KChIP1 polypeptide, or another
5 splicing variant of a KChIP1 polypeptide or polymorphic variant thereof. Thus, for example, the invention pertains to DNA molecules comprising a sequence that is different from the naturally occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a KChIP1 polypeptide of the present invention. The invention also encompasses nucleic acid molecules encoding portions
10 (fragments), or encoding variant polypeptides such as analogues or derivatives of a KChIP1 polypeptide. Such variants can be naturally occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more
15 nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a KChIP1 polypeptide. In one embodiment, the nucleic acid sequences are fragments that comprise one or more polymorphic microsatellite markers. In another
20 embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a KChIP1 gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates),
25 charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules
30 include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

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The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (e.g., nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 114-258. In another embodiment, the invention includes variants described herein that hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence encoding an amino acid sequence or a polymorphic variant thereof. In another embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a KChIP1 polypeptide.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (e.g., under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (e.g., when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, e.g., conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (i.e., 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (e.g., 70%, 75%, 85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., "Current Protocols in Molecular Biology", John Wiley & Sons, (2001)), the entire

5 teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 10 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample 15 can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (2001), which describes the determination of washing conditions for moderate or low stringency conditions. 20 Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that 25 hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

30 For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate

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stringency wash can comprise washing in a pre-warmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in pre-warmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent homology or identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first sequence for optimal alignment).

The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions x 100). When a position in one sequence is occupied by the same nucleotide or amino acid residue as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, nucleic acid or amino acid "homology" is equivalent to nucleic acid or amino acid "identity". In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, for example, at least 40%, in certain embodiments at least 60%, and in other embodiments at least 70%, 80%, 90% or 95% of the length of the reference sequence.

The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl.*

Acad. Sci. USA 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (e.g., W=5 or W=20).

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Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1): 11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 114-258, or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, that encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

30

Probes and Primers

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand
5 of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500 (1991).

A probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, for example about 20-25, and in certain embodiments about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous
10 nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 114-258 or polymorphic variant thereof. In other embodiments, a probe or primer comprises 100 or fewer nucleotides, in certain embodiments from 6 to 50 nucleotides, for example from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the
15 contiguous nucleotide sequence, for example at least 80% identical, in certain embodiments at least 90% identical, and in other embodiments at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or
20 enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic
25 oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs: 1, 114-258 or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press,
30 NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19: 4967

(1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

5 Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The
10 latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be labeled, for example, radiolabeled, and used as a
15 probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can be obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct
20 analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Additionally, fluorescence methods are also available for
25 analyzing nucleic acids (Chen *et al.*, *Genome Res.* 9, 492 (1999)) and polypeptides. Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs: 1, 114-258 and/or the
30 complement of one or more of SEQ ID NOs: 1, 114-258 and/or a portion of one or more of SEQ ID NOs: 1, 114-258 or the complement of one or more of SEQ ID NOs:

1, 114-258 and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (e.g., reagent kits) for use in the screening and/or diagnostic assays described herein.

Vectors and Host Cells

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1, 114-258 and the complements thereof (or a portion thereof). The constructs comprise a vector (e.g., an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Expression vectors are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

In certain embodiments, recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence"

is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct

5 constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The

10 expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, e.g.,

15 bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

20 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding

25 generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (e.g., *E. coli*), insect

30 cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.*, (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the

invention has been introduced (e.g., an exogenous KChIP1 gene, or an exogenous nucleic acid encoding a KChIP1 polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. NO: 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by KChIP1 nucleic acids ("KChIP1 polypeptides," or "KChIP1 proteins," such as the protein shown in SEQ ID NO: 2) and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (e.g., other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (e.g., in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less

than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO: 1, optionally additionally comprising one or more of SEQ ID NOs: 114-258; or the complement of such a nucleic acid, or portions thereof, or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide of SEQ ID NO: 1, optionally additionally one or more of SEQ ID NOs: 114-258; or a complement of such a sequence, or portions thereof or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, in certain embodiments at least about 70-75%, and in other embodiments at least about 80-85%, and in other embodiments greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to of SEQ ID NO: 1 or any one of 114-258 or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding SEQ ID NO: 1 or any one of 114-258 or a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention.

5 Similarity is determined by conserved amino acid substitution where a given amino acid in a polypeptide is substituted by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl
10 residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

15 A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical
20 regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution,
25 insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1082-1185 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant
30 molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by

structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

5 The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising SEQ ID NO: 1 and optionally comprising one or more of SEQ ID NOs: 114-258; or a complement of such a nucleic acid or other variants. However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6
10 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise
15 a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

20 Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the
25 carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide.

30 "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus

or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition*, 8:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry*, 270,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992).

Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

5 The isolated polypeptide can be purified from cells that naturally express it, can be purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the
10 expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

 The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a
15 labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent,
20 *e.g.*, ligand or receptor, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

 Polyclonal antibodies and/or monoclonal antibodies that specifically bind one
25 form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen
30 binding site that specifically bind an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment

thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or a fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4: 72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.*, (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to

identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, e.g., *Current Protocols in Immunology*, *supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981)). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog NO: 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog NO: 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent NO: 5,223,409; PCT Publication NO: WO 92/18619; PCT Publication NO: WO 91/17271; PCT Publication NO: WO 92/20791; PCT Publication NO: WO 92/15679; PCT Publication NO: WO 93/01288; PCT Publication NO: WO 92/01047; PCT Publication NO: WO 92/09690; PCT Publication NO: WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9: 1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246: 1275-1281 (1989); and Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. The antibody can be coupled to a detectable substance to facilitate its detection. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of Type II diabetes; of a susceptibility to Type II diabetes; or of a condition associated with a KChIP1 gene, as well as in kits (*e.g.*, useful for diagnosis of Type II diabetes; a susceptibility to Type II diabetes; or a condition associated with a KChIP1 gene). In one embodiment, the kit comprises primers which contain one or more of the SNP's identified in Table 10.

In one embodiment of the invention, diagnosis of a disease or condition associated with a KChIP1 gene (*e.g.*, diagnosis of Type II diabetes, or of a

susceptibility to Type II diabetes) is made by detecting a polymorphism in a KChIP1 nucleic acid as described herein. The polymorphism can be a change in a KChIP1 nucleic acid, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such change may be present in a single gene. Such sequence changes cause a difference in the polypeptide encoded by a KChIP1 nucleic acid. For example, if the difference is a frame shift change, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a disease or condition or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid can be a synonymous alteration in one or more nucleotides (*i.e.*, an alteration that does not result in a change in the polypeptide encoded by a KChIP1 nucleic acid). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the gene. A KChIP1 nucleic acid that has any of the changes or alterations described above is referred to herein as an "altered nucleic acid."

In a first method of diagnosing Type II diabetes or a susceptibility to Type II diabetes, or another disease or condition associated with a KChIP1 gene, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds, John Wiley & Sons, including all supplements through 1999). For example, a biological sample (a "test sample") from a test subject (the "test individual") of genomic DNA, RNA, or cDNA, is obtained from an individual, such as an individual suspected of having, being susceptible to or predisposed for, or

carrying a defect for, the disease or condition, or the susceptibility to the disease or condition, associated with a KChIP1 gene (*e.g.*, Type II diabetes). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of
5 cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a KChIP1 nucleic acid is present, and/or to
10 determine which splicing variant(s) encoded by the KChIP1 is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain, for example, at least one polymorphism in a KChIP1 nucleic acid (*e.g.*,
15 as set forth in Table 10) and/or contain a nucleic acid encoding a particular splicing variant of a KChIP1 nucleic acid. The probe can be any of the nucleic acid molecules described above (*e.g.*, the gene or nucleic acid, a fragment, a vector comprising the gene or nucleic acid, a probe or primer, etc.).

To diagnose Type II diabetes, or a susceptibility to Type II diabetes, or
20 another condition associated with a KChIP1 gene, a hybridization sample is formed by contacting the test sample containing a KChIP1 nucleic acid with at least one nucleic acid probe. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length
25 nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 114-258 or the complement thereof, or a portion thereof. Other suitable probes for use in the
30 diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a KChIP1 nucleic acid.

"Specific hybridization", as used herein, indicates exact hybridization (e.g., with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and KChIP1 nucleic acid in the test sample, then the KChIP1 has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the KChIP1 nucleic acid, or of the presence of a particular splicing variant encoding the KChIP1 nucleic acid and is therefore diagnostic for a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. et al., eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition associated with a KChIP1 gene (e.g., Type II diabetes). For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a KChIP1 nucleic acid, or of the presence of a particular splicing variant encoded by a KChIP1 nucleic acid and is therefore diagnostic for Type II diabetes or a susceptibility to Type II diabetes or a condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents NO: 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA

mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be
5 designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes). Hybridization of the PNA probe to a KChIP1 gene is diagnostic for Type II diabetes or a susceptibility to Type II diabetes or a condition associated with a KChIP1 nucleic acid.

10 In another method of the invention, alteration analysis by restriction digestion can be used to detect an altered gene, or genes containing a polymorphism(s), if the alteration (mutation) or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a
15 KChIP1 nucleic acid (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the alteration or polymorphism in the KChIP1 nucleic acid, and therefore indicates the presence or absence of Type II
20 diabetes or the susceptibility to a disease or condition associated with a KChIP1 nucleic acid.

Sequence analysis can also be used to detect specific polymorphisms in a KChIP1 nucleic acid. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene or
25 nucleic acid, and/or its flanking sequences, if desired. The sequence of a KChIP1 nucleic acid, or a fragment of the nucleic acid, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the nucleic acid, nucleic acid fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene or
30 cDNA (*e.g.*, one or more of SEQ ID NOs: 114-258 or a complement thereof) or

mRNA, as appropriate. The presence of a polymorphism in the KChIP1 indicates that the individual has Type II diabetes or a susceptibility to Type II diabetes.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a KChIP1 nucleic acid, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a KChIP1 nucleic acid, and that contains a polymorphism associated with a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a KChIP1 nucleic acid can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a KChIP1 nucleic acid and its flanking sequences. The DNA containing the amplified KChIP1 nucleic acid (or fragment of the gene or nucleic acid) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified KChIP1 nucleic acid is then detected. Hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the KChIP1 nucleic acid, and is therefore indicative of a disease or condition associated with a KChIP1 nucleic acid or susceptibility to a disease or condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

The invention further provides allele-specific oligonucleotides that hybridize to the reference or variant allele of a gene or nucleic acid comprising a single nucleotide polymorphism or to the complement thereof. These oligonucleotides can be probes or primers.

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer, which hybridizes at a distal site. Amplification proceeds from the two primers, resulting in a detectable product, which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, *e.g.*, WO 93/22456).

With the addition of such analogs as locked nucleic acids (LNAs), the size of primers and probes can be reduced to as few as 8 bases. LNAs are a novel class of bicyclic DNA analogs in which the 2' and 4' positions in the furanose ring are joined via an O-methylene (oxy-LNA), S-methylene (thio-LNA), or amino methylene (amino-LNA) moiety. Common to all of these LNA variants is an affinity toward complementary nucleic acids, which is by far the highest reported for a DNA analog. For example, particular all oxy-LNA nonamers have been shown to have melting temperatures of 64°C and 74°C when in complex with complementary DNA or RNA, respectively, as opposed to 28°C for both DNA and RNA for the corresponding DNA nonamer. Substantial increases in T_m are also obtained when LNA monomers are used in combination with standard DNA or RNA monomers. For primers and probes, depending on where the LNA monomers are included (*e.g.*, the 3' end, the 5' end, or in the middle), the T_m could be increased considerably.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a KChIP1 nucleic acid. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also

described as "Genechips™," have been generally described in the art, for example, U.S. Pat. NO: 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See 5 Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. NO: 5,143,854 (see also PCT Application NO: WO 90/15070) and Fodor *et al.*, PCT Publication NO: WO 92/10092 and U.S. Pat. NO: 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using 10 mechanical synthesis methods are described in, *e.g.*, U.S. Pat. NO: 5,384,261; the entire teachings of which are incorporated by reference herein. In another example, linear arrays can be utilized.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and 15 scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. NO: 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well-known amplification techniques, *e.g.*, PCR. 20 Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is 25 scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and 30 thus be capable of analyzing multiple, specific polymorphisms. In alternative arrangements, it will generally be understood that detection blocks may be grouped

within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional uses of oligonucleotide arrays for polymorphism detection can be found, for example, in U.S. Patents Nos. 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of nucleic acid analysis can be used to detect polymorphisms in a Type II diabetes gene or variants encoding by a Type II diabetes gene. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. NO: 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In one embodiment of the invention, diagnosis of a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes) or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes) can also be made by expression analysis by quantitative PCR (kinetic thermal cycling). This technique, utilizing TaqMan[®], can be used to allow the identification of polymorphisms and whether a patient is homozygous or heterozygous. The technique can assess the presence of an alteration in the expression or composition of the

polypeptide encoded by a KChIP1 nucleic acid or splicing variants encoded by a KChIP1 nucleic acid. Further, the expression of the variants can be quantified as physically or functionally different.

In another embodiment of the invention, diagnosis of Type II diabetes or a susceptibility to Type II diabetes 5 or a condition associated with a KChIP1 gene) can be made by examining expression and/or composition of a KChIP1 polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a KChIP1 nucleic acid, or for 10 the presence of a particular variant encoded by a KChIP1 nucleic acid. An alteration in expression of a polypeptide encoded by a KChIP1 nucleic acid can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a KChIP1 nucleic acid is an alteration in the qualitative polypeptide expression (*e.g.*, 15 expression of an altered KChIP1 polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of the disease or condition associated with KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid is made by detecting a particular splicing variant encoded by that KChIP1 nucleic acid, or a particular pattern of splicing variants. 20

Both such alterations (quantitative and qualitative) can also be present. The term "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a KChIP1 nucleic acid in a control 25 sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or 30 condition associated with a KChIP1 nucleic acid. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly

different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. Various means of examining expression or composition of the polypeptide encoded by a KChIP1 nucleic acid can be used, including: spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by an altered KChIP1 nucleic acid (*e.g.*, a KChIP1 nucleic acid having one or more alterations as shown in Table 10), or an antibody that specifically binds to a polypeptide encoded by a non-altered nucleic acid, or an antibody that specifically binds to a particular splicing variant encoded by a nucleic acid, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or altered KChIP1 nucleic acid, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid. The presence of a polypeptide encoded by a polymorphic or altered nucleic acid, or the absence of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid, is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes),

as is the presence (or absence) of particular splicing variants encoded by the KChIP1 nucleic acid.

In one embodiment of this method, the level or amount of polypeptide encoded by a KChIP1 nucleic acid in a test sample is compared with the level or amount of the polypeptide encoded by the KChIP1 in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the KChIP1 nucleic acid, and is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid (*e.g.*, Type II diabetes). Alternatively, the composition of the polypeptide encoded by a KChIP1 nucleic acid in a test sample is compared with the composition of the polypeptide encoded by the KChIP1 nucleic acid in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid (*e.g.*, Type II diabetes). In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid.

The invention further pertains to a method for the diagnosis or identification of a susceptibility to Type II diabetes in an individual, by identifying an at-risk haplotype (*e.g.*, a haplotype comprising a KChIP1 nucleic acid). The KChIP1-associated haplotypes, *e.g.*, those described in Table 2 and Table 5, describe a set of genetic markers ("alleles"). In a certain embodiment, the haplotype can comprise one

or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular "alleles" at "polymorphic sites" associated with KChIP1. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules), is referred to herein as a "polymorphic site". Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism ("SNP"). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP. Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an "allele" of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are referred to as "variant" alleles. For example, the reference KChIP1 sequence is described herein by SEQ ID NO: 1. The term, "variant KChIP1", as used herein, refers to a sequence that differs from SEQ ID NO: 1, but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are KChIP1 variants. The variants of KChIP1 that are used to determine the haplotypes disclosed herein of the present invention are associated with Type II diabetes or a susceptibility to Type II diabetes.

Additional variants can include changes that affect a polypeptide, *e.g.*, the KChIP1 polypeptide. These sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence

of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such sequence changes alter the polypeptide encoded by a KChIP1 nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with Type II diabetes or a susceptibility to Type II diabetes can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 10, Table 11, Table 12 or Table 13, are found more frequently in individuals with Type II diabetes than in individuals without Type II diabetes. Therefore, these haplotypes have predictive value for detecting Type II diabetes or a susceptibility to Type II diabetes in an individual. The haplotypes described herein are a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites, such as the methods described above.

HAPLOTYPE SCREENING

In the methods for the diagnosis and identification of susceptibility to Type II diabetes or Type II diabetes in an individual, an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one which confers a significant risk of Type II diabetes. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at

least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

The invention also pertains to methods of diagnosing Type II diabetes or a susceptibility to Type II diabetes in an individual, comprising screening for an at-risk haplotype in, or comprising portions of, the KChIP1 gene, where the haplotype is more frequently present in an individual susceptible to Type II diabetes (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of Type II diabetes or susceptibility to Type II diabetes. Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In a preferred embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the KChIP1 gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual has Type II diabetes or is susceptible to Type II diabetes. See, for example, Tables 6, 7, 9, 11 and 13 (below) for SNPs and markers that can form haplotypes that can be used as screening tools. These markers and SNPs can be used to design diagnostic tests for determining Type II diabetes or a susceptibility to Type II diabetes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 10, Table 11, Table 12 and/ or Table 13. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. Haplotype analysis involves

defining a candidate susceptibility locus using LOD scores. The defined regions are then ultra-fine mapped with microsatellite markers with an average spacing between markers of less than 100kb. All usable microsatellite markers that found in public databases and mapped within that region can be used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome can be used.

The frequencies of haplotypes in the patient and the control groups using an expectation-maximization algorithm can be estimated (Dempster A. *et al.*, 1977. *J. R. Stat. Soc. B*, 39:1-389). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase can be used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis where a candidate at-risk-haplotype, which can include the markers described herein, is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups is tested. Likelihoods are maximized separately under both hypotheses and a corresponding 1-df likelihood ratio statistics is used to evaluate the statistic significance.

To look for at-risk-haplotypes in the 1-lod drop, for example, association of all possible combinations of genotyped markers is studied, provided those markers span a practical region. The combined patient and control groups can be randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis is then repeated and the most significant p-value registered is determined. This randomization scheme can be repeated, for example, over 100 times to construct an empirical distribution of p-values.

The at-risk haplotypes identified in Table 2 (haplotypes identified as A1, A2, A3, A4, A5, A6, B1, B2, B3, B4 and B5) or Table 5 (haplotypes identified as D1, D2, D3, D4 and D5) are associated with Type II diabetes or a susceptibility to Type II diabetes. In certain embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S879, DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S1058 and DG5S37 at the 5q35 locus; or DG5S1058, DG5S37 and DG5S101 at the 5q35 locus; or DG5S881,

DG5S1058, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S879, DG5S1058 and DG5S37; or DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; DG5S953, DG5S955, DG5S13 and DG5S959 at the 5q35 locus; or DG5S888 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955 and DG5S124 at the 5q35 locus; or DG5S888, DG5S44 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955, DG5S13, DG5S123, and DG5S959 at the 5q35 locus. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

Also described herein is a haplotype associated with Type II diabetes or a

susceptibility to Type II diabetes comprising markers DG5S13, KCP_1152, and

D5S625 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In one particular embodiment, the presence of the -4, 1, 0 haplotype at DG5S13, KCP_1152, and D5S625 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers DG5S124, KCP_1152, KCP_2649, KPC_4976 and KPC-16152 at the 5q35 locus. In one particular embodiment, the presence of the 0, 1, 1, 3 and 0 haplotype at DG5S124, KCP_1152, KCP_2649, KPC_4976 and KPC-16152 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers KCP_173982, KCP_15400, and KCP_18069. In one particular embodiment, the presence of the 0, 1, 1 haplotype at KCP_173982, KCP_15400, and KCP_18069 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

In additional embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S124, KCP_1152, KCP_2649, KCP_4976, and KCP_16152 at the 5q35 locus, as well as one of the following 3 markers: KCP_197678, KCP_197775, and KCP_202795 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In particular embodiments, the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP_197679, KCP_1152, KCP_2649, KCP_4976, and KCP_16152; the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124,

KCP_197775, KCP_1152, KCP_2649, KCP_4976, and KCP_16152; or the presence of the 0, 1, 1, 1, 3, 0 haplotype at DG5S124, KCP_202795, KCP_1152, KCP_2649, KCP_4976, and KCP_16152; is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

5 Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to altered or to non-
10 altered (native) KChIP1 polypeptide, means for amplification of nucleic acids comprising a KChIP1 nucleic acid, or means for analyzing the nucleic acid sequence of a KChIP1 nucleic acid or for analyzing the amino acid sequence of a KChIP1 polypeptide as described herein, etc. In one embodiment, the kit for diagnosing a Type II diabetes or a susceptibility to Type II diabetes can comprise primers for
15 nucleic acid amplification of a region in the KChIP1 nucleic acid comprising an at-risk haplotype that is more frequently present in an individual having Type II diabetes or who is susceptible to Type II diabetes. The primers can be designed using portions of the nucleic acids flanking SNPs that are indicative of Type II diabetes. In a certain embodiment, the primers are designed to amplify regions of the KChIP1 gene
20 associated with an at-risk haplotype for Type II diabetes, as shown in Table 10 and 13, or more particularly the haplotypes described in Tables 2 and 5.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

 The invention provides methods (also referred to herein as "screening assays")
25 for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the
30 sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1, 114-258, or the complement

thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs: 2, or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In one embodiment, high stringency conditions are conditions
5 appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a KChIP1 nucleic acid), and the contacted sample is assessed for the presence or
10 absence of hybridization. In another embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

15 In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to
20 the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which
25 otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, KChIP1 binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with KChIP1 binding agents (*e.g.*, receptors
30 or other binding agents); or which alter posttranslational processing of the KChIP1 polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide

from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a KChIP1 polypeptide, a cell, cell lysate, or solution containing or expressing a KChIP1 polypeptide, or another splicing variant encoded by a KChIP1 gene (such as comprising a SNP as shown in Table 10 and/or 3), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of KChIP1 activity is assessed (e.g., the level (amount) of KChIP1 activity is measured, either directly or indirectly), and is compared with the level of activity in a control (i.e., the level of activity of the KChIP1 polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a KChIP1 polypeptide. An increase in the level of KChIP1 activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) KChIP1 activity. Similarly, a decrease in the level of KChIP1 activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) KChIP1 activity. In another embodiment, the level of activity of a KChIP1

polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters KChIP1 activity.

5 The present invention also relates to an assay for identifying agents which alter the expression of a KChIP1 nucleic acid (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which
10 otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a KChIP1 polypeptide (*e.g.*, a KChIP1 gene or nucleic acid) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can
15 be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of KChIP1 expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a
20 control (*i.e.*, the level and/or pattern of the KChIP1 expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of a Type II diabetes gene. Enhancement of KChIP1 expression indicates that the agent is
25 an agonist of KChIP1 activity. Similarly, inhibition of KChIP1 expression indicates that the agent is an antagonist of KChIP1 activity. In another embodiment, the level and/or pattern of KChIP1 polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent
30 that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters KChIP1 expression.

In another embodiment of the invention, agents which alter the expression of a KChIP1 nucleic acid or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the KChIP1 gene or nucleic acid operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the KChIP1, as indicated by its ability to alter expression of a gene that is operably linked to the KChIP1 gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of KChIP1 activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of KChIP1 activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a KChIP1 nucleic acid (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a KChIP1 binding agent. For example, a cell that expresses a compound that interacts with a KChIP1 polypeptide (herein referred to as a "KChIP1 binding agent", which can be a polypeptide or other molecule that interacts with a KChIP1 polypeptide, such as a receptor) is contacted with a KChIP1 in the presence of a test agent, and the ability of the test agent to alter the interaction between the KChIP1 and the KChIP1 binding

agent is determined. Alternatively, a cell lysate or a solution containing the KChIP1 binding agent, can be used. An agent which binds to the KChIP1 or the KChIP1 binding agent can alter the interaction by interfering with, or enhancing the ability of the KChIP1 to bind to, associate with, or otherwise interact with the KChIP1 binding agent. Determining the ability of the test agent to bind to a KChIP1 nucleic acid or a KChIP1 binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a KChIP1 polypeptide or a KChIP1 binding agent without the labeling of either the test agent, KChIP1 polypeptide, or the KChIP1 binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (*e.g.*, CytosensorTM) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide.

Thus, these receptors can be used to screen for compounds that are agonists or antagonists, for use in treating a susceptibility to a disease or condition associated with a KChIP1 gene or nucleic acid, or for studying a susceptibility to a disease or condition associated with a KChIP1 (*e.g.*, Type II diabetes). Drugs could be designed to regulate KChIP1 activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more KChIP1 polypeptides, as described herein.

For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more KChIP1 polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (e.g., nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a KChIP1 polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the KChIP1 polypeptide, splicing variant, or fragment or derivative thereof (e.g., a KChIP1 polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (e.g., mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the KChIP1 polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a KChIP1 polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the KChIP1 gene or nucleic acid, the KChIP1 polypeptide, the KChIP1 binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include

microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a KChIP1 nucleic acid, KChIP1 polypeptide, or a KChIP1 binding agent to be bound to a matrix or other solid support.

5 In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a KChIP1 nucleic acid is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or
10 polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified
15 as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting
20 mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a
25 modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent.

30 Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an

agent identified as described herein can be used to alter activity of a polypeptide encoded by a KChIP1 nucleic acid, or to alter expression of a KChIP1 nucleic acid, by contacting the polypeptide or the nucleic acid (or contacting a cell comprising the polypeptide or the nucleic acid) with the agent identified as described herein.

5

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein (*e.g.*, a KChIP1 polypeptide); comprising polypeptides described herein and/or comprising other splicing variants encoded by a KChIP1 nucleic acid; and/or an agent that alters (*e.g.*, enhances or inhibits) KChIP1 nucleic acid expression or KChIP1 polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a KChIP1 nucleic acid receptor), an agent that alters KChIP1 nucleic acid expression, or a KChIP1 binding agent or binding partner, fragment, fusion protein or pro-drug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters KChIP1 polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

20 Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

30 The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution,

suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl
5 pyrollidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle
10 acceleration devises ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For
15 example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a
20 hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be
25 mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments,
30 powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting

agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze
5 bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms.

Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and
10 those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a
15 particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms, and should be decided according
20 to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical
25 compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug
30 administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or

kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is
5 intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic
10 and/or therapeutic) for certain diseases and conditions associated with KChIP1. In particular, the invention relates to methods of treatment for Type II diabetes or a susceptibility to Type II diabetes, using a Type II diabetes therapeutic agent. A "Type II diabetes therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) KChIP1 polypeptide activity and/or KChIP1 nucleic acid expression, as described
15 herein (*e.g.*, a Type II diabetes nucleic acid agonist or antagonist). In certain embodiments, the Type II diabetes therapeutic agent alters activity and/or nucleic acid expression of KChIP1.

Type II diabetes therapeutic agents can alter KChIP1 polypeptide activity or nucleic acid expression by a variety of means, such as, for example, by providing
20 additional KChIP1 polypeptide or by upregulating the transcription or translation of the KChIP1 nucleic acid; by altering posttranslational processing of the KChIP1 polypeptide; by altering transcription of KChIP1 splicing variants; or by interfering with KChIP1 polypeptide activity (*e.g.*, by binding to a KChIP1 polypeptide), or by binding to another polypeptide that interacts with KChIP1, by altering (*e.g.*,
25 downregulating) the expression, transcription or translation of a KChIP1 nucleic acid, or by altering (*e.g.*, agonizing or antagonizing) activity.

Representative Type II diabetes therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly
30 nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a

nucleic acid encoding a KChIP1 polypeptide or active fragment or derivative thereof, or an oligonucleotide; or a complement thereof, or fragments or derivatives thereof, and/or other splicing variants encoded by a Type II diabetes nucleic acid, or fragments or derivatives thereof);

5

polypeptides described herein and/ or splicing variants encoded by the KChIP1 nucleic acid or fragments or derivatives thereof;

10

other polypeptides (*e.g.*, KChIP1 receptors); KChIP1 binding agents; or agents that affect (*e.g.*, increase or decrease) activity,

antibodies, such as an antibody to an altered KChIP1 polypeptide, or an antibody to a non-altered KChIP1 polypeptide, or an antibody to a particular splicing variant encoded by a KChIP1 nucleic acid as described above;

15

peptidomimetics; fusion proteins or prodrugs thereof; ribozymes; other small molecules; and

20

other agents that alter (*e.g.*, enhance or inhibit) expression of a KChIP1 nucleic acid, or that regulate transcription of KChIP1 splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed).

More than one Type II diabetes therapeutic agent can be used concurrently, if desired.

25

A Type II diabetes nucleic acid therapeutic agent that is a nucleic acid is used in the treatment of Type II diabetes or in the treatment for a susceptibility to Type II diabetes. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease or condition, but also preventing or delaying the onset of the disease or condition, and also lessening the severity or frequency of symptoms of the disease or condition. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a KChIP1 polypeptide in an individual.

30

For example, a Type II diabetes therapeutic agent can be administered in order to upregulate or increase the expression or availability of the KChIP1 nucleic acid or of specific splicing variants of KChIP1 nucleic acid, or, conversely, to downregulate or decrease the expression or availability of the KChIP1 nucleic acid or specific splicing variants of the KChIP1 nucleic acid. Upregulation or increasing expression or availability of a native KChIP1 gene or nucleic acid or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native KChIP1 gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The Type II diabetes therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a KChIP1 polypeptide, such as one of SEQ ID NO: 1 or a complement thereof); or another nucleic acid that encodes a KChIP1 polypeptide or a splicing variant, derivative or fragment thereof (*e.g.*, comprising any one or more of SEQ ID NO: 114-258), can be used, either alone or in a pharmaceutical composition as described above. For example, a KChIP1 gene or nucleic acid or a cDNA encoding a KChIP1 polypeptide, either by itself or included within a vector, can be introduced

into cells (either *in vitro* or *in vivo*) such that the cells produce native KChIP1 polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene, nucleic acid or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native KChIP1 expression and activity, or have altered KChIP1 expression and activity, or have expression of a disease-associated KChIP1 splicing variant, can be engineered to express the KChIP1 polypeptide or an active fragment of the KChIP1 polypeptide (or a different variant of the KChIP1 polypeptide). In certain embodiments, nucleic acids encoding a KChIP1 polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (e.g., microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a Type II diabetes gene is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the KChIP1 polypeptide, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the KChIP1 polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then

inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides, which are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*BioTechniques* 6:958-976 (1988)); and Stein *et al.*, (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the KChIP1. The antisense oligonucleotides bind to KChIP1 mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA*

86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication NO: WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication NO: WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or
5 intercalating agents. (See, *e.g.*, Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express KChIP1 *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*,
10 antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense
15 oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous KChIP1 transcripts and thereby prevent translation of the KChIP1 mRNA. For example, a vector can be introduced *in*
20 *vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to
25 prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous KChIP1 polypeptide expression can also be reduced by
30 inactivating or "knocking out" the gene, nucleic acid or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985);

Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene or nucleic acid (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene or nucleic acid (either the coding regions or regulatory regions of the nucleic acid) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene or nucleic acid *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the gene or nucleic acid. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-altered genes or nucleic acids can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene or nucleic acid, *e.g.*, a nucleic acid comprising one or more of SEQ ID NOs: 114-258 or the complement thereof, or a portion thereof, in place of an altered KChIP1 in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a Type II diabetes polypeptide variant that differs from that present in the cell.

Alternatively, endogenous KChIP1 nucleic acid expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a KChIP1 nucleic acid (*i.e.*, the KChIP1 promoter and/or enhancers) to form triple helical structures that prevent transcription of the KChIP1 nucleic acid in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the KChIP1 proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a Type II diabetes gene mRNA or gene sequence) can be used to investigate the role of KChIP1 or the interaction of KChIP1 and its binding agents in developmental events, as well as the normal cellular function of KChIP1 or of the

interaction of KChIP1 and its binding agents in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other Type II diabetes therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to a disease or condition associated with a Type II diabetes gene. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (e.g., a transgenic animal, such as U.S. Pat. NO: 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (e.g., administration of non-altered polypeptide in conjunction with antisense therapy targeting altered mRNA of KChIP1; administration of a first splicing variant encoded by a KChIP1 nucleic acid in conjunction with antisense therapy targeting a second splicing encoded by a KChIP1 nucleic acid) can also be used.

The present invention is now illustrated by the following Exemplification, which is not intended to be limiting in any way. All references cited herein are incorporated by reference in their entirety.

EXEMPLIFICATION

The study was done in collaboration with the Icelandic Heart Association, who provided an encrypted list of 1350 diabetic patients. In 1967-1991 the Heart Association started a study of cardiovascular disease and its complications.

Measurements of blood sugar were included in a thorough check-up of the participants which results led to many individuals being diagnosed with diabetes. The list of participants is an unbiased sample of about a third of the Icelandic nation. Individuals diagnosed in the years following 1991 were either diagnosed at the Icelandic Heart Association or at one of two major hospitals in Reykjavik, Iceland.

All participants in the Type II diabetes study visited the Icelandic Heart Association where each answered a questionnaire, had blood drawn, a blood sugar

assessment, and measurements taken. Height (m) and weight (kg) were measured to calculate the body mass index. In serum, the fasting blood glucose and triglyceride levels were measured as well. Diagnoses of Type II diabetes were based on the diagnostic criteria set by the World Health Organization (1999). All patients with
5 fasting glucose above 7 mM were diagnosed as having Type II diabetes and individuals with fasting blood sugar between 6.1 – 6.9 mM were diagnosed with impaired fasting glucose. If the participants had no prior history of diabetes, they were requested to come in for another test to have their diagnosis confirmed. All individuals on diabetic medication were classified as Type II. The questionnaire
10 included questions regarding age at diagnosis and type of medication. All patients were requested to bring two relatives who's DNA was used to confirm the genotypes of the patients.

Since the patients had participated in a study that was conducted between 1967-1991 a considerable time had passed, in some instances, since they had visited
15 the Heart Association. Therefore, all the patients were required to have another fasting blood glucose test to check on their blood sugar level at the time of participation in the study. Thus, all patients were labeled unconfirmed, meaning that results of blood glucose levels were pending, for this particular study. A label of confirmed diabetic was given to the patient when the measurements were received.
20 Linkage analyses were done with confirmed patients and unconfirmed patients were included only if they were close relatives of a confirmed index patient. The initial list of patients included 1350 Type II diabetics, but during this study new patients were diagnosed who were relatives of the index patients. All participants with no previous history of diabetes but with elevated fasting glucose were diagnosed according to the
25 WHO criteria as described above. At present date, 1406 Type II diabetics and 266 patients with impaired fasting glucose have participated in the study, together with 3972 of their close relatives.

This study was approved by the Data Protection Commission of Iceland and the National Bioethics Committee of Iceland. All patients and their relatives who
30 participated in the Study gave informed consents.

Outline of the study

This particular genetic study, which has the aim of identifying a genetic variant or a gene that may contribute to type II diabetes by using a positional cloning approach, can be divided into three steps:

- 5 i. *Genome-wide linkage study*, where excess allele sharing among related type II diabetics is used to identify a chromosomal segment, typically 2 – 8 Megabases long, that may harbor a disease susceptibility gene/genes.
- 10 ii. *Locus-wide association study*, where a high-density of microsatellite markers is typed in a large patient and control cohort. By comparing the frequencies of individual alleles or haplotypes between the two cohorts, the location of the putative disease gene/genes is narrowed down to a few hundred kilobases.
- 15 iii. *Candidate gene assessment*, where additional microsatellites and/or SNPs are typed in all genes that are identified within the smaller candidate region and further association analysis is used to identify which of the genes shows strong association to the disease.

20 Linkage analysis*Pedigree Construction*

For the linkage analysis, blood samples were obtained from 964 Type II diabetics and 203 individuals with impaired fasting glucose. The patients were clustered into families such that each patient is related to (within and including six
25 meiotic events) at least one other patient. In this manner, 772 patients fell into families - 705 Type II diabetics and 67 with impaired fasting glucose. The confirmed Type II patients were treated as probands and clustered into families that each proband is related to, within and including six meiotic events. The other patients, unconfirmed Type II and IFG patients, were added to the families if they were related
30 to a proband within and including three meiotic events. The rationale behind this was to include as many patients as possible in the study. Impaired fasting glucose is an

immediate diagnosis, and we assumed that the more closely related these patients are to the confirmed diabetics, the likelier they are to have or to develop the disease.

The families were checked for relationship errors by comparing the identity-by-state (IBS) distribution for the set of 906 markers, for each pair of related and genotyped individuals, to a reference distribution corresponding to the particular degree of relatedness. The reference distributions were constructed from a large subset of the Icelandic population. Individuals were excluded from the study if their relationship with the rest of the family was inconsistent with the relationship specified in the geneology database.

The remaining material that was available for the study was the following: 763 now confirmed Type II patients in 227 families together with 764 genotyped relatives. Of the patients, 667 were confirmed Type II patients, 35 unconfirmed Type II patients, 52 confirmed patients with impaired fasting glucose (IFG) and 9 unconfirmed patients with IFG.

Stratification of the Patient Material

The patients were classified into two sub-phenotypes based on their BMI: non-obese Type II diabetes are patients who have BMI less than 30, and obese Type II diabetes are patients who have BMI at or above 30. The reason for fractionating the diabetics into non-obese and obese groups is that other factors may be influencing the pathogenesis of disease in these two groups. Obesity alone could be contributing to the diabetic phenotype. Therefore, this factor was separated. Obesity is most likely due to a combination of environmental and genetic factors. This fractionation into non-obese and obese diabetics practically separates the material into two halves; 60% of the patients are in the non-obese category (20% with BMI below 25 (lean) and 40% with BMI between 25-30 (overweight)), and 40% of the patients are in the obese category (BMI above 30).

An affected-only linkage analysis for each of those sub-phenotypes was performed, using the same set of families as above, but classifying patients not belonging to the particular sub-group as having an unknown disease status. Restricted to a particular sub-phenotype, some families no longer contain a pair of related

patients classified as affecteds and hence do not contribute in the linkage analysis. Such families were excluded from the analysis of the particular sub-phenotype. The number of patients and families used in the linkage analysis is summarized in Table 1 below.

- 5 Table 1: The number of patients and families that contribute to the genome-wide linkage scan, both when all the patients are used, and when the analysis is restricted to obese or non-obese diabetic patients, respectively.

Table 1: Phenotype and Patients

Phenotype	Total Number of Patients	NO: of families contributing to the analysis	NO: of patients contributing to the analysis
All diabetics	763	227	763
Obese	296	92	219
Non-obese	467	154	413

10

Genome wide scan

- A genome wide scan was performed on 772 patients and their relatives. Nine patients were excluded due to inheritance errors so the linkage analysis was performed with 763 patients and 764 relatives. The procedure was as described in Gretarsdóttir, *et al.*, *Am J Hum Genet.*, 70(3):593-603 (2002). In short, the DNA was genotyped with a framework marker set of 906 microsatellite markers with an average resolution of 4cM. Alleles were called automatically with the TrueAllele program (Cybergenetics, Co., Pittsburgh, PA), and the program DecodeGT (deCODE genetics, ehf., Iceland), was used to fractionate according to quality and edit the called genotypes (Palsson, B., *et al.*, *Genome Res.*, 9(10):1002-1012 (1999)). The population allele frequencies for the markers were constructed from a cohort of more than 30,000 Icelanders that have participated in genome-wide studies of various disease projects at deCODE genetics. Additional markers were genotyped within the locus on chromosome 5q, where we observed the strongest linkage signal, to increase the information on identity by descent (IBD) sharing within the families. For those
- 15
- 20
- 25

markers, at least 180 Icelandic controls were genotyped to derive the population allele frequencies.

The additional microsatellite markers that were genotyped within the locus were either publicly available or designed at deCODE genetics; those markers are indicated with a DG designation. Repeats within the DNA sequence were identified that allowed us to choose or design primers that were evenly spaced across the locus. The identification of the repeats and location with respect to other markers was based on the work of the physical mapping team at deCODE genetics.

For the markers used in the genomewide scan, the genetic positions were taken from the recently published high-resolution genetic map (HRGM), constructed at deCODE genetics (Kong A., *et al.*, *Nat Genet.*, 31: 241-247 (2002)). The genetic position of the additional markers are either taken from the HRGM, when available, or by applying the same genetic mapping methods as were used in constructing the HRGM map to the family material genotyped for this particular linkage study.

Statistical Methods for Linkage Analysis

The linkage analysis is done using the software Allegro (Gudbjartsson *et al.*, *Nat. Genet.* 25:12-3, (2000)) that determines the statistical significance of excess sharing among related patients by applying non-parametric affected-only allele-sharing methods (without any particular disease inheritance model being specified). Allegro, a linkage program developed at deCODE genetics, calculates LOD scores based on multipoint calculations. Our baseline linkage analysis uses the S_{pairs} scoring function (Whittemore, A.S. and Halpern, J., *Biometrics* 50:118-27 (1994); Kruglyak L., *et al.*, *Am J Hum Genet* 58:1347-63, (1996)), the exponential allele-sharing model (Kong, A. and Cox, N.J., *Am. J. Hum. Genet.*, 61:1179 (1997)), and a family weighting scheme which is halfway on a log scale between weighting each affected pair equally and weighting each family equally. In the analysis, all genotyped individuals who are not affected are treated as "unknown". Because of concern with small sample behavior, we usually compute corresponding P-values in two different ways for comparison. The first P-value is computed based on large sample theory; $Z_{1r} = \sqrt{(2 \log_e (10) \text{ LOD})}$ and is approximately distributed as a standard normal

distribution under the null hypothesis of no linkage. A second P-value is computed by comparing the observed LOD score to its complete data sampling distribution under the null hypothesis. When a data set consists of more than a handful of families, these two P-values tend to be very similar.

5 All suggestive loci with LOD scores greater than 2 are followed up with some extra markers to increase the information on the IBD-sharing within the families and to decrease the chance that a LOD score represents a false-positive linkage. The information measure we use was defined by Nicolae (D. L. Nicolae, Thesis, University of Chicago (1999)) and is a part of the Allegro program output. This
10 measure is closely related to a classical measure of information as previously described by Dempster *et al.* (Dempster, A.P., *et al.*, *J. R. Statist. Soc. B*, 39:1 (1977)); the information equals zero if the marker genotypes are completely uninformative and equals one if the genotypes determine the exact amount of allele sharing by descent among the affected relatives. Using the framework marker set
15 with average marker spacing of 4 cM typically results in information content of about 0.7 in the families used in our linkage analysis. Increasing the marker density to one marker every centimorgan usually increases the information content above 0.85.

Results

20 The results of the genome-wide linkage analysis with the framework marker set are shown in FIG. 4 which depicts the allele-sharing LOD-score versus the genetic distance from the p-terminus in centimorgan (cM) for each of the 23 chromosomes. The analysis was performed with the three phenotypes: all Type II diabetics (solid lines), non-obese diabetics (dashed lines) and obese diabetics (dotted lines). A LOD-
25 score of 1.84 is observed on chromosome 5q34-q35.2 with the framework marker set when we use all Type II diabetics in the analysis. When the linkage analysis is restricted to non-obese diabetics, this LOD-score increases to 2.81. The obese diabetics do not show linkage in this region.

Additional markers were genotyped in this area to increase the information
30 content and to confirm the linkage. The information on the IBD-sharing at this locus was about 78% with the framework marker set. In order to increase the information

content, another 38 microsatellite markers were genotyped within a 40 cM region that includes the observed signal. Repeating the linkage analysis including the additional markers increased the LOD-score to 3.64 (P -value = 3.18×10^{-5}) for the non-obese diabetics. For all patients, the peak LOD-score increased to 2.9 (P -value = 1.22×10^{-4}).

5 This is shown in FIG. 5.

The peak of the LOD-score is centered on marker D5S625 and the region determined by a drop of one in the LOD is from marker DG5S5 to marker D5S429, centromeric and telomeric respectively. The one-LOD-drop is about 9 cM and estimated to be about 3.5 Mb. This 1-LOD-drop roughly corresponds to the 80-90%
10 confidence interval for the location of a putative disease associated gene.

Locus-wide association study

Genotyping to Narrow Down the Region of Linkage

In order to narrow down the region of interest, the linkage analysis is followed
15 by a comprehensive association study of the 1-LOD-drop. This is necessary as the linkage analysis has limited resolution; it compares sharing among closely related individuals that share on average large chromosomal segments. For the association analysis, we identified a large number of additional microsatellite markers located in the 1-LOD-drop and typed those markers in both our patient cohort and in a large
20 number of unrelated controls randomly selected from the Icelandic population.

We identified and typed 67 markers in the 1-LOD-drop in addition to the 17 markers already typed and used in the linkage analysis (locus-wide association micorsatellites; Table 6). The new polymorphic repeats (dinucleotide or trinucleotide repeats) were identified with the Sputnik program. We subtracted the smaller allele of
25 CEPH sample 1347-02 (CEPH genomics repository) from the alleles of the microsatellites and used it as a reference. A total of 84 markers were available for the association analysis, *i.e.*, an average density of one marker every 42kb or one marker every 0.107 cM. All those markers were typed for 590 non-obese diabetics and 477 unrelated controls.

Statistical Methods for Association and Haplotype Analysis

For single marker association to the disease, we use Fisher exact test to calculate a two-sided P-value for each individual allele. When presenting the results, we use allelic frequencies rather than carrier frequencies for microsatellites, SNPs and haplotypes. Haplotype analyses are performed using a computer program we developed at deCODE called NEMO (NEsted MOdels) (Gretarsdóttir, *et al.*, *Nat Genet.* 2003 Oct;35(2):131-8). We use NEMO both to study marker-marker association and to calculate linkage disequilibrium (LD) between markers, and for case-control haplotype analysis. With NEMO, haplotype frequencies are estimated by maximum likelihood and the differences between patients and controls are tested using a generalized likelihood ratio test. The maximum likelihood estimates, likelihood ratios and P-values are computed with the aid of the EM-algorithm directly for the observed data, and hence the loss of information due to the uncertainty with phase and missing genotypes is automatically captured by the likelihood ratios, and under most situations, large sample theory can be used to reliably determine statistical significance. The relative risk (RR) of an allele or a haplotype, *i.e.*, the risk of an allele compared to all other alleles of the same marker, is calculated assuming the multiplicative model (Terwilliger, J.D. & Ott, J. A haplotype-based 'haplotype relative risk' approach to detecting allelic associations. *Hum Hered* 42, 337-46 (1992) and Falk, C.T. & Rubinstein, P. Haplotype relative risks: an easy reliable way to construct a proper control sample for risk calculations. *Ann Hum Genet* 51 (Pt 3), 227-33 (1987)), together with the population attributable risk (PAR).

In the haplotype analysis, it may be useful to group haplotypes together and test the group as a whole for association to the disease. This is possible to do with NEMO. A model is defined by a partition of the set of all possible haplotypes, where haplotypes in the same group are assumed to confer the same risk while haplotypes in different groups can confer different risks. A null hypothesis and an alternative hypothesis are said to be nested when the latter corresponds to a finer partition than the former. NEMO provides complete flexibility in the partition of the haplotype space. In this way, it is possible to test multiple haplotypes jointly for association and to test if different at-risk haplotypes confer different risk. As a measure of LD, we use

two standard definitions of LD, D' and R^2 (Lewontin, R., *Genetics*, 49:49-67 (1964) and Hill, W.G. and A. Robertson, *Theor. Appl. Genet.*, 22:226-231 (1968)) as they provide complementary information on the amount of LD. For the purpose of estimating D' and R^2 , the frequencies of all two-marker allele combinations are
5 estimated using maximum likelihood methods and the deviation from linkage disequilibrium is evaluated using a likelihood ratio test. The standard definitions of D' and R^2 are extended to include microsatellites by averaging over the values for all possible allele combinations of the two markers weighted by the marginal allele probabilities.

10 The number of possible haplotypes that can be constructed out of the dense set of markers genotyped in the 1-LOD-drop is very large and even though the number of haplotypes that are actually observed in the patient and control cohort is much smaller, testing all those haplotypes for association to the disease is a formidable task. Note that we do not restrict our analysis to haplotypes constructed from a set of
15 consecutive markers, as some markers may be very mutable and might split up an otherwise well conserved haplotype constructed out of surrounding markers.

The approach we take to the problem of identifying those haplotypes in the candidate region that show strongest association to the disease is two-fold. First, we restrict the haplotypes we test to span a sub-region small enough that the included
20 markers may be expected to be in substantial LD. In this study, we only consider haplotypes that span less than 300kb. Second, we apply an iterative procedure that gradually builds up the most significant haplotypes. Starting with haplotypes constructed out of 3 markers, we select those haplotypes that show strong association to the disease, add other nearby markers to those haplotypes and repeat the association
25 test. By iterating this procedure, we expect to identify those haplotypes that show strongest association to the disease.

Results

For the association analysis, we genotyped 590 non-obese Icelandic Type II
30 diabetes patients and 477 unrelated population controls using a total of 84 microsatellite markers. These markers are distributed evenly across a region of

approximately 3.5 Mb. The region is centered on our linkage peak and corresponds to the 1-LOD-drop. We then applied the procedure described above and looked for single-markers and haplotypes consisting of up to 5 markers that showed association to the disease. The result is summarized in FIG. 6. In FIG. 6, we show the location of a marker or a haplotype on the horizontal axis and the corresponding P-value from the association test on the vertical axis. This is shown for all haplotypes tested that have a P-value less than 0.01. The horizontal bars indicated the size of the corresponding haplotypes and the location of all markers is shown at the bottom of the figure. All locations are in Mb and refer to the NCBI Build33.

We observe a series of correlated haplotypes that show strong association for non-obese diabetics in two locations within the 1-LOD-drop. We denote those regions A (168.37 – 168.83Mb) and B (169.70 – 170.17Mb), and in Table 10 we list the most significant haplotype in each of those regions. For each haplotype, the table includes a two-sided single-test P-value for association, calculated using NEMO, the corresponding relative risk, the estimated frequency of the haplotype in the patient and the control cohorts, the region the haplotype spans, and the markers and alleles (in bold) that define the haplotype.

Note, however, that some of the haplotypes listed within each of the two regions are very correlated and should be considered as a single observation of association to the disease. This is demonstrated for region B in Table 3, which lists the pairwise correlation, both D' and R^2 , between the haplotypes. Based on the correlation, we observe that haplotypes B2 and B4 are strongly correlated and should be considered as a single observation of association to this region. Likewise, haplotypes B1 and B5 are strongly correlated. However, haplotypes B1, B2 and B3 are all weakly correlated with each other, and in fact, B1 and B2 are mutually exclusive, *i.e.*, never appear jointly on the same chromosome. These three haplotypes hence constitute three almost independent observations of association to non-obese diabetes of this region within the locus. It is possible to test haplotypes B1, B2 and B3 together as a group for association to non-obese diabetes. This test yields a P-value = 8.5×10^{-8} with a corresponding relative risk of 5.2, a population attributable

risk of 13.9%, and an allelic frequency of 0.089 and 0.018 in the patient and the control cohorts, respectively.

Table 2

	P-value	RR	Aff.fr q	Ctrl.fr q	Span (Mb)	Haplotype
A1	0.000005	> 10	0.033	0.000	168.37- 168.72	0 DG5S879 4 DG5S881 -4 D5S2075 0 DG5S883 4 DG5S38
A2	0.000006	3.81	0.053	0.015	168.55- 168.77	4 DG5S1058 -6 DG5S37
A3	0.000008	3.64	0.054	0.015	168.55- 168.83	4 DG5S1058 -6 DG5S37 0 DG5S101
A4	0.000015	6.18	0.046	0.008	168.40- 168.72	4 DG5S881 4 DG5S1058 -4 D5S2075 0 DG5S883 4 DG5S38
A5	0.000015	4.42	0.047	0.011	168.37- 168.77	0 DG5S879 4 DG5S1058 -6 DG5S37
A6	0.000018	6.94	0.045	0.007	168.40- 168.72	4 DG5S881 -4 D5S2075 0 DG5S883 4 DG5S38
B1	0.000011	> 10	0.039	0.000	169.87- 170.17	0 DG5S953 0 DG5S955 0 DG5S13 5 DG5S959
B2	0.000023	> 10	0.034	0.000	169.65- 169.87	27 DG5S888 0 DG5S953
B3	0.000023	5.26	0.049	0.010	169.87- 170.04	0 DG5S953 0 DG5S955 4 DG5S124
B4	0.000031	> 10	0.034	0.000	169.65- 169.87	27 DG5S888 0 DG5S44 0 DG5S953
B5	0.000060	> 10	0.034	0.000	169.87- 170.17	0 DG5S953 0 DG5S955 0 DG5S13 0 DG5S123 5 DG5S959

Table 2: Haplotypes within the 1-LOD-drop that show the strongest association to non-obese diabetes. For each haplotype, we show (i) a two-sided P-value for a single test of association to non-obese diabetes, (ii) the corresponding relative risk (RR), (iii) the estimated allelic frequency of the haplotype in the patient and the control cohort, (iv) the span of the haplotype (referring to NCBI 33) and (v) the alleles (in bold) and markers that define the haplotype. The haplotypes are separated into two groups, A and B, corresponding to two different regions within the 1-LOD-drop.

Table 3

		D'				
		B1	B2	B3	B4	B5
R ²	B1	-	0	0	0	1
	B2	0	-	0.4	1	0
	B3	0	0.1	-	0.35	0
	B4	0	0.96	0.7	-	0
	B5	0.92	0	0	0	-

Table 3: Pairwise correlation between the five haplotypes in the B-region that show the strongest association to non-obese diabetes. Estimates of D' are shown in the upper right corner, and estimates of R² are shown in the lower left corner. The haplotypes are labelled B1, ..., B5 as in Table 2.

Investigation of Region B

10 Genes in Region B

We next identified all genes in and around region B (UCSC). In the region defined by the five most significant haplotypes, 169.70 – 170.17 Mb, there are four genes, *LCP2* (lymphocyte cytosolic protein 2), *KCNMB1* (potassium large conductance calcium-activated channel, subfamily M, beta member 1), *KCHIP1* (Kv channel interacting protein 1) and *GABRP* (gamma-aminobutyric acid (GABA) A receptor, pi). Of those genes, *KCHIP1* is by far the largest, stretching from 169.7 to 170.1 MB, or almost the entire span of the observed haplotype association. The other three genes are small. In addition, there is a big gene, *RANBP17* (RAN binding protein 17), just telomeric of the location of the observed association signal. The relative location of all the genes is shown in FIG. 7, which shows the location of the exons of *KCHIP1* as solid bars, and the location of the other genes as shaded boxes. In addition, FIG. 7 shows the location of the microsatellites (filled boxes) that we have typed in this region and the location of the at-risk haplotypes B1, ..., B5 (gray horizontal lines).

25

Description of new Splice Variants of KChIP1 Identified by RACE and PCR

The published sequence for KChIP1 comprises exons 1 to 8. New exons belonging to the KChIP1 gene and four different splice variants were discovered by performing RACE or PCR (primers within the exons) using as template human
5 Marathon cDNA and cDNA prepared from rat pancreatic INS1 beta cells. In all, 6 new exons located in the 5' region of the gene were discovered.. An alternative exon 1 was found that we call exon 1a. Here, we label the published sequence for exon 1 with a "b" to distinguish it from the alternative exon 1, exon 1a. Four exons are called UTR 1, UTR 2, UTR 3 and UTR 4, or untranslated region 1 - 4, because they
10 lie upstream of exon 1b and they are not translated. The last exon to be identified is called Ins-r, or insert rodent, because it was known to be present in mouse and rat, and has recently been demonstrated by others to be present in humans as well (Boland *et al.*, *Am J Physiol Cell Physiol* 285, C161-170. (2003)). See nucleotide sequences of the new exons below, as well as their location in the genomic sequence of NCBI build
15 33. Even if not mentioned, all new variants of KChIP1 found and described below include exons 2 - 8 of the published sequence.

Splice variant 1 consists of exon 1a, UTR1, UTR2, UTR3, UTR4 and exon 1b. Exon 1a is untranslated and the resulting protein is identical in amino acid sequence to KChIP1 described by An *et al.* (*Nature* 430, 553-556 (2000), see also FIG.2). This
20 variant was observed in human heart and testis and the rat INS1 cell line.

Splice variant 2 consists of exon 1b and the Ins-r exon giving rise to a protein that is identical in amino acid sequence to KChIP1 described by Boland *et al.*. This variant was observed in human brain, heart, pancreas and the rat INS1 cell line.

Splice variant 3 consists of exon 1a and is identical in nucleotide sequence to
25 AL538404, an EST in NCBI. The amino acid sequence of the N-terminus coded by exon 1a is unique (see sequence below) but the amino acid sequence coded by exons 2 - 8 is that of the published sequence. This variant was observed in human brain, heart, pancreas, skeletal muscle, adipose tissue, liver, hypothalamus, small intestine, testis and the rat INS1 cell line.

Splice variant 4 consists of exons 1a and UTR1, which would result in a protein translated from exons 2 - 8. The second methionine in exon 2 has a Kozak sequence. This variant was observed in human heart.

The nucleotide sequences of the new exons are as follows (the genomic locations given are from NCBI build 33, see also Table 8):

Exon 1a: 169716298 - 169716511 (Build 33)

GGCTTCAGGGGTGCATCCGTCACCTCAGGGTTCATTCACCCAGGCAGGCTCCAAGT
 TCCTGGGGTGCACAAGGTGGGCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTG
 GCTCCCCTCCGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTTGGGTTCGTG
 AAATTGCCCAGACCATCTTTAAGCTCATCACTGGGACCCTCAGCAAAG (SEQ ID
 NO: 4)

UTR 1: 169848417-169848523 (Build 33)

ACTCAGCATCATCAAGACTGGAGGGACAGAGCATTGGAATCATCAGACGCTGGGC
 CAGACGTCACCCACGCGTTTCTCATTTTATC GTCCTAAGAAGCCCAGAAG (SEQ
 ID NO: 5)

UTR 2: 169861083-169861154 (Build 33)

CCTGAATGCAATTTGCAATGAGGAGATGATTTGATTTTCTTCAGCCCTAGACCTCC
 AGCTTCCTGAGAGCAG (SEQ ID NO: 6)

UTR 3: 169864589-169864679 (Build 33)

GGGTTCCCCAGGAGACCACGACAGAGGCCTGGAACCCAAGTTCTAATCCACATC
 CTGGCTGGGCAACTTCAGGCAAATTTCTAACACAAG (SEQ ID NO: 7)

UTR 4: 169867066-169867173 (Build 33)

GGTAGGGGAGGGGCGGGCCCGGGTCCCAACTCGCACTCAAGTCTTCGCTGCCA
 TGGGGGCCGTCATGGGCACCTTCTCATCTCTGC₂AACCAAACAAAGGCGACCC
 (SEQ ID NO: 8)

Ins-r 170075401-170075433

ACATCGCCTGGTGGTATTACCAGTATCAGAGAG (SEQ ID NO: 9)

The nucleotide sequence derived from splice variant 4 (KChIP1.4) with the ATG and a Kozak sequence ((G/ANNATGG) underlined is as follows:

ATAAGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCCGAGGGACT
 GGAGCAGCTCGAGGCCAGACCAACTTCACCAAGAGGGAGCTGCAGGTCCTTTAT
 CGAGGCTTCAAAAATGAGTGCCCCAGTGGTGTGGTCAACGAAGACACATTCAAGC
 AGATCTATGCTCAGTTTTTCCCTCATGGAGATGCCAGCACGTATGCCATTACCTC
 TTCAATGCCTTCGACACCACTCAGACAGGCTCCGTGAAGTTCGAGGACTTTGTAAC
 CGCTCTGTGCGATTTTATTGAGAGGAACTGTCCACGAGAACTAAGGTGGACATTT
 AATTTGTATGACATCAACAAGGACGGATACATAAACAAGAGGAGATGATGGAC
 ATTGTCAAAGCCATCTATGACATGATGGGGAAATACACATATCCTGTGCTCAAAG
 AGGACACTCCAAGGCAGCATGTGGACGTCTTCTTCCAGAAAATGGACAAAAATAA
 AGATGGCATCGTAACTTTAGATGAATTTCTTGAATCATGTGTCAGGAGGACGACAAC
 ATCATGAGGTCTCTCCAGCTGTTTCAAAATGTCATGTAAGTGGTGACACTCAGCCA
 TTCAGCTCTCAGAGACATTGTAATAACAACCACTTAACACCCTGATCTGCCCTT
 GTTCTGATTTTACACACCAACTCTTGGGACAGAAACACCTTTTACACTTTGGAAGA

ATTCTCTGCTGAAGACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATT
GCCAACTCTTCCYCTTTCTTCTTCTTGAGAGAGA (SEQ ID NO: 10)

5 The protein sequences resulting from the splice variants are as follows:

KChIP1.3

(The amino acid sequence derived from splice variant 3 (KChIP1.3), the underlined amino acids are coded by exon 1a.)

10 MSGCSKRCKLGFVKFAQTIFKLITGTLISKDKIEDELEMTMVCHRPEGLEQLEAQTNFT
KRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSV
KFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKEEMMDIVKAIYDMMGKYTY
PVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQEDDNIMRSLQLFQNV (SEQ
ID NO: 11)

15 KChIP1.2

(The amino acid sequence derived from splice variant 2 (KChIP1.2), the underlined amino acids are coded by exon Ins-r.)

20 MGAVMGTFFSSLQTKQRRPSKDIAWWYYOYORDKIEDELEMTMVCHRPEGLEQLEA
QTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTT
QTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKEEMMDIVKAIYDMM
GKYTYTPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQEDDNIMRSLQLFQNV
M (SEQ ID NO: 12)

25 KChIP1.4

(The amino acid sequence derived from splice variant 4 (KChIP1.4).)

30 MVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDA
STYAHYLFNAFDTTQTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKE
EMMDIVKAIYDMMGKYTYTPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQE
DDNIMRSLQLFQNV (SEQ ID NO: 13)

Identification of SNPs and Microsatellites

35 In order to identify SNPs across KChIP1, all exons of KChIP1 and their
flanking regions were sequenced on 94 non-obese diabetic patients. As a
consequence, 31 SNPs were identified (Table 9). Additional SNPs were identified
across the gene by selecting SNPs from the public domain (US National Center for
Biotechnology Information's SNP database) and designing SNP assays for them.
(Table 10).

40 We genotyped SNPs on 470 non-obese diabetics and 658 population-based
controls using a method for detecting SNPs with fluorescent polarization template-
directed dye-terminator incorporation (SNP-FP-TDI assay) (Chen, X., Zehnauer, B.,
Gnirke, A. & Kwok, P.Y. *Proc. Natl. Acad. Sci. USA* 94, 10756-10761 (1997)).

Association Study of Genes in Region B

We tested all the genes in and around Region B (*LCP2*, *KCNMB1*, *KChIP1*, *GABRP* and *RANBP17*) individually for association to non-obese diabetes. In the analysis of each gene, we included all SNPs identified, and previously typed

5 microsatellites, in and close to that gene. The association analysis was carried out in the same way as the locus-wide association, i.e., using the iterative approach, we search for haplotypes, shorter than 300kb, that showed strongest association to the disease.

The strongest association observed was for *KChIP1*. For *KChIP1*, we tested

10 25 markers, 7 microsatellites and 18 SNPs, for association (Table 11). The strongest association signal was observed in the 3'-end of the gene; a three marker haplotype with a P-value = 9.2×10^{-5} , relative risk 12, and allelic frequency 3.6% and 0.3% in the patient and control cohorts, respectively. This haplotype, which extends over the last 8 exons of *KChIP1*, from 169.96 to 170.11 Mb, is listed in Table 4 as D1. We also

15 observed another haplotype in the same region that showed association to non-obese diabetes, albeit less significant than D1, with a P-value = 0.037, relative risk 1.69 and allelic frequency 7.8% and 4.8% in the patient and the control cohorts, respectively. This haplotype is labelled D2 in Table 4. For risk haplotypes, the corresponding population attributable risk is PAR = 4.9% for D1 and PAR = 4.7% for D2. However,

20 as D1 and D2 are independent haplotypes, i.e., they do not appear jointly on the same chromosome, their population attributable risk can be added together.

Table 4

	P-Value	RR	Aff.frq.	Ctrl.frq	Haplotype
Icelandic					
D1	9.20E-05	12	0.036	0.003	-4 DG5S13 C KCP_1152
D2					0 D5S625
	0.037	1.69	0.078	0.048	0 DG5S124 C KCP_1152 C
					KCP_2649 T KCP_4976 A
					KCP_16152
Danish					
D1	0.052*	2.98	0.031	0.011	-4 DG5S13 C KCP_1152 0
D2					D5S625
	0.002*	2.74	0.098	0.038	0 DG5S124 C KCP_1152 C
					KCP_2649 T KCP_4976 A
					KCP_16152

* One-sided P-value

Table 4: *Microsatellite* and SNP haplotype association within *KChIP1*. The two independent haplotypes D1 and D2 are located in the 3'-end of the gene, from 169.96 - 170.11 Mb. Shown are results of a test of association for non-obese diabetics vs population controls for both haplotypes in a cohort of Icelandic diabetics (top) and a replication in a cohort of Danish diabetics (bottom). Note that we report one-sided P-values for the test on the Danish cohort as that is a replication of association results previously observed in the Icelandic cohort.

Replication in a Cohort of Danish Diabetics

We typed the markers that define the two at-risk haplotypes, D1 and D2, in a cohort of 149 non-obese Danish females that have been diagnosed with diabetes and/or measured >7mM glucose who participated in a Danish PERF (Prospective Epidemiological Risk Factors) study. As controls, we used 346 females from the same study that answered no to a question about their diabetes status and/or measured <7mM glucose.

The results of the association test for the two at-risk haplotypes, identified in the Icelandic diabetes cohort, are listed in Table 4. Both haplotypes appear in higher frequency in the non-obese Danish diabetics than in the control cohort. For haplotype D1, the association to non-obese diabetes is only marginally significant, with a one-sided P-value = 0.05, and the relative risk of the at-risk haplotype is $RR = 3.0$, somewhat less than is observed for the Icelandic non-obese diabetics. Note, however, that the estimated frequency of haplotype D1 is very low, especially in the control cohorts, hence the estimates of the relative risk are not very reliable. For haplotype D2, on the other hand, we do observe a statistically significant association with a one-sided P-value = 0.002 and relative risk = 2.74. Note that as the test of association of haplotypes D1 and D2 are attempts to replicate the association we have observed for Icelandic non-obese diabetics, it is appropriate to report one-sided P-values for those tests.

Additional SNP Genotyping for KChIP1

Having observed association to the 3'-end of *KChIP1*, both in Icelandic and Danish non-obese diabetics, we subsequently sequenced 94 Icelandic individuals, 1/3 non-obese type II diabetes patients with the observed haplotype D1, 1/3 additional non-obese type II diabetes patients and 1/3 controls. The purpose of the sequencing

was to identify additional SNPs. We identified 725 SNPs (Table 12). Many of those SNPs were completely correlated so we removed several redundant SNPs from further genotyping. Some SNPs with very low minor allele frequencies were also ignored. Of the 725 identified SNPs plus what was originally identified, 108 were
5 selected for further genotyping in the Icelandic cohort (Table 13).

We performed a single-marker test of association to non-obese diabetes for each of the additional SNPs we typed, although none of the SNPs showed a strong association. We did, however, observe that three of the SNPs, KCP_197678, KCP_197775 and KCP_202795, increased the specificity of haplotype D2, if added to
10 that haplotype, while still retaining most of its sensitivity. This is shown in Table 5, both for the association in the Icelandic and in the Danish cohorts. This increases the value of the at-risk haplotype as a diagnostic tool. Note that the three SNPs are very correlated to each other, with pairwise correlation coefficients $D' \approx 0.96$ and $R^2 \approx 0.9$, hence the association of haplotypes D3, D4 and D5 to non-obese diabetes should be
15 considered as a single observation.

In addition to the refinement of the at-risk haplotype D2, we observed another refinement of the at-risk haplotype, consisting of three SNPs only, that was very correlated with the three at-risk haplotypes, D3, D4 and D5, with pairwise correlation coefficients $D' \approx 0.83$ and $R^2 \approx 0.59$. This haplotype is included in Table
20 5 as D6.

25

30

Table 5

	P-Value	RR	PAR	Aff.frq.	Ctrl.f rq	Haplotype
Icelandic						
D2	0.037	1.69	6.3%	0.078	0.048	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152
D3	0.022	2.19	5.5%	0.052	0.024	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197678
D4	0.052	2.03	4.6%	0.046	0.023	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197775
D5	0.023	2.14	5.5%	0.052	0.025	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 C KCP_202795
D6	0.054	1.77	4.0%	0.046	0.027	A KCP_173982 C KCP_15400 C KCP_18069
Danish						
D2	0.002*	2.74	12.0%	0.098	0.038	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152
D3	0.0046	2.60	9.0%	0.076	0.030	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197678
D4	0.0004	3.69	11.3%	0.078	0.023	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197775
D5	0.0002	3.67	11.7%	0.084	0.024	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 C KCP_202795

* One-sided P-value

Table 5: Microsatellite and SNP haplotype association within *KChIP1*. Shown is association of the at-risk haplotype D2, and of further refinements of that haplotype; haplotypes D3, D4 and D5, to non-obese diabetes. This is shown both for the Icelandic and the Danish cohorts and, as in Table 4, we report one-sided P-values for the association test in the Danish cohort. Finally, we include the result of association to non-obese diabetes, in the Icelandic cohort, of a 3 SNP haplotype, D6, that is strongly correlated with the at-risk haplotypes D3, D4 and D5.

Allele Numbering System

SNP alleles are indicated by the letters found in the DNA sequence. In general the alleles can be references by A=0, C=1, G=2 and T=3. For microsatellite alleles, the CEPH sample (Centre d'Etudes du Polymorphisme Humain, genomics repository) is used as a reference, the lower allele of each microsatellite in this sample is set at 0 and all other alleles in other samples are numbered according in relation to this reference. Thus allele 1 is 1 bp longer than the lower allele in the CEPH sample, allele 2 is 2 bp longer than the lower allele in the CEPH sample, allele 3 is 3 bp longer than the lower allele in the CEPH sample, allele 4 is 4 bp longer than the lower allele

in the CEPH sample, allele -1 is 1 bp shorter than the lower allele in the CEPH sample, allele -2 is 2 bp shorter than the lower allele in the CEPH sample, and so on.

Table 6:

- 5 The DNA sequence of the microsatellites employed for the C05 locus wide association (including Build 33 locations).

Y= C or T; S = C or G; R = A or G; W = A or T; M = A or C; K = G or T.

TABLE 6

Name	Position	Nucleic Acid Sequence	SEQ ID NO:
DG5S5	167638990 - 167639163	TCCTCAGAACAGGTGCAACACAGTGTGTTTTGCTGGGG AAAAGGGATGTCAAGCAATCTATGACGGGGGTGCAGG GAGTCTGGGGAGAAACACAAGGAAGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGAATGTGTGTGTGTGTGAGAG AGAGAGCTGGTGTGTTGTGTCCA	SEQ ID NO: 14
D5S671	167657904 - 167658237	GGAATGTGCCAAGACATTCTTTAGGGTTGGTAACCAG AGACGCTATTTTGTCTTGGTGGCTAAGAAATCACTTT TCTGACTGAAGGNCCATTTGACTTACTTCTTTTAAATT CAGGGGAATGGGTGGGCATCTCCATGATTCAGGTAAG GAAAAATCCAAGGNAAATAAACACACACACACAC ACACACACACACACACACACGGAGTAGAAATTTTTAG TGCAATTTTTTGTCTCACAGCATTAAATTAATTGCAGGG ATATAACTACCTTGGCAGAATTTTTTCTCCCCAACCCA CCACCCCCCGGAATAAGTTTGGCTCTTTTCAGCT	SEQ ID NO: 15
DG5S870	167719773 - 167719939	TGCCCACTCATAAGATGCTGAGGTTACAACGTGTTAATA AGATATTAAGATACTGTCTTTTTCTTCTCTCTCTCTCT TACACACACACACACACACACACACACACTTTTTG GGCCAACTGGAAATTCATACATTCTCCCCAGCACTGGA GCTCAAAGCGTCTG	SEQ ID NO: 16
D5S671	167657904 - 167658237	GGAATGTGCCAAGACATTCTTTAGGGTTGGTAACCAG AGACGCTATTTTGTCTTGGTGGCTAAGAAATCACTTT TCTGACTGAAGGNCCATTTGACTTACTTCTTTTAAATT CAGGGGAATGGGTGGGCATCTCCATGATTCAGGTAAG GAAAAATCCAAGGNAAATAAACACACACACACAC ACACACACACACACACACACGGAGTAGAAATTTTTAG TGCAATTTTTTGTCTCACAGCATTAAATTAATTGCAGGG ATATAACTACCTTGGCAGAATTTTTTCTCCCCAACCCA CCACCCCCCGGAATAAGTTTGGCTCTTTTCAGCT	SEQ ID NO: 17
DG5S870	167719773 - 167719939	TGCCCACTCATAAGATGCTGAGGTTACAACGTGTTAATA AGATATTAAGATACTGTCTTTTTCTTCTCTCTCTCTCT TACACACACACACACACACACACACACACTTTTTG GGCCAACTGGAAATTCATACATTCTCCCCAGCACTGGA GCTCAAAGCGTCTG	SEQ ID NO: 18

DG5S85	167721558 - 167721918	TTGTTGTTGTTGGTGGTGGTGGGGTGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTTTCGAGACAGACTCTC ACTCTGTCACCCAGGCTGGAGTGCAGTGGCAGCATCT GGGTTCACTGCAACCTCTACTTCCTCAGCTCCAAGGAT CCTCTCACCTCCACCTCCCAAGTAGCTGGGACTACAGG TACGCGCCACCATGTCTGGCTAATTTTTTTGTATTGGA GAGACAGGGTTCCACCATGTTGCCCCGGGCTAGTGTTCG ACTCCTGAGCTCAGGTGATCCACCCACCTCAACGTCCC CAAGTGCTGGGATTAGAGGCGTGAGCCACCACGTCTG GCCTATACACTATAGAGTTT	SEQ ID NO: 19
DG5S90	167766290 - 167766502	TCTGGACAGGACCAGGAGTTGGCTGCTGTCAGCCTTTG CCCCACCTCTCTGTGGCTACTGGGTATGTGAATCTCTC AAGGCCTGAAGAGAGGACAGCTGAGGAATTTGGAAAT CCTAAAACACATGCATACACACACACACACACACACA CACACACACACACACACACTTTTCTTTCCCTTAAAAAA AAAAAGATTTCATTACCCGTGTGCA	SEQ ID NO: 20
DG5S874	167846718 - 167847065	CTGTCTACACTACCCACCCATTAGTCACTTATTAGCCC TCTGAATTACTGGATTGAAAAAACATAGTATATATATA GGGCTTGGTACTATTACGGTTTCAGGCATCCACTGAG GGGTGTTGCAATGTATCTCCACGGATAAGGAAGGAC TGGTATATTAACACTTTTATTTGATTTACAAAAATAAG GATAGTTTATATAGTTCTGGGTAAAATTAATTAATTAA TTTAAAAGGAAAAAAGATAAAGGCAAACCTTTAAGCTT GTTAAAATTAAGTAAAATAATTTGGATTATTTAATTG GACAAAGAGGACTGGCTTTGCCAATGAAACAATATGG CCGACATG	SEQ ID NO: 21
DG5S88	167864864 - 167865059	GGACCTTCTTTCTGCCCTAAAACCGCAATATCATTATA ATAACAAATATATATATATATATATATATATTTTTTTT TTTAAAACAATCTTGCTATGTTGCCTAGGCTGGTGTGG AACTCCTGGCCTCAAGTGATCCTCCACCTCGGCCTCC CAGAGTGCTGGGATTATAGACATGAACCTACCATACCC AGCCA	SEQ ID NO: 22
DG5S7	167910343 - 167910651	CACAGCCATCAAGTTTCCAACCTTACTGCCTCACATATT AAGATGATTTTTTTTAAACAACTTAACAGGCGATGGAT ACTCCATTCTCCATGATGTGCTTAATTCACATGCATGC TTGTATCAAAACATCTCACATACTCCATAAAGCCTGTA ATCCCAACACTTTGGGATGCCAAGGTGGGTGGATCAC TTGAGCCCAGGAGTTTGAGAACAGCCTGGACAACATG GCGAAACCCCATTTACACACACACACACACACACACA CACACACACCACACAAACAAAATGAAACAAACACCTA ACCAACAA	SEQ ID NO: 23
DG5S6	167952553 - 167952858	TCCTAACGGCTGCTACCACTAAAGATCTTAGCATGGTG TGTGTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTGGTGGGGCTATTAGTAAGGCTAGAAGTGAAA AAGCTAGTAGAAAGCCCATGGTGATGGAGAATGGAGG AAGACTGATTAGGGAGCTCCTCAGCAGTATAAGGAAG GACTAAGAGCACATAAGGACAGGATCATAGAATCCG CATCTCAGGATTTTTGAGGCTGCCACTGCCTTAGCTGT GAGGCCAGTGCATATAAGAATAGTTTGCACAGTTCTG CTGTGG	SEQ ID NO: 24
DG5S87	167992779 - 167993149	CCTCTGGGATTAGCCTCTCAGGGTACAGATATAACGAT GATTGAGTTGGCTTATGTATGTGTGTGTGTGTGTGTG TCTGTGTGTGTGTGTGTGAGAGAGAGAGAGAGAGAGA GAGAGAGTGACAGAGAGAGAATGAGAGAGAACTGGA AGTTGTCAACAAGAAGAGTCAAACCTCTGTAAATATT TGAAGAGATTTATTCTGAGCCAAATAGGAGTGCCACA	SEQ ID NO: 25

		GCCCCGGGAGATCCTAAGAACATGTGCCAGAGTAGT CAAGCTATAGTTTGGTTTTATACATTTTAGGGAGACAT AAGACATCAGTCAATACATGTAAGATGCACATTGATA CACTGGTTTAGTAGGGAAAGGTGGGACAACTCGAA	
DG5S91	168014827 - 168015078	GGTGCCAATTAAATCCAACAAGGTAGCTGAGTGTGGT GGTGCACGCTGTAGTCTAGCTATGCAGGAGGCTGA GGTGGGAGGATCACTTGAGCCTGGGAGGTCGAGGCTG CTGTGAGCTGTGATTGCACCGCTGCATTCCAGCCTGGG AGACAGAGCAAGATCCTGACACACACACACACACACA CACACACACACACACACACACACACATTCCAACAAGG TAATGTGTAGGAGGAAGTACCCGAGCTT	SEQ ID NO: 26
DG5S92	168065529 - 168065864	CAACTCCTGCAGCCCTTTACGCCAAGCACAGAAATCC AGGAGGCAGAGCCTAGCGCTTGATGACATGGTAATTG GGCCTGGAAGTGGGGATTTCTGTCACTTACCTCTCCTT GAAAAATAATCACTATTGCCAACGCCTGGTTAATTAGC CTGATTCAATTCTCTTCAGCCTCATTTTGCTCAAATCTA CCAGATTTGTGGTGTCTCCTTGGTCTCCACCACACTTT CTACCCCTCATCCCCTTTGTGTGTGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT TGGCCAGGAATCCTGACTGGCTTCCTTTAAA	SEQ ID NO: 27
DG5S491	168081175 - 168081342	AAGACCACCCTCCTGTTGTGTCTCTCCTGAAATGTATTC ATATCCACCCATACACACACACACACACACACACACA CACACACACACACACACACACACACACATTCTCTCTCT CTCTCTCTTTCTCTCTCTCTCTTAAATGTCAGTTTTCTCT TCCTGCTTTCCAGA	SEQ ID NO: 28
DG5S9	168139425 - 168139680	CTTGACATTGAGGCGCTTCTGAGTACATCATCTTGTC AGAAACACTGAACTATTTCAGTACACAACAGGTCAGAG GTGCCCATTTGATAGCCTGAGGATGGAATCCTTATTGC AGCATTTTGCATGATGCCACATATATGTGTTTTTCAAT CCTCCTCTGTTTTAAAAATTGGAAAATTTTCATACAACA CACACACACACACACACACACACACACACACACACAC ACCCCCCATACACACCACACCACATCA	SEQ ID NO: 29
DG5S876	168266982 - 168267134	AGCCTCTGACTCTCCTCTGTGGGGCTAATCCAGAAAAT CTTACTTTAGAAATAACAATAATAATAATAATAAT AATAATACCTCATTATCTTTACTTATCATGTGCTAGT ATGTTTCTAAGCCTTTTGGCATAGCCTTCAATGTCCCT	SEQ ID NO: 30
DG5S97	168286866 - 168287096	CTCTTCCCAGTCTGCTTCTCTCCTTCCCTGCGGGTTGG GACCCAGTACCCTCCATCTCTCTCACTCCTCCCCTCTCA AACCTTCTTTTTAGGAAAGGAGTCCAAATCGACCACTT ACACCTCAGTTCAATGCAAGCCAGTATAATTAATAAG GAACATTTAAGGGTGTGTAAAGGGTGTGTGTGTGTGTAT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT C	SEQ ID NO: 31
D5S2052	168324273 - 168324633	GATCACCAGGGAATCTAGATGGAATCCATAGTNCCTNC CCTGCAAGAAATGCTGCAATTCTGTACCGTGGAGGNGC CAACAGAATCACCAGGCTCTGTGACTCAGTCACAACA CCCTGACCTGCCCTGTCCATTCTCCATATCATACCCA GAGTGGTCTTTTCAAAGCACAGCTTTGACCAATTCTCT GTCTTTTACACATACACACACACACACACACACACAC ACATGCGTGCATGCATGCCTGAAATAGTATAGTATTGC TCTTAAGATAAACATTAANGTTCTACCATGGTACAGA AAATATATGTNGTTAGGCCCGTGGCTCTTTCTTTTCC AGACTCCTCTTACCCCTTTGTG	SEQ ID NO: 32
DG5S879	168369069 - 168369202	AAATCTTCCATTGCAGACCAATTAATAATTAAAGATTT TCTCTCTCTTTCCCCTCTTCTCTCTCTCTCTCTCTCT CTCTCTCACACACACACACACACACACACACAACTCTC	SEQ ID NO: 33

		TCACCTCTTGGGCCGTGATGATGATGAGGGAGAGGAGC AGT	
DG5S38	168715977 - 168716367	TATTTGCCTGCCTGGGTTAGATGATTCTCCAGGCTTCT ACACAATTTTATGTTTATATGAAAATAGCCACAAAGG GAAAAGAGGACAATAAAACAAGAGATATGAATAATA ATGTATTGTATACTTGAATTTTGCTAAAAGAGTAGATC TCAAGTGTCTACATACACACACACACACACACACAC ACACAAAGGTAATGAATGAGATGATAGGTGTTAATTA ACTTGATTGTGGTAATCACTTCACAATGTATACATATA AAAACATCATGTTTTACAACCTACATTTATACAATTCC TCAATTATATATCAATAAACCTGGAAAAATAAAGATG TATAAAAAAGATTTACAAATAAGATTTTAAAAAAGG ATTGTGAGGAAACAAAG	SEQ ID NO: 41
DG5S37	168770226 - 168770418	ACCAGCTAACCTGCCATGAGACTGTTGTGTAGCCATCT TCACCTCCTCATCTTCAGGGAAGGGGATGAAAATATCT GTGCACTGCAAATGTTAACTATATATACACACACACAC ACACACACACACACGTACAGTAGGCCCTCCATAACCT GAGGTTCCACATCTGCATATTTTACCAACTCTGGTCCC TGC	SEQ ID NO: 42
DG5S886	168803195 - 168803445	TTGTTCTGAATGGGAGGAGGACTGGTGAGTGAGGGG GAAAGAATGGAGACAGGACTGAGAAGAACCAGAAAT TAAAATAATAGTAGTAATAGCCTAACATGTACACGTA TATGAGATCTATCTATCTATCTATCTATCTATCTATCTA TCTATCTATCTATCATCTATATATCTATCATCCATCATG TATCTATCTATTTGCATATATAAGCTATAATATCTGGC TCTGTTCTAATTGTTT	SEQ ID NO: 43
DG5S101	168833451 - 168833700	CCAGGCTTGGATGAGAGAATAATCTTAAGGAAGTCAG CATATGTTCTAGAAACATTGAGAAGACAAAAGAGTCT GTTATGAAAGAACAAGTATTTGTAATAATAAATTGA ATGTTACATGGACACACCCAGACATACACACACAGAC ACACACACACACAGTTTTTCTTCTCTCTCTCTCTCCC CACTCCCCTCTCTCATACTTTGCAAACAAGCTCCTCAG CAGCTGGTAAGCTGTTCCCTGTCC	SEQ ID NO: 44
DG5S102	168895047 - 168895352	TCCTGACTGCTCAAAGCTCAAGGTGTTGCCTTTTTCAA ATGGGATGCAATAGCCTACTCATTTTCCAAGATTAAAG CTAGAGAGAAGAATGAATGAATGAATAAATAAATAAA TAAATAAATAAATAAATAAATAAATGAGCAAAGTTAA TATTAGCTGGAAAAAATAGGGTACAGGTGGAAGGAAT GAACCCATATTGAGAGTCCACTATGTGTCAAATTCCTT GCATGGAATCTCTAAGGTCTGTCTAGCTTAAAGCAAT GCCAGCCTTGCTATCTGTACTTGATGAGGAGATGGATC GGAA	SEQ ID NO: 45
DG5S39	168920224 - 168920577	CCAAACTGCAAACCCAACTTCTACAATGAATTCATGT GCAACTTATTCTAAAAGATCTATACACACACACACAC ACACACACACACACACACACACACACTTCCTGTCTCT ATTGCTCTTCACTACTTCCTTCATCTCTGTGCTACAATC TGGGTTTCATTTTTCTTCCCCTTGAGTAATTTATTATGTT TTTTACAGTGAGTCTGTTGCTCAAAAATTCCTTTAGTAT TTATTTGTATAAAAAGTCTTAATTTTGTCTTCATATAAA ATTTTGTGTTGACACTCTATTATAAATTGACTGTTATTCT CTTTCCATGTTTTCCGGACATAGTTCCATTGTCTTCTGA CTCCA	SEQ ID NO: 46
D5S1456	168968063 - 168968256	TTCNACCTTATGGGTATATCGAATTGTAACCCCGTTGT AGGTCAAGGAGCATCTNCATATATACATACATAGATG ATAGATAGATAGATAGATAGATAGATAGATAGATAGA TAGATAGATTTAATTCTAAANTTTCCAAATACTCTTTC	SEQ ID NO: 47

		ATTTAAATGATTATAGTTTTACAACAATTTTCATATATT NTATAGGTAGGAGAATTAGGGTTTTCCAGAGAAATAG ANNCAATAGGCTGTGTGTGTATATAANGATTTANTTTN AAGA	
DG5S106	169021310 - 169021609	GTTGGGCATGATGGTGTGTACCTATAGTCCTAGCTACC TGGGAGGCTGAGGCAGGAGGATCCCTTGAGCCCAGGA GTTTAAGACTAACAAGACTCCATCTCTGAAAAATAAG GCAAAAAAAGTATGAAGAATAAAATAACAATCACTTA CATTCCAACCACTATAAATTAATCATTGCCAACACCTG AGGATATTTTGCTTCCAATCTACAAGACTGCATTATTAT TATTATTATTATTATTATTATTATTATTATTATTATTATT ATTATTGAGATGGGGGTTTCTCTTTGTTGCCAG	SEQ ID NO: 48
DG5S40	169067041 - 169067434	GCAGACAGGGTTCAAATTCAGCCTCCCTCATATTAG CTGTGTGATCTTAGGCAAGTTTATTCATGTGTAAAAAG AAATAATAACCTCTTCTCGTGGGGTTGCAGGTTAAACA AAAGAGTAGGTATTAACAACAATAAAAGAGTATGATT GGATTGTTTATAACACAAAGGATAAATGCTTGAGGAC ATGGATCCCCATCTTCCATGATGTGATTTTTATGCATT GTATGCCTCTATCAAAACATCTCATTACTCCATATAT ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTGTGTATGTGTATGCACACACTATGTGCCACACA AAAATTAAAAATTTTAAAAATTAAAAATTTTAAAAAT AAACATGCTGCTGGGC	SEQ ID NO: 49
D5S504	169142805 - 169143006	AGCTGCCAGCACACAAGGCCAGAGGTACTTTATTGG ATGCCAAATTCTTTTAACACACCATGAGAAAAGAAGT TGACAACTTTCCCATGCATTTTGGAAGGTGTGTTAGAA CGATTCAACACACACACACACACACACACACACACAC ACACACACACACATTTATTGGGTTGGGGGAGCCTT AAAACCTACAAATCT	SEQ ID NO: 50
D5S1961	169173385 - 169173631	AATTTCTTACCCTTTATCCCGTCTTCTACTCCCATTCC ACATGCCCCCACCCTCATGAATGATTGTCTAATGC GTTGAATATGCACGTGTGGTTTTGGGTGCATGTATGTT TACACACACACACACAGACTCTCTCTCTCTCTCTCA CACACACACACACACACACACACACACACACACTCAT GCCTCTCCTTTGAAGAGGATCAGATATGGACAGCAA GGCATTAGCATCTTAGCT	SEQ ID NO: 51
DG5S108	169203019 - 169203370	GCTCCAAAGTTCCTGATTCCAAAGCCTAAGTTAAGCCA TCTTAACTTATATTTTCAAGGTGACTAGTGGAATTTTTAT GCCAGTGTAGGTGGTAATGACGATGGAGATATGGCG ATGATGATGATGATGATGATGATGATGATGATGATGA TGGCAGTAGTGGTGGTGGTGTGGTGATGGTGTGAA GATCACCATGTCTGACCACTGTTGTCTGTGTCCTTTGT ACAATTGTTTCAAGTGCAGTGTCTGGTTGTCACATAGA TGTCTCTGACTGTTTTACAGGCCTTCACCTACCACCAT ATCCAGGAGATCATGGTCCAGCTGCTGCGGACAGTGA ACCGGACAGTCA	SEQ ID NO: 52
DG5S41	169277936 - 169278300	TTAACCCTGCTCCCATTTTGCTGGTGGAAAACTGAA AACCAAAGAGATTAAGTCATTTACCCAAGGTCATGTA ACTAATATATTGAATCTCAGATGTTTTAATGATTTTGA CTCATTTCCAATTTGCCTGGCTATATAGAGAAAAATATT TGAGGAATTGACAGGGAACACACACACACACACACAC ACACACACACACACACACACACACAGAGGGAGGGAG GGGAGAGAGAGAGACAGAGACAGACAGAGACTGAAC AGATTATTTCTCCACTGATGTTTATTATTAGATCTATT TTCAACATTTAAAGGCAATTGTCAGCATAGTCAATTCA GCCATTTTAAACCATCAAGGGCCAATG	SEQ ID NO: 53

DG5S42	169285983 - 169286144	GCAACCTATTTTGTAGCAGCACATGCGTGCGTGTGCAT GCACGTGGGCACACACACACACACACACACACACA CTCTTTGCAGGGGAATTTTGAGCCAGAAATTTATCTGT AGGCCCATATTCAATTCCTTTTTGCACATTTCTATTGTGA CCTTGGGCA	SEQ ID NO: 54
DG5S10	169356049 - 169356318	CAATTCCACACAGCTGGAGAGTAACAAAGCCAGAAAT CACATCCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTC CAAATCCTGTGATTCCAGTGCCAGGATACACTGTCTTC CGTGTTCAACAGTCATGAAAGTATTTTAATGAACACCT GGCCCTGCAGTGCCTGATGTAGCAAATGCTGCAGATA CTCCACCCACCGACTCTTGGACCACCCAAAATCCACTG GCAGCTTCAGTGAGGCTTTCCTACTTCTTTCTTCCCTG GGCT	SEQ ID NO: 55
DG5S110	169391090 - 169391341	CACTGGACTTGGAGTCAGGACATCATTTTAACAGCTTT ATCGAGATGTAATTTACATGCCATACAATTTACCCAAA GTGTACAATCATTGACTCTTAGTATGTTACAGAGCTA TGTAACCATCACACAATCAATTTTACAACATTTTCAT TACTCCTAAAAAGCAAACCTGCACCCCTTAGCCACTGC TCTGCCAACACACACACACACACACACACACACACGC GTGCGCACACACACCCAAACACTC	SEQ ID NO: 56
DG5S11	169409260 - 169409401	CGCGTGTAACCTCCACATAGATGTTTGCCAATGCCTATG CCCAAGACACACACACATACACACACACACACACACA CAGGATACATTCAAGCACACACTAATGTATGTGCACTT GCCTGCACAGAGTCCACATCACACAGGC	SEQ ID NO: 57
D5S1973	169424532 - 169424861	AGCTTCTAGTCTGCTATGTTGCTAATTGTCTTCTTGGTC ATCTTTTAAAACCATTTCTGTGAAATTATAGCCTCCTT ACTCCCTTACCCTGAGTCTGGATGTTTCTGAAGATGAC TGATCTCTACAGTGAGAAGGCCCTGGGAATTGACTGA CTCACTCTCTGTCTCTCTCTCTCTCTCTCTCTCACACAC ACACACACACACACACACACTCATATACATACACA CATAGATACACATATACATGCATCCACACATGCACAC CCTGGGCACACCCACACACCCTACAACCTGCACATGCA TGCACACACATAATGTAACTGAAGG	SEQ ID NO: 58
D5S397	169542970 - 169543287	AGCTTTTGGCTATGGAACCTTAGGCAAGATGTTTCATAA ACCCTTTAATCTCTAGTGCCCTTGTTTCATAAAAAGAAG TGAATCGGATCCCTGCAGGACTGTTTTTGTATTCACTG CACAGGTGTGTGTGAAGACACCCAGCATGTTGCCAGG CACACAGAGATGTCTACCTTGATACTTTTCTCTCCTCCT CCCCGCAAATACACACACACACACACACACACACACA CACTCACACACTCTTATTTTGATCTTGGCCTGAGGC TGACAAGCCCCAGATTAGTGATCAGTGACAATTCGG CTTTATCAGCT	SEQ ID NO: 59
DG5S115	169586308 - 169586550	CGAGGATGCACACCTCATTAATTGAGGAGCTAGGATT TAGATCCAGAGCCTCATGATTCTAAAGCCTGTTTTTG TTGTTTGTGTTGTTGTTTGTGTTTGGCCACACTAGGTT TCTAGAACTTCCAGTTCCTTCTTAAAAGTCCTTTTTGG GCATTCCGGCCTAAATCCCAAAACTGTGGTCTGGGTAC AAGAGAGAATTAGGCCAGTGAGAAAAATTTAAACCAC CCTGCCCTCTAAAT	SEQ ID NO: 60
DG5S888	169653226 - 169653848	CTTGATGTCTTCTTTTACCATCCCCTGGCACCCGCCTAT ACATTTATTACTTGAAACAGACTGACCTTTATTTGGTT AGGCCACTGTGGTCAGGTTTCTGCAACATGGGGTCAC ATGCCCTCCCAACTGACACAAGTCTCAAGCTCCTTTTC TCTTCTTTTTATACTTCTAGAAGCATAGCTTCTACCAG ATAAGGATCTAACCTTTTCAAGTGGAACAAAAATGG CAAAGAAGTAAAGAAAGAAGAGAGAGAAAGAAGAAA	SEQ ID NO: 61

		GAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG AAGAAAAGAAAAGAAAAGAAAAGAAAAGAGAGAAAAGAAAAG AGAGAAAAGAAAAGAGAGAAAAGAAAAGAGAGATGGAGAG AGGGAAGGAAGGAAGAAAAGAAAAGAGAGGGAGAAAG AAAGAAGACAGGGAAGGAAGGGAAAGGGAAAAGAG GGAAGGGGAGAGGGGAGGACAAGGGAAGGGGAGAG GGGAGGACAAGGGAAGGGAGGAAGGAAGGAAGGAAGGA GGAAAAGAGGCAGGAAGGAAGGAAGGAAGGAAGGAAGGA AGAAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA GCCTTTCACTTTTGCCTTCAATAGCAGAGTGGCCCTGG ATAT	
DG5S44	169661202 - 169661574	TATTGGCAGAGGGTGAGTCCAGTGTATAAAAGCAACT ATATTTGTGCAATAAGGCAACCTCTAAACACAAGTTAC TACTTCATCTAATGCCACACACACACACACACACACAC ACACACACACACGAGTCATCTGTTCCAAGGCTGTTGCC TTTACTAAGTGATGCTATGTTGGTCCTTGAGGTGGTGC CTTCCTGAGGGTTTTCAAGCATAGCTTTGGCCATGCAC AGTTTTCTTCTTATACACACTCTGAGGAGCCCCGCCGT CACGGTAATGCACCTGCCTCACAAGCTGGTGGGCAGC TTAAATGAAATACACATTTTGCTCCAGGCCAGCACTA GCTCATCAATGTGAGCTGGTGTAGCCTCACC	SEQ ID NO: 62
DG5S45	169693772 - 169693912	CAGTAGCCAGGAAGCTGAGGAACACACACACACACAC ACACACACACACACACACACACACACAAACACACCCCTTCC TGGCTCCAGTTCCGCACCACCCCAACCCCCAACACCG GAAGTAGATTTCTCAATAGGCAGGGCTG	SEQ ID NO: 63
DG5S46	169702377 - 169702678	TTTGCCAGAATGTCCTCACACCAAATAGTGGACCCCTT CTTTTGCTGATTTATCTGCTATTGTATAGGTGTATGTGT GTGTGGGTGTGTGTGTGTGTGTGTGTGTGTTAAGGCAGGT GGTAGTATGTGTAGGGTAGGGTTTTCCCCAGTCACCTGG AGCCCTGAGTGCCTGCTTCCCTAAACTAGGCCAGTTTA GCTGACTGGCTTCCCTTTGTGTATTGGTCCATTCTGCATC AAAAGCATCTGAATTTTCAATCAATCTCTCTCTGAAT TTTCACTTTTTAAAAACCTGACCAGTCCCTTGTTG	SEQ ID NO: 64
DG5S47	169788696 - 169788899	CTCCTCCATGGTAGGGACTGGTTCTCTTAGGCCCTGT ATCCTCAGGCCCAGCATGCTTGGGAAAATGTTTGCTAA TGCTTTGTGACTCAAAAGGAATCACACACACACACAC ACACACACACAAACACACACACACAGTTTTTAATATT ATCAGTCATATCAGCCCCCTGAGGCAGCTGCTCTGTTT CAGACAAACCCTGTT	SEQ ID NO: 65
DG5S119	169843903 - 169844041	GGGTACAGGAGAGTTGTGGTGGGCATTAGTACTACTC CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT AGTGACAGAGTGGGAAAATATTAAAGTTGAGTTCAC ATTAGTGTTCCAGTTTAGCGTGAGC	SEQ ID NO: 66
DG5S953	169866165 - 169866415	CCATGAGTTCAGGCAGTGGGTAAATAAGATTTCCCTT GAAGTCGAATGAAATCACAATGCACCACACACAGGGA CACACACACACACACACGCACGCACGCACATCACACA CACACACACACACACACACACACACACACACACATAC ACACACACAGTCTCCCTGGGGCCAATCTACTGCCCCCT GAACCTCACCCATCAGCCAGGTGCCTGGCCCCGGGTCT GTCTCTTAGGGTTACATGCTCCCGG	SEQ ID NO: 67
DG5S955	169951970 - 169952619	ACTTATGGAACCTACTCAGTGCCAGGTATTGTTGTA GATGCCAGGAGTACAGCAGGGAATAAAACAACATCCC TGTCCTCGACACAAACACACAAGTAAATAGAGAAGGT CAGAGATAAATGCTGTGCAGGAAAACAAAGCAAAGTG AGGGATGGAGAGTGCGGAAGGTTGGGGCACTTTTGT TCAGATGAGTGTGAGGGAAGCCCCCTTGGAGGAGGCA	SEQ ID NO: 68

		CTGTAAGGGGCACAGAATCGAATGAAAGGAGTATGTGA AGGTGCTTAAATTGTTTCTGTTTGGTTTGGTGTGGTGT GATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT GTGGTGTGGTGTGGTGTGGTGTGGTGTGATGTGATGTG GTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGTG GTGTGGTATGGGTTGAGGCTGGCCTTAGGAGCCTGTTG GCCTTCCAGGCCAGTCCTGAAGCCCAGCCCAGAGCAC CAGACTCTGCAGTCAGTCAGTGGAGGGCCCCACATCTC AGCCAATGCATGGCTTTGGGTGGTGACTTCATCTCCCC TAGTGTTCCTTTCCCCCTCTGCAAAATGGGAATGGGA TGGCTCAGAACTCCAGCGGGAGTTAGGAGGAATAAT GTATAGGAAGTATGAGCAGAGTGCCTGG	
DG5S13	169961410 - 169961530	TGATGTGCTCGTTCCCATAGCCCCGCTGTGTGTGTGTG CGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTTTGGTGGGGTGGGAGGGGAGGCAGAAGAGGAAG AGAGGGCA	SEQ ID NO: 69
DG5S123	170015858 - 170015997	TGGTGATCAGCTCAGTGTCTTGGAAAAGAGCAGAAA GTGGTATCACGAACATATCTTCTCCTTTGCTTCCTTCTC CTCACTCTTCATCATCATCATCATCATCAAAAT ATGGATCTGTGAGGCTACCTCTGGG	SEQ ID NO: 70
DG5S124	170041996 - 170042336	GGAGGAGAGACCAGCATTACATTGATTATTGTTGTT TTAAATCCATTACGCACATACATAGGAGAAAATTTCA GCAACAGTCACCCTCTGAACCCAGTTCCTCAGTTCTCT CCAGAGGCAACTAAAATGCTCAATTATTAGTGTATCCT TTTGAAAATATTTTATGTATATGACAGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT AAATAATATTAACATTGGTAATAGTGGTACTAAACAA CTTAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTATCTTTCCAGGAAAAGATACATGGATGTGCCACA	SEQ ID NO: 71
D5S625	170105556 - 170105787	TCAATAAATGATTCTGGGGATGTGTCTGTCTGTCCATC TGTCTCTCTCNAGANACANATACACACACACACACAC ACACACACACACACACACATCCTGTTAGTTCTGTTTAC CTGGAGAACCTTGACTAACATACCCATTAAACCCAAA ATATGTCCTTCAGGGTGTAAATGTTTGGTTGAAGAAAC ACAGAAGTTTAACAATTGTATCAGGCTGGGCACGGCC TATAATCCCAGCATTTTGGGAGGCCACAATGAGNGGA TCACTTGAGCCCAGGAGTTCTAGACCAGCCTATGCAAC ATAGTGAGACAAAAAATGAANAAAATTAGGGGTGTG GTGGAGCGCACCTGTAGTCCTAGCT	SEQ ID NO: 72
DG5S959	170167429 - 170167616	GAGTTCTATGGAACAGCATTTATTGAATAATAACATTT CAGGAAAAAATATAAGCTTTACTGTATATTAAAATAC ATATATACGTTTATATATTATATATTATATTATATTATA TATTATATATATTATATATATTATAATTTTATATATTA TATAGATATAAATCAACTACAAGATCCAGTTCAA	SEQ ID NO: 73
DG5S960	170203240 - 170203459	TTGCCTAAGATCTAGGTGTTCAAAAGAATTTCTCCAAT CCACTTCAGCCTGTTATTATGTATGTATTCTGTTTTAAA TGAGAAACAAGAGTCATTTCTCCAGAATAATAGAAC CATAGTGACACTTGAAGTAAGTCCAGTGGTCCTGATAT GATAATAATAATAATAATAATTATTATTATTATTATTA TTATTTTGAGACGAGGTCTGTATCTGTTG	SEQ ID NO: 74
DG5S16	170280782 - 170281084	ATGGAGAGACACGGAGTTGCTTGAGGGTACAGTGCCT GTAGATACTCAATAAATATTTGTTTAATTAAGAAAATT TCTGTTATTTGTGTGCTCATACATACCATTTTCACTCTGG TGAGTATTGTTCTTTCTAGAGTTTACTTTTAATCTTAA GTATTTTCCAGGTCTTTGTTGACTTCTGTTTAAACCAC AGTACACACACACACACACACACACACACAACTTTGTG	SEQ ID NO: 75

		TACTATAATAGCTTCCCCAAAATTATAATTTAGTCATT GTGATGCAGATCTTCTTCCAAGGCTCTACTTTGG	
DG5S962	170338421 - 170338789	AAACAAACAAACAGAAACACCAAAATGGATTCCAGCA TCTTATAAGTGCTTTCTCTTATGATCGAGAGTAAGACA AGCATGGCTACTCCCTTCTCTCTATTAAATATTGTACT AGGGGTTCTATTGAGATAAATAGGCAAAAAACAAAAC AAAACAAACAAAAAGGCATCCAGATTAAAAA AAGGAATCTAGGAATAAAGGGATTACATCTCTACTTG CAGATGACATGATCTTATGTATAGGAAATCCTAAGGA TCCACTGAAAACTGTTAGAACTAATAACATCAGTAA GTTTGCAGGATTATAAGATTAAATACAAAAACTCGACT GAATTTCTGTGCACTTGCAATAAACACCCAAA	SEQ ID NO: 76
DG5S132	170442700 - 170442947	TCTGCCACACACTTTATGCTTTAAACAAAAGGCCAT GTTGAACCTGTAGAACCAATGATTGCTAATTACTTGG GGCGATACTAGTGATATATTATCTTACATACACACACA CAAAACACACACACACACACACACACACACACACAG GCTTGAGTCCAGCATGGCCTACTGATTTTAAATAGGA AATGACAGTGTAATGCCAGGATAAAGGACAAAGTGC TCTGACCTGTTGCCAAACCTT	SEQ ID NO: 77
DG5S136	170469573 - 170469843	GGGTTTAGGACCCACGTATCTTTTGTGTTGTTGTTGTTG TTGTTGTTGTTTGGAGTTCAACATGTTTATGGTGTGTA GCCATGGTTGAAAGCTTTTATTTTATAAGATAGACAAA GCAGGAATTATTCTCATTTTACAGGAGAAAAACA GAAGGGCTATGTGGTTTGTAAAAGGCCACACAGACA GTAAAGAACACAGCCTTTACATGGTCAGCCTCACATTC TAGTACTCATTTTATTACACTGCTCTTCTCTCTGTGCTG CTG	SEQ ID NO: 78
DG5S133	170480360 - 170480621	CTGGCCTCTTTGCCCATTTTCTAATTGGATTATATGTGG GGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT TGCTGTTGTGACGTTAGAGTTCCTTGTATATTCTAGAT ATTAATCCCTTGCCAATTAATAGTTTGCCAGTATTTCT CCCATCCTGTAGGTTGTTCACTCTGATGATTGTTTCCTT TGCTGTGCAGAAGGTATTTAATTGATATAATCCCATT TATTTACTTTTGTGTTCTGTTGCCTGTGA	SEQ ID NO: 79
DG5S17	170499980 - 170500284	CCATCCAGGGTCTAACTCCAGCATTTGTATAAACTTGG ACAATACTTTTGCTACAGGGTTGTCATTGAAAGTATTG CCTCATTATATTTCTTAGTGGTCCCTGTATGAAGCCAT ATAAGAGAACTTCTTAATTTAGCACTAGGAAATGCTT CTGTTGACTTGAGATGTGTGTGTGTGTGTGTGTGTGTG TGTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTG GTGTATTCCCTAATTGATAAACTATAAAATAATCTTT CTCTTTTCACTTTGGCCATCTGGAAATTTGCCACCAA	SEQ ID NO: 80
DG5S137	170644993 - 170645364	TGGCTTCCCAATCCTAGAAAAGGAAGAAAGCTGCATG TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT TGTTAGATGGAGTTTCTGTGCGCCAGGCTGGAGTGCA GTCACATGATCTCAGCTCACTGCAGCCTCTGCCTCCCT GGTTCAAGCAATTCTCCAGTCTCAGCCTCCCAAGTAGC TGGGATTACAGGTGCGCACCACCACTCCAGGCTAATTT TTTGATTTTATAGTAGAGACGGGGTTTCACGATGTTGG CCAGGCTGGTCTTGAATCCTGACCTCAGGTGACCCAC CTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG AGCCACCGCACCTGGCTGAAAGCTGCAT	SEQ ID NO: 81
DG5S53	170673106 - 170673364	GCCTTCGCAGATTGTACCTCTTCTTTCACCTTCTCGC TGGCCTGTGCTTCTCTCTCCATCGTGGTCTCCACGCCT TGGTTTCTCCTCCATCCCCATCCCCATCTTTCGTGAGCC CCTCCAACCTCTCTCCCCGTGTTTGTACGGTCTCCTGCG	SEQ ID NO: 82

		TTCAC TTGATTTCTCTCACCCACCCCGCCCCAAACA CACAGGCACACACACACACACACACGCGCACACAC ACGGGCCTCTCGCACTCTCCTTCTCCT	
DG5S968	170675807 - 170676033	TGACTCTTGGCCTCTGTGTGTCTCTGGGTTTCTTTGTCT CCCTCCTCTCCACGGTCTCTTGTCTTTTGTCTTCCCT TTCTTGTTTCTTGAATCTCTTTGCCTTTATGTATCTGTCT TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT TCTTTCCCTTTCTCCCTGACTCCCTCTCTCCCTCTTCCAG GCCCAGCTCCCGTAGCTCCTAAGGCAA	SEQ ID NO: 83
DG5S904	170735417 - 170735632	CATTTGGGATAAATGTTGTCTTTAGTTTTCAACTACTTT TTCTTTGGCTTATTCTCTCTCTCTCCCTCCCTCCCTCTCT CTCTCTCTCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTG TGTGTATTTCATGTTTTCTTAATCTATCTGAATTGTTGTG TCGGTTTTCCATGCGAATTTCCAGTTACCTCCACAGTA TTCGTTTCAGAATGCTTCT	SEQ ID NO: 84
DG5S906	170820130 - 170820505	TTGCAGTTTCATGAACCAAGTATTACTGCCTCAACAAT TAAAAACAACAGACAAATTATTTAAAAAACCATGAGG CGAGTGGTGGCTGGTGGCTGGTGGCAGGGCGGGGCA GGGTGGCCTCTGTGTCTCATGCTTTCTGGTTGGTCTGT GGTCTTTGCACTGAGAGCTAGGGCCTTGCACATTCATT CATTCAATTCATTCAATTCATTCTTTGAATTCAACAT TACTATGCACCAGGCGCTGAGAAGGCAGCCTTAGACA GATGGAAATCCTTGCTTTCCGGGAGATTCCATTCTAAT GGGTCAATGATTCAAGTGGCCTCTTCAGTCATTTGTTCA TATGCATTTACTCGTACCTCTCATGTGCCA	SEQ ID NO: 85
DG5S141	170910447 - 170910786	AACTGAACCTGGGCTGTGTCAAGTCTAAGACTTATGCTT GGAACCTGTAAGAAGAACAAGTGTGCGTGCATGCATG TGTGTGTGTGTGTGTGTGTGTGTTTGGAGGGATAGTGA AGTTTTTTCCTACAGCTACAAATAGAACATGCTTTCT ATACAATTGTACTAATCAATATTATTTCTTACATTATC TCCAGCCATTTCCCTATAATTAGACATTCAGATTATTT CAAGGTTGTTATTCCTATAAACAGTGATGTGATGAATT TTTAAAGTTGGTTCTCACAATCCGTCTGTTCTTGTA TGTATCCATCATAGAACTGGACCACAAAGGTTGG	SEQ ID NO: 86
DG5S909	170941109 - 170941259	GGGAGTTCTCTTTCTTCAAGTGCTTAGGGGAGAAAATA AGTGAGAAAAAGAGAGATAGAGGAAGGAAGGAAGGA AGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA AGAAGAAAAGGAAACGAAAAGGAAAGGAAGGAAG AAAGGA	SEQ ID NO: 87
DG5S910	170946679 - 170947010	TCCATGTTATTCTCTACCTGTTGGTTCCTTCCTCATTGA AAATTGGTGTATAGATGGTAGATAGATAGATAGATAGA TAGATAGGTAGATAGATAGATAGATAGATAGATAGAT AGATAGATAGATAGATAGATAGATTTTATTTTGGTC TATCTCCTTTACTAAACAGTAAGCTCCATGAAAATATG GATCATCACTGTCTTATTCACCATTAATTCTCAGCAT ATGGTATTGTCCTGGTATAGAATAGATTCTCAATAAAT GCTTGCTAAATGAATGCATTCATGAGTGAGTGAATGA ATGAATATGCGAGTGGATGAGTGTGTGGA	SEQ ID NO: 88
DG5S911	170985696 - 170986066	TGCTTGAGGGCAGGATCTATATGTAATTCCTTTCTGGA AAACCAGGGATTGAAACAGGATCTGGCATGCAATGGG CTGGATGGGTGAATGGAGAAATAGATGAATGACAGAT GGATGGACAAACAGATGGAAGGAAGGATGGATGGAT AGATGGATGGATGGATGGTTGGATGGATGGATGGATG GATGGATGGATGGATGGATGGATGGATGGATGGACAG ATGGATTGGTTGGTAGATGTGTGGATAGATGGATGGG TGAACAAGCGAGTAGATGGATGAGTAAATGGCTAAAT	SEQ ID NO: 89

		CTGGTGCTTTTCTTCCAGAATCCTGGATTCTGAAGGGA GGCTTTGCAGCCCTTCCTCGTGGATCACTTGCTCTG	
DG5S143	171018986 - 171019237	GGCTGAATTACTGGGCATGTTTCTGAGAAGAAAGAAC TTCTATTTTAATTATATATCTACAGAAACCAAATTGCC TGCTTACAGTTTTACATGTCTGATGATTGGAAGTTTTT GTTTGTTTGTTGTTTGTTTGTTTGTTTCCACAGACTAG CCTCTGACTCCATATATTTCAAACCTTTGTTCTCTTCCA CTACCCACATATTTCTGATGTGAGACATTCTAGAAAAA TTTCATATTGCAAGACGGCTTC	SEQ ID NO: 90
DG5S513	171039003 - 171039366	TTGGCAGGATTTCAGTTCCTCATGGGCACCAGACGGAG AGTCTCAGCAAATCACTAGCTGGTGAAGTGCAGCCACC GCAGTTCTTTATCAGTGGTTCTCTCCATAGGGCAGTT CACAGTGTGGTAACTTGCTTCATCAGAGCAAGCCAGG AAGAAGACCCAGAGACAGACAGAGAGAGAGAGAGAG AGAGAGAGAGAGAGAGGAGGCCTCTGAAAGAGAGAGAG AAGAGAGAGAGAGCAAGAGAGAGAATGAGAACTCCAGA AGTCACTGTCTTTTATAGCCTAATCTTGAAAGTGACAT TCATCACTTTCACTACATTTTCTTCCCCAGCAGTGCTCA GTGGGAGGGGATTATACACGGCCATGGAT	SEQ ID NO: 91
DG5S145	171040948 - 171041151	GCACATTTGCAGAGGTTTGGAGGTCCCATTAGCCAT GCTTCTTGGTTCCTGCACTATGAGTATACGTATGTGGG CTGATGGCCTCATTCACTGGATACACACACACACAC ACACACACACACACACACACACACACCTCACCAGGGA CTTGGGAGTATCTAAATGTTTGAGAATCATAGAGCAG GGAGACATCCAACAC	SEQ ID NO: 92
DG5S146	171073796 - 171074122	GGGCACATACAGCTTTCCTTGCAGGAAAAAACCTGC TTAACTTTGTTTATTATATATTATTTGATCTGTGCTTCA TATATTATTCATATATTATTTGATCAAGTTGCTTCATGT ATTATTTGATCAAGGAATCATGTGTGTCTACAGCACCT ATTAAAAATTCCTGGCACTGAAATTCTGTAGAAAAACCA TTTAGGAAAAAGTTGATCTAACTGTATAATTATTAGTAA AACATATACACACACACATACACACACACACACACAC ACACACACACACCACAAGCAAACAAAAAACCAC CTTAATGGTCTCCTAACCAAGGCA	SEQ ID NO: 93
DG5S147	171107565 - 171107831	GCATGTTCCGCACAGAGATTCAATTAATTTAAATAGGT AGAGGACTTGGGGCAGTGCCTAGGACAACATTACACT CAGGGATGGTGATGATGATGATTATAATGATGATGAT GATGTTGATGATGATGATGTTGATAATGATGATGATGA TGATGATGATGATGATCATGATGATAATGGAAAAGAA GATAGAGGAGGTAGAAGAGGAGACAATCATGATGTTG GAGGTAGACTCCAATCTTCAGAATCAGAAGCTCAGGG TTGGA	SEQ ID NO: 94
D5S462	171134297 - 171134396	AGCTTAATCTATTATTTNAGAGGCAGAAAGTTAACTTG CTTATCCTGAAAAGAAAGTGCAAATATATCCCAAAAGT GCCATTCTTTCATTTCATCCACTCAAACAGATACACACA CACACACATACACACACACACACACACACACCCCTTTTC ACCCCTTGGTAGTGTACAGTCTCTGAGTTGTAAAAAAT AGTCATTNCTTTCTGCTTGAAAGACTGTATTAGCT	SEQ ID NO: 95
DG5S148	171140975 - 171141303	CCAGCATGATCCTATGAATCCTTATAAAAGGGAGATG GGAAAATTTACACACACACACACACACACACACACA CACACACACACACACACAGATAGAGACAGAGAGAAG AGGATAAGGCAATGTAACCATGGAGGCAGAGATGGG AGTGCTGTAGCCACAAGCTAAGGAATGCTGGCAGCCA CAGATGCTGGAAGAGTTGAAGAATGGGTTCCCCCTGA GGGAGCACAGCCAGATGCATGCTTTGAGAGTTTCAGCC CAGTGCTACTGACTTTAGACTTATGGTTTCCAGAATA	SEQ ID NO: 96

		CAAAAAATTAATTTCTGTCGTTTCAAACCATCC	
DG5S914	171219902 - 171220159	CAAACGTCGCTGACCTGAGTCTGACCTGGGCTGCCTCG TGTTACCAACATGAAAAGGGAGTGAGAAAATCTGAGG CCAATTAACCTCTCTCCCTCTCTCTCTTTTCTCCCCT TGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC TCTCTCTCTCTCTTTTCCCTCCTCTTCTTGGAGAC ATGATGAAATTTCTGAAACAAAACCTCGCAGCCCGT TCAATAAAATGCTTTCGCCTTTGGTG	SEQ ID NO: 97
DG5S150	171232854 - 171233077	ACAGTTGCCATTTGCTCATTTAAATGTTAGTGAGGTGT TTTAAAGAGGGTTTGTTCATTTACCAAAAAGGGAAA AAAAGGGAAAAGAAGAACTTATTGTTGAACGAACAC ACACACACACACACACACACAAAGAGCCTGGCTTAAT TTAGGGATAAAGCAAAGAAGTCAATACCCCCACATCA ACTATTGAAACCTAAGCTATTGCTGGAGTTGACAGCG	SEQ ID NO: 98
D5S429	171276128 - 171276490	AGCTCTNCCTAGCATTGTTTTCTTTGCTTCATTTCTC TTAAATGTGTTGGATGCACTTNGTTCCTGCTAACTAAT CTATCTTNCAGTTTCAAATCAAATGAACCCAGAGAAT TTATTTTACATTATTATCTTCAGATTTAGATTTGTTT GCTTTTAATCCTGTCTTCATGAAGGGGAAAGCCATGTG TACCAGCATGGTTGATAAACCACCAAATCGTGAAACT TTGCTTGCTCCCCAAACCCCAACACACACACATACA CACACACACACACACATACACACACACACACACAC ACACACACACACACACACACCTGGGAAATTGGGNAG AAAACCTGGCAAACCTTAAACTAG	SEQ ID NO: 99

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Table 7 The DNA sequence of the microsatellites employed for the association studies across KChIP1 (including Build 33 locations).

NAME	POSITION	SEQUENCE	SEQ ID NO
DG5S1173	169653708 - 169653840	AAGGGAAGGGAGGAAGGAAGAAAGGAAGGAAAG AAGGCAGGAAGGAAGGAAGGAAGGAAGGAAGAA AGGAAGGAAGGAAGGAAGGAAAAATAACTAGGG CCTTTCACTTTTGCCTTCAATAGCAGAGTGGCC	SEQ ID NO: 100
DG5S44	169661202 - 169661574	TATTGGCAGAGGGTGAGTCCAGTGTATAAAAGCAA CTATATTTGTGCAATAAGGCAACCTCTAAACACAA GTTACTACTTCATCTAATGCCACACACACACAC ACACACACACACACACACGAGTCATCTGTTCCA AGGCTGTTGCCTTTACTAAGTGATGCTATGTTGGTC CTTGAGGTGGTGCCTTCCTGAGGGTTTTCAAGCAT AGCTTTGGCCATGCACAGTTTTCTTCTTATACACAC TCTGAGGAGCCCCGCCGTACGGTAATGCACCTGC CTCACAAGCTGGTGGGCAGCTTAAATGAAATACAC ATTTTGCTCCAGGCCAGCACTAGCTCATCAATGT GAGCTGGTGTAGCCTCACC	SEQ ID NO: 101
DG5S45	169693772 - 169693912	CAGTAGCCAGGAAGCTGAGGAACACACACACACA CACACACACACACACACACACACAAACACACC CCTTCCTGGCTCCAGTTCGACACCACCCACACCCC CAACACCGGAAGTAGATTTCTCAATAGGCAGGGCT G	SEQ ID NO: 102
DG5S46	169702377 - 169702678	TTTGCCAGAATGTCCTCACACCAAATAGTGGACCC CTTCTTTTGCTGATTTATCTGCTATTGTATAGGTGT ATGTGTGTGTGGGTGTGTGTGTGTGTGTGTGTGTA AGGCAGGTGGTAGTATGTGTAGGGTAGGGTTTCCC CAGTCACCTGGAGCCCTGAGTGCCTGCTTCCCTAA ACTAGGCCAGTTTAGCTGACTGGCTTCCTTTGTGTA TTGGTCCATTCTGCATCAAAAGCATCTGAATTTTCA TTCAATCTCTCTTCTGAATTTTCACTTTTAAAAACC TGACCAGTCCCTTGTG	SEQ ID NO: 103
DG5S1178	169745438 - 169745539	GTGCTCAATGGCTGTTGAATAAATAAATGAGAGGA GGAAAGAAGGAACAAGGAAGGAAGGAAGGAAG GAAGGAAGGGAGGGAGAGAGGGAGGGAAGGAGG	SEQ ID NO: 104
DG5S47	169788696 - 169788899	CTCCTCCATGGTAGGGACTGGTTCTCTTAGGCCCT GTATCCTCAGGCCCAGCATGCTTGGGAAAATGTTT GCTAATGCTTTGTGACTCAAAAGGAATCACACACA CACACACACACACACAAACACACACACACAGT TTTTAATATTATCAGTCATATCAGCCCCCTGAGGCA GCTGCTCTGTTCCAGACAAACCTGTT	SEQ ID NO: 105
DG5S1592	169794522 - 169794686	TTGAGCTGTTTGGCCTCAATGGCATTATCTCTCT CTCTCTCTGTGTCTCTCTTTTCTTTTTTTTTTTT CACATTGAGCCATCTTCTTACAGCTGAGGTTTTTCA ATAAAAAAGCAAGTTGCTGGTTTCTCTTTAAAGT AGGGCAATCTGGCAGTTCT	SEQ ID NO: 106

DG5S119	169843903 - 169844041	GGGTACAGGAGAGTTGTGGTGGGCATTAGTACTAC TCCTGCTGCTGCTGCTGCTGCTGCTGCTGTGTCCAC TGTTAGTGACAGAAAGTGGGAAAATATTTAAGTTGA GTTACATTAGTGTTCCCAGTTTAGCGTGAGC	SEQ ID NO: 107
DG5S955	169951970 - 169952619	ACTTATGGAACACCTACTCAGTGCCAGGTATTGTT GTAGATGCCAGGAGTACAGCAGGGAATAAAACAA CATCCCTGTCCTCGACACAAACACACAAGTAAATA GAGAAGGTCAGAGATAAATGCTGTGCAGGAAAAC AAAGCAAAGTGAGGGGATGGAGAGTGCAGGAAAGGT GGGGCACTTTTGTTCAGATGAGTGTCAGGGAAGC CCCCTTGGAGGAGGCACTGTAAGGGCACAGAATC GAATGAAAG GAGTATGTGAAGGTGCTTAAATTTGTTTCTGTTTGGT TTGGTGTGGTGTGATGTGGTGTGGTGTGGTGTGGT GTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT GTGGTGTGATGTGATGTGGTGTGCGGTGCGGTGCG GTGCGGTGCGGTGCGGTGTGGTGTGGTATGGGTTG AGGCTGGCCTTAGGAGCCTGTTGGCCTTCCAGGCC AGTCCTGAAGCCCAGCCCAGAGCACCAGACTCTGC AGTCAGTCAGTGGAGGGGCCACATCTCAGCCAATG CATGGCTTTGGGTGGTGACTTCATCTCCCCTAGTGT TCCTTTCCCCCTCTGCAAAATGGGAATGGGGATGG CTCAGAACTCCCAGCGGGAGTTAGGAGGAATAAT GTATAGGAAGTATGAGCAGAGTGCCTGG	SEQ ID NO: 108
DG5S13	169961410 - 169961530	TGATGTGCTCGTTCCCATAGCCCCGCTGTGTGTGTG TGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTGTTTGGTGGGGTGGGAGGGGAGGCAGAAAG AGGAAGAGAGGGCA	SEQ ID NO: 109
DG5S123	170015858 - 170015997	TGGTGATCAGCTCAGTGTCCTTGAAAAGAGCAGA AAGTGGTATCACGAACATATCTTCTCCTTTGCTTCC TTCTCCTCACTCTTCATCATCATCATCATCATCATC ATCAAAATATGGATCTGTGAGGCTACCTCTGGG	SEQ ID NO: 110
DG5S124	170041996 - 170042336	GGAGGAGAGACCAGCATTACATTCAAGTTATTGTT GTTTTAAATCCATTACGCACATACATAGGAGAAAA TTTCAGCAACAGTCACCCCTCTGAACCCAGTTCCCTC AGTTCTCTCCAGAGGCAACTAAAAATGCTCAATTAT TAGTGTATCCTTTTGAAAATATTTTATGTATATGAC AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TTCCCTTCCAATATTAAAAATAATTAACATTGGTA ATAGTGGTACTAAACAACCTTAGGGTGTGTTTTTTT CATTTAATAGTATATTTTTAGTATCTTCCAGGAAA AGATACATGGATGTGCCACA	SEQ ID NO: 111

D5S625	170105556 - 170105787	TCAATAAATGATTCTGGGGATGTGTCTGTCTGTCC ATCTGTCTCTCTCNAGANACANATACACACACACA CACACACACACACACACACACATCCTGTTAGTT CTGTTTACCTGGAGAACCTTGACTAACATACCCAT TAAAACCAAAATATGTCCTTCAGGGTGTTAATGTT TGGTTGAAGAAACACAGAAGTTTAAACAATTGTATC AGGCTGGGCACGGCCTATAATCCCAGCATTTTGGG AGGCCACAATGAGNGGATCACTTGAGCCCAGGAG TTCTAGACCAGCCTATGCAACATAGTGAGACAAAA AAATGAANAAAATTAGGGGTGTGGTGGAGCGCAC CTGTAGTCCTAGCT	SEQ ID NO: 112
DG5S959	170167429 - 170167616	GAGTTCTATGGAACAGCATTTATTGAATAATAACA TTTCAGGAAAAAATATAAGCTTTACTGTATATTAA AATACATATATACGTTTATATATTATATATTATATT ATATTATATATTATATATATTATATATATTATAATA TTTATATATTATATAGATATAAATCAACTACAAGA TCCAGTTCAA	SEQ ID NO: 113

Table 8: The Build 33 location and size of KChIP1 exons.

EXON	START (NBCI33)	END (B33)	Size (bp)
1a	169716298	169716511	214
UTR 1	169848417	169848523	107
UTR 2	169861083	169861154	72
UTR 3	169864589	169864679	91
UTR 4	169867066	169867173	108
1b	169867120	169867180	61
Ins-r	170075401	170075433	33
2	170081305	170081429	125
3	170082868	170082937	70
4	170084380	170084450	71
5	170085260	170085367	108
6	170095347	170095451	105
7	170096383	170096445	63
8	170098306	170098353	48

Table 9. The Build 33 location of SNPs found across KChIP1 after the first round of sequencing that was limited to the exons and flanking sequences.

START (B33)	MARKER	VARIATION
169716196	KCP_e1a_249924	C/G
169716299	KCP_e1a_250027	C/T
169716321	KCP_e1a_250049	A/C
169740666	KNB_24222	A/G
169740703	KNB_24259	A/G
169741172	KNB_24728	G/T
169746339	KNB_29895	C/T
169747941	KNB_31497	A/G
169751683	KNB_35298	A/T
169751753	KNB_35370	C/G
169751753	KNB_35399	A/G
169848476	KCP_UTR1_382206	C/T
169848542	KCP_UTR1_382272	A/C
169861338	KCP_3UTR2_395068	A/G
169864750	KCP_3UTR3_398480	C/T
169864875	KCP_3UTR3_398605	C/T
169866181	KCP_e1b_399912	G/T
170081291	KCP_1152	C/T
170081464	KCP_1324	G/C
170081473	KCP_1333	A/G
170082788	KCP_2649	C/T
170085097	KCP_4957	C/T
170085115	KCP_4976	C/T
170085151	KCP_5011	A/T
170085191	KCP_5051	C/T
170085217	KCP_5077	A/T
170085342	KCP_5202	A/C
170095344	KCP_15204	C/T

170095540	KCP_15400	C/T
170096291	KCP_16152	A/G
170098209	KCP_18069	C/T

Table 10. The DNA sequence of the SNPs identified across KChIP1.

NAME	SEQUENCE LISTING	SEQ ID NO.
KChIP1	See FIG. 1	SEQ ID NO 1
SG05S872	<p>TGGCTGTCCCCTCTGCCTGGAGCAGGCTTTGCCAGATGTCTCTC CTGGCTCACTCCCTCACCTCCTTATGTCTTGACTCAGAGGTCAC CCTTCCAGATTAGACTGCCTGACCCCTTCTGTGCTTTCTGTTTT CTCCTTATTACAAATGAATCTGCACCATATTTCACTGATTGTGT TTGCTGCATGCATGAGGGCTCACATAAGGATGTGCTTTTTGTCC ACTTTGTTTCATTGCTGAATCACTAGCACTGACAGCTGTACCTGG CACAACTGGGTGCTTAAGAAATATTCTTGAATCAAGGAATCAA TAAATGAATGTTATAGAGAAAGCAGGAGAATAGATGATAATTGA GAAACTGAAGCCCAGAGATGGGAAGTCACTGGCCCCATGTCAC ACAGCAGCAAATGCAGAACCGGTCCTGGAACCTCAGCCTCTCAG CCCCGGCCCTGTCTCTCTGTGCTTCTCACCCTTTATGTAAG TTTTTTCTTTATTTGTGGAGCTCTCAGCAGGCATTTTTCTCTCT GTGCTCAGTTGGCATTTTTCCCTTGAACCAGCTGTGTCTTCACT CTCTTCCCCATTTTCTCCAGAATATGTTCTTCTGTTAACTGAA TGTTCTCTTTTTCTGCAGGTCTGGCCCACTGCAATATCCAGAG ACTTTTCGGGTGCATATGAAAGAAAAGGAGCAGGAAGCCAAGAT GCCCCACCTGGCTTCTACATCAGGGTGATCTGCATAGTAAGATG CAAAGACACTGACATATGCCTGGGGGTAACGAGGGCAGTGGGGG GAGGGAGCTAAGCCAAGATAAGCCTCCTCCCCACCAAACATAGG TGCTACTGAGCAATGATAGGGGGCATGCTGTCTGCTCTGGTACT TGCGTAGGGAATGCTCTGAGAAACCTCACTAAATCTGCCCTCTA GAGTAGAGCAACCTGGGAGCTCAGGCTTCCCTTTCCTCTGTGTG ATGGGTTGGCGGTCCTTAGAGCCAGCCATTTT [A/G] TCCTGCT CCTTCTCTCCTCCCCCTTCTGACCAATAAAGATTGTGTGCTTCT GCCCAGTCAGCAGGGTGGGCTCTCACTCCATCCTGCCTCTGGTA TGACAGCACAAATCCCTCATTCTTTATAATCATTATAAAATAA AATAACTACCTTTTAGAATACTTATTTGATATGAGGCACCTTGC AAACCCACAGTCCTGCATATCCCATTTGACATATCAGGATGCTG GGCTTACAGGTTACCCCAGGGGTGGAGTTGGGCTCAATCCTAGG ATTGTCTGCATCTGATTCTGAAGCTTGTCTTTTCCCTTATA CACAATCATTCACTTCACTTCAAGTAATTTTAAATTGAGACA TACTATGTACCAGCACCTGTTCTAAGCATTTGATTATGGTGATG AATGAGGCAGACAGGGTCTTCCCACAAATAACTCACTTATTC AAGCAGTGGGAGAAAAGCAATGAATGGGAAATAAATGCACAAA TCAAGTAATGTTGGATGGGACAACCTGCTGTGGTCCCATTGAAAC AAGCCCAGAGTGAGCCCAGTGTAGGGACTTCTTCACTGACTGGT TGGGAATTGAGTGACAATCGGTTGCTGCATGCTGATGGGTGCCA AATACAACCGTAAGGAAACACTCCCCTGGGAGGGAGGCGGGATC CAGGTTAGGAAAGAGCCTTGGATTGAGGCAGAGTGTCAGGAAGT GGGGAGGTACGCAGCTGACCTTGGAGAAAATCCCTGAGTGGTGTC</p>	SEQ ID NO. 114

	AGATCTCTTGAATCTCTGAGTGGCTCAGAGTCTTCCTGGAAATG CAGAAATCCCCATGCCACTTAGGGGCATCTTCATTCATCTCCAG CCCTCCTTTATTAAAGTCATGTATACCATCTCCTCTCTTATGCTT AATGTCATGCCACTCTTCAATCCTTGTCCTTCTTTCCCTCTGT GCCTGCTTGTGGTTTACTCCTGCTGACACCAAAGGCTGAGGAGG ATGAAAGAACAATTCCAGCCCTGAC	
SG05S873	GGTAATTCTTAAGCTGGCTGGGCCTAAAACTGCAAACTGGTATT GGGCATGCCAGAAGGTAACCATAAAATGGGCTATTTGGAGATTTT TAGGAAGAAGAATGACATTTTGTTCATTCCATTCCATTTTCATT TCATTCCATTAATACTAAAAATATTAATAAGCATCATTTCTA CTATATATCCAGAAGAGAACATGGTCTTAGGTCTTTTAATAAAT GAACTTCAGTTGCAAACTTTCTGCTGTGACGTTATATTTCTCTT TCCACCCTAGACCAGCCCCAATGGGGCCATGAAGTCAGATTTT TGGTTCATGGTGTGTCGGGGCAGCATAGCCAGAATTCCACTT CCTTCCCTGAGGACACATTTATTCTGGTAGATGTGCTGTTTTCC ATTTAAATGTCCTTTTGGCAATAAAAGAGCTGGCTCCAACAGCAG ACCACGGGGCTGGCTTTGTGCGGCAGACACCACGTGTTTCATGACT GGCAGCTTTGTCTGGAAGAGGGAGCTTTTAAATGCAGTTCTAT GCTGACTCTTTGGAGTCTTCCAGGAAGATAACTGCTATTGCAT TGCATGCTTAATTTAGAGCACCTATTTTTCCCTCTCCTTCAAGG TTTCTGTATATCTTCTCAGTTCATGAAATTAATTATTTGGGTAC AATAATTGTACAAAGGCACCTTTATCAGACACTTCGTATAAATTA TTTCTCATTCTCAAGGCAACTTGGAAAGGTCAGTCTAGGGGTCA GCTGCTACTTTTGGTGATCAGGCATCACCCCTCCTTCTCTTA GTACGTTATGACAGTGGCAAGTGAGCATTACCTGTGGACCCCAA AGGAGTTCATTTCCCTAGAGCCAGCCATTCTCAGTTAATCTGG TCTGTGACACACTCTGTCCCAGGACACTGAGCCTTGAGCATGTG AAGGTGTGGGCTCTGCTGGGGGCTTGGCAGCCAGCACCTGTCTG TGTATCACCTGGCTCCTGCGAGCGAGAACCTGC [A/G] GTGTGAT TTCTGCAGCCTGGCCCTCTGAGATTCCATGGCTGCTGACCATTT TCCACTTTCCAAGACTGTTACATTCCCAGCAATTCTGTGAGGC CCTGGCCTTCAAAGGTGTTCAATACATTCTTTTTTTTTTTTTTT TTTTTTTTTTTGAGACAGAGTCTCACTCTGTACCCAGCCTGGAG TGCAGTGGTGCCATTTACAGCTCACCGCAACCTCCACCTCTCGGG TTCAAGCAATTCTTCTGCCTCTGTCTCGCAAGTAGTTGGGATTA CAGGCACACATTGCCACTTACGGCTTTTTTATCATTATTATTAT TATTTATTTTTTAGTAGAGATGCAGTTTTGCCATGTTGGCCAGGC TGGCCTTGAACTCCTGGTCTCAAGTGATTACCCACCTCAGCCT CCCAAGTGCTGGGTTTACAGGCGTGAGCCACTGTGCTGGGCCC CATTTGTTATTTAAGGGAGAGTCCGTTTCTGCTGTTTGTAACCTA AGGACCTGTCTGATCTCTAGGAATTATTGACCCAGTTTTTCAGA TAAAGAAGTTAAGCTTGAGGTTAGAGCTTTTGAGCAAAAACCTCC TCTCCTAGAGAACTCAAGTATCCAGGAATACTCGGTCAAGGCTG GGCTGGACCAGGTCTGTAATCCTGATATTCAGAAAAGGGATGAT TTCTCCTCTTTGGTTTGGTTTCTCACTGAGGCCTGCACACCAG TTTATTTCTGACTTGTGCATTCAACATGGGCAATCCAGGTCA ACAAAGACTGGCAGCTTATTCCTGAGTACAGTTCCACCAGGTAT GGCACACAAAGTGATATGAGTTAGAACACAGATGGATATAGATG TTTTACAAATGTAAGTTTGCATAACACACACACACATTGCTA TGTGTTAGAAAAATACAATAAGCTCATCTAATTTATTATTTTCAT GTGTCTTATTGCTCAGAAAGAGGAAAAGATTTTATTGAAGTTGA	SEQ ID NO. 115

	GAAAAGAAATTGAATTAATAATA	
KCP_rs31 5773	AGAAACTCCGACTGTCTTTCAGCACACAGAAGACACTGTACTGG ACCCGGACATTAGGCAGACACCCACGCCTGACTTTCAGGAGAAA AGAGAACATGACTAACGGATATTCTTAGTAGATGGTTTATTAGA AAAGAGAACATCTTCCAGCATGTGTCTCGGGGTGATGGGTGTGG GAAGCACTCAGTCCATAGTCCTGGTCCCTGGCTTCCCCAAGCCC AGCACCATGAATGTACAGTGGAAAGCAGAGGGTGCAGCGTCTCA GAAAGATGCTTCCACTCACAAGGATTGGAGCTCACAAGTGAGCT CCATAACCTGCAAACCAGAGAAACCTGAGACACTGCCCTTGGC CATTTTATCAACGGAGACTTTATTGTGATTATCCCGGCAGGGGG CCGAGCTCTCCTCTCTGCAACAGGAAATGCTCTTTAGTGAAAAT GCAGCATTCTCTCAAGGGTAACAAAGCTGAACGCCTGCTTAGCT TATGAACCCCTCAGTTGGCCTAGGTGGTGCAAAGACCCTGCTGTT ACTGCTTTGATCATCAGTACTGTGGACTGTACCAGGAGATCCCT GGGAATGTGCTCTGGGCGGAAGCAGCTTTTATCTTTGGCCCTCA CCCATGCTTTATATGGTGAGGTTGGGAAAATGGCACAAGGCTTC TCCTGAACCTCAAATCAACACCCTTGCCCCATTTAGATCCTATC TGGCTGTTTCTTGCTAATATTACTGCATCACTGCACCATCTTTC CTATTTACAGCAAAGTGGAGTCATGTGTGGTTTATGGGGTAGATG GACCCCAAACCTGATAATATGAATCAAGCTATGGTGTCTTACTCC CTAGGAAATGCACAATTTTCTGGAAACCTACAGAAGCTTCAAA TGCAATTCGCCATGCAAAGCTAAGTCAGCAGAACCAACCGTTTGG CTTTGGAGGCTAGTTCAGTTCCGCGGACAGGGAGAAAGATGAGG CAGACTGTGGTTTTTTCAGTTCTGAGCTTAC [A/G] GAGCTCC AAAGCTCCCTCTCTTCCACCCTGGCTGCACTGTTCTTAATTTT AGATAATACCCTGCCTTCTCGTATTGCTGCTGAGCTCCTAGCAT CCTCAGTTTATCTGTCTGTGAAATGAAAAATCTAATGTTAAATT TTTTACCTATGGCATGAGAGAGATGGCTATGGCTCTTGTGAGCC TCTCTGCAGCCCCTCTTTTCTTCAATCACCCCTCTGTCTCTCCT GCCTTCTGCTTATTCTCTCTCTCCTCCCTCATCCCCACTTTCCAG TGGGTCTCTGTCTCTCTTTTTTTTTTTCTTTTAAATCTCTCTA TGCCTCCAGCCGAGAAGATAAAGAGTGATACATCTTCTGTTAA AAAGTTTGTCTTTGCAGAAACACAGCCAATTTATGATTCTGGCC TTCCAGCTAGGGACAGTGTTCATTTACATTTAGGACCATGAGG AGAGAGGCTTAGCTGTGTGTTTCTGAGGCCGGAGAAAATTACAG TGATATATAACAGTGTGCACTCATAGAGGTGCTGAGCCGGGGT TGGGCTCAGGCGGCCGCTAAGCTCAGAGTGGAAGTTTCAGAGG GGAGGCAGAAAGGAGAGGTCTATAGCTCCTCCAGATTCTAGGTA TTAATTTACTAAGATATTCCTAAGCCAGAAAAACAGAGACAGAAG ACAAAGAGAAAGAGGGAAGAAGAGCAAGACAGAGAGTTAGAGAG AGACAAAGAGAGAGAGTTAGAGACAAAGAGAGAGTGAGAGGAG AGAGAGCAAATATTGAAAGGAAAAGGAAAAGAAAGAAACCTGA CAGCTCATGAACTTTTTAAAAAGTTACAAATTAGATTTGAAGAG ATGGGCAGAGGTTTAAGATTTCTTCATTAGGCTGGGTGTGGTGG CTCATGCCTGTAATTGCAGCACTCTGGGAGGCTGAGGGTGGCAG ATCATCTGAGGTGAGGAGTTCGACACCAGACAGGCCAACATGGT GAAACCCTGTCTCTACTAAAAATAC	SEQ ID NO. 116
SG05S876	TATATACAACCTGGAAGCTCTTTTCCAAACCATATCACAGACAA AGAAATTGAGGCTTGTAAGGTGAAGGGGCTGCCTTTCTTTG CTCACAGGAATGTGAGGATGATACAAAAGTGAAGGATATTGGCA TTCTTCAGGCAGGGAGATAACCTGGACAGGGGTGGTGCAGCAGG CATGTGCATAAAAGGAGCAAGAGAAGCCTTCTGTCTGTGAGCA AGCTTGCAAGCCAGATGGAGAAAAATGAAGTAAAGTCACCCCAA AGCCTGGATTCTCATCTGGAGTGCCTCTTGCCCTCTTGCCCTTCC CAGAACGCTCCAGCTTGGCACTGGGCTGGAATTCCTACTAAGAAT TGAGTTGATTTCTCATCTGAGGCCCTGGGCACAATGACAAGGG	SEQ ID NO. 117

	<p>TGGTTTTCTCGGATCTGCAGTGAGCATTACACCAGAGTGTGGGA AACAGTGCCTACTCAGGGACCCCACTCTGGGACCCAGGGCAAAC TTGCCATCGTCTCCAGTCAGCTCATTAGCCGCCAGGACTCTGC CAGCCCATCCAGGCAGTGATGTAATTACCAAAATGGAGATGAAT ATTTAAAGGGACTCTTACTTAACCGATATACTTCTCTCCAAGT TCCCTCCTTCACCGGCTCTGGATGAATTTCTGGAGGGATTGCTC TGACATAGGCCCAGAGCTACCTGTGGTTTGACCTCATCATGAGG CCTTTCTTCACCCCTTCTTGGTGGCTTGCCCTTGAGGGTGTAGG AGATGGTCCATTGTCTGACTGTGAACAGCAGGGCAGCTCTTATA TTCTCCATCAATGGATCTCTGGGGACAAGACCCAGATGGGTGGG GGGACAGGGGAAGGAAACATAAAAGCCAAAGGGACTGGATACCT GTAACATAATTACCCCTTACTGTTTCTGTCAACAGACCTTAGTG CCACAAAGGATTGGGGGTCAATTTGTGACAATGTATGTTGTAAAA TGTAATATGCAAGTGACCACAAATCTGAAAGC [A/G] GTATAGA GCTTTGGTTAAATAATGCAGGCTCTCCACTGGCATTATTATTG TTGTTAGGAGAGTCTGGTGTCTGTTCAAGGGCTTTTCTGTGCT ATGGATTATCTCTGTTTAGCACAAATATCTTGTGTCCCTGGAA ACCCCTTAGTCCTGAGAAAACAGGGCAGTTGGTCACCCCTTG TTCAATGCAGGCATCAGTTCCACTAGGTAGGGGGTCTTAGCTGC ATTTTAAAGATAAGGAAATAAAGACTTAATGGGTTGGAATAACT GGGTATGTGCACATAGCTAAAGAATGGTTACACAAACAACCTC AAGTCAAATATTAGACCTGCGTATTCCTAAAATCCCTATGGCTG TTTGCAATAACTTGAGGCCAGCCTCCCTCTCTCTTTTCTAAGC CCTCTTTACCTTTCTGTGTCTCTGATGGCTGTTGTTTATCAAG GCAACCATCGTGATTACATCCTCAAAGCAGCTTTGAAATTCTAC TCCTATAGGCTCCAAAACCTTATTATCCAGGTTCAAGTATTGCT CTAACTAGGTGAGGTCTGAACAGACCCAGATTTCAAGCATAT TCAGGTGGATTTGTTTAAACAGAGTGTGGCTACTGGAACATCTGG AGCCCAAAGTACACAGGAGGCAGGAGAGAGCCTACTTTCCTGAA GAGAGGGACGGGCCAACTGTCCGACAAAGAGGAGGTGGGCATT TTTCTTTGTAAAACAAAAGTATCTGAGACAGGGGTCAAGTCAA TTCAGAAGCTTATTTTGCCAACTTATGGACCATAACCCATGAC ACAGCCTCAAGAGGTCTTGAGAACATGTGCCCGAGGTGGCTGGG TTACATCTTGGTTTTTACATGTTTGAGGGAGACTGAAGACATCAG TCAATACATGTGAGGCATACATTGGTTGGGTCCAGAAAGGCGGG ACAACCTCAGAGGTGGGGAGTGGCTTTTAGGTCATGGGTGGATT CAAAGATTTTCTGGTTGGCAATTGG</p>	
KCP_rs95 2767	<p>AAAAGTAGCATCGAGAATCAATTTGCATCTCAGAATTGGGATCC CTGCCCTAATCTCTCTACTTTATGCGGCCGTGTCTGCTTTTCA TGACTCTAGAAAGCAGAGGAGAAAGTGGATGTAAGATATAAATT AGTCTGTCTTGTAGGGCTTTCTCTTGGTCCCATTCTGGGACCAG CCAGTGTCCATACCTGTGGCCTTTGGTATCCAATTTAAGGCAGT TCTTCTCTTTCCATGATCACACAGTAAAGGAGCCCCCGTATACA GTGCTCCAGGACTGAGTCCAGTTTTTAGTGTAGCGTGCAACAAG AGCAGAAAAGGCAGAGTTGGGAAGGACATGTCAACGGGCAGCAA TGAGGTGGTATAAAGACCCTGGGCATTGAGGGAACAGAGGGA GAAAGGTCTGCTTCAAGGACCAACTTGGTCTCTTCCTATCTCTG CCCTGGCAGCACCAGCAGCTGCACATTGGCCCTTCTTACCCTT CCATGGCAAAACCAAG [G/T] TTTCTCTACCTCGCCTAGCCGGC CCCTGCAGACTTGCTGACACAGCTGAGTGCGGAGTGATCTAGA CCCCAATGAGGCGCCCTTCTCTCAAAACAAATGAGCCTTCGA AACTCCAGCAAACAGTGCTAATGAATTGCCCTCGGCTTCTTAGG CATCATTTTCTCGTAATTATAATGGGAAGAAGACATGGAGTCCC ACTGAGAACGTGGAGCTAGCCTGCCCTAGAGCAAGGCAAAATC CCTCTCTGAGGACCACACTCAAGCAGAACTGATTTTCTAAGAC TTAGAGAAGAAACAAATCTGATTTAATCTTAGGAAATTGCTT TTTTTAACCCACCTGTGTAAGCCTGTATTTAAATGCTAATATAT</p>	SEQ ID NO. 118

	TTGGCCTGCCGGGATGCCACATTTATTTTCTTCCTTAGCAGCAA CAAAAATCATTATTTATGTAGAAATTCAGCTCCTACCTGCTCTC CTGAGTTCCTCATCTTCATTTCCATCTACCAGCTGGA	
KNB_2422 2	GAGGGGTTTTTAAGATTGTGTGTTCTGAATGGCCTGTCTCTGAC TGGAACCCAACTCCGTCCCCAGACCCACTTCCATCTTTTTCTGT GAGGGGGACACACTCTTCAACTTTTCCAAAATGGCATCTACCA TGGCTTTTCTGATTAAAAGCAAACGAAACACACCCTTCCTATAA TCAAAAATTTAGAAAAGCAGCAAAAATAAAAAGGGGATAAGGAA GAAAACAGAAATTAACCACCATCCC [A/G] CCGCTAAAATTTTG ATGAGTTCTCATGTGTTTCTTNCAGCTGATTGTTGTTTGGCAT ACATTTATTAA	SEQ ID NO. 119
KNB_2425 9	CACTTCCATCTTTTTCTGTGAGGGGGACACACTCTTTCAACTTT TCCAAAATGGCATCTACCATGGCTTTTCTGATTAAAAGCAAACG AAACACACCCTTCCTATAATCAAAAATTTAGAAAAGCAGCAAAA ATAAAAAGGGGATAAGGAAGAAAACAGAAATTAACCACCATCCC NCCGCTAAAATTTTGATGAGTTCTCATGTGTTTCTT [A/G] CA GCTGATTGTTGTTTGGCATAACATTTATTAATATTGGAATTAATA ATATATATGGCACTTTATATCCTAGAAAATAGTAATACTGTAAA TGTGTTCTAGAAATGGGAGCTGCTGTTGCTCTTATTAGAGAATT CAAACAAAGAAGGGAGGCTCGCTGGGGACAGCTTCTGGGGGAGG ATGGGTACCGCTTTGAGACA	SEQ ID NO. 120
KNB_2472 8	AGGTATGAGTCAGTTGAGTGGGGACAGGTAATAGAGAGCTAGAA CTGGCTGGCCTTATGGCCTCCAAGGCATTGGGGAGCCACTGTAC ATTCTTGAGCAGGCAATGACTTCACAAAAGGATTTCTCAAAGGT TAGTCCTGCAACAGAAGACAGCGTGGATTGGACTGGAAGAGTGG GAGGGCAGGTGGAGAAGGCATTG [G/T] CTGCAAGTGGGGAGCA GCCCCTGGGGGCCCAGCCAGTCCCCTGTGCCCTGACAAGTGGTAT GGCATGGATGGATGGCTCTACTTCTGGGCCGCCAGGATGGACAG GTACTGGTTGCTCTTCACCATGGCGATAATGAGGAGGCCACCGG TCAGCAGGAAGGTGGGCCAGAAGAGGGAGAGAGAGGGCCTGG GGCCCGTAGAGGCGCTGGAAT	SEQ ID NO. 121
KNB_2989 5	CCCCATCCCTCCAGTTCAGTACCTGCTGGTTCTGGTCCCGAGTG TCCTCCGTGTGGTACAGCACAGCCCACCTGCCGGCAGCTGACAC GTTGACCCACAGGCATGGGTACTGGGGCACCTTCTTGCCCTTCA GCT [C/T] CTCCTGGTCCCTGATGTTGGTCTCAATCAGGTGGCA CTTGGAATCCTGGGTCCACACGCTGAGGAGACCACACACATGCA CACATACACATCTCAGAAGTGGGTGACACACAGAACACCCATT GAACCCATTATCCCTGGGAGCCTCTAGAGGGATCCAGGACTGG GCTCCTCATCTTGTCTTCAGCATCCAGCAATAAAGGCACAT	SEQ ID NO. 122
KNB_3149 7	TTCCCTGCACTTGAACCCTAGAACCCTAAGAATGAGCATCGTCTT GACCCCTGCTGCCTTGAATGAGGGTCAAGGAGAGGGGTGAGTAGA AGGCCAGGGTTCCCTTACAGATGCCAGACCCCTTAGGAGAGGGTTG GGGGGTGGGCAGGCCNGGAGAGCTCAGTACCTTTTCTGGTAGAG GGGCAGCACAGTCGTGACCAGGATGTAGTAGGTGATGACGGCAC ACACCACCATGGTTACACCCAG [A/G] CAAAGGGCTCGTGTCTC TCCCCGCTTCTGGGCCATCACCAGCTTCTTACCATATTCAGTG GGGGCAGTGATCATTTCTAGGTCCACAGAAGCAAACAGAAGTGA GATCAGCCCAGTTCACAGGTGATCCACAGAAAGAGAGGACAGGT GAGAGGGGAAGGTACTCAACTATTAATATCACTCTTGTTTATAT TTGGAGCTTTGCAACTTCCAGAAGTCTTGCTTTTGGACCCCAT GTA	SEQ ID NO. 123
KNB_3529 8	AGAGGAAGGGAGTCCCTGCCTGCCTCCCTCCCTGCCCCGTGG CAGGCTGCTTTCCCC [A/T] GTCTCCCTCCAGCCCGGTCTTCAG AGAAATCACTTCCCAAGTGCTTTTCAGGCCCGGTACTCACAGTCT TCCCCGCGTCTGTGGGTCTTGAGCAGCAGACAGTTTCTTTCTG CCTGGACCC	SEQ ID NO. 124
KNB_3537	AGCCCCGTCTTCAGAGAAATCACTTCCCAAGTGCTTTTCAGGCC	SEQ ID

0	GGTACTCACAGTCTTCC [C/G] GCGTCCTGTGGGTCTTGAGCA GCAGACAGTTTCTTTCTGCCTGGACCCCCGCCCCACCCCAAAA GAGGCCACAGAGCTTCA	NO. 125
KNB_3539 9	AGCCCGGTCTTCAGAGAAATCACTTCCCAAGTGCTTTTCAGGCCC GGTACTCACAGTCTTCCCGGCGTCCTGTGGGTCTTGAGCAGCAG AC [A/G] GTTTCTTTCTGCCTGGACCCCCGCCCCACCCCAAAA GAGGCCACAGAGCTTCA	SEQ ID NO. 126
KCP_rs31 4129	CTTATCTCCACCCTTCACTTGACCCAAGAATCAAAGAACCTGAA ACTGAGACTTGGAGGCTTGAAGTCACTGGTGCAACCCCTAGGGGC CAGAACTAGATTGGAAGCTGGCCCTTCCAGATGGCACAGCTTGG TCTGTCTCTGATGACCCTGGGGCTGCTCTGAGACATTAAAAATC ACCTCGATCATAACAGTAAGCTGCCACCTGAGGCTCTGGAGGTCA CCCTGAGTTTCCCCAGCCCCCAGGGAGGTGGGTGCAGCCTGGCC TTCCCTGCTGAGCGAGCTCACCACCTTCCCTCCCTCCTGCCTCCA GCAGGCGCGAAATGAAGGCAGCCACTCAGGCCTCCCTGACACAC TCTCAGGCGGTGAGTGCCCTTCTCCACCCCTTTCTTAATTGAAT CTTATTAACAGGAGACTACAGTGTCTGTTAATGGGCACCATAG CACCAGAGGGTCTAAGACCAGCTTCAAGCCTTGACAGGCAGATTG ACAGAGGGATGTAGGA [C/T] CTGGAATTCAATCTCAGAAGAGC AATTTTCCAAGGATGATCCTCTGTCCACTCAGAAGCAGGAAAAG TCCTCCTGGGGCTAATCCAGAAATGCCAGGCCCCCTCCTGCTT CCCTGGGGGAGAGATACACAGTGCAACAGGCTGCCATTTATGAG TATAACCGAAGGGCTCCTTGCTCGTGATACTCTGAATAAGTTAT TAAGGGCTACATATTATTTGGAAATCATAACAACTTTAGCAT TCTTCCCAAGGGAAGGTGGGAACAAACAGGGAAGGGGGGCCGTG GGGTCTTCTGCTCCCCCTAAATGAGCCACAACCAAAAGGCATTG ACAAGCCCTGTCTCGAGGGTTTGTGGGTGAAAACCCAGGTCCT TTGCTGGCTGCGGGGTTGTGTGTGACAGATGGCTACAGGTGGAG GGCAAGAAAATAACAATGCTGCAACAATAAATATTGACGGTTTG CATTAGTACGGGTGTGACAGATCACAATAATCTTC	SEQ ID NO. 127
KCP_rs18 3398	TACTTTTCAGCCTGAGGTCTCCTCCTCACCCTAACACCCTTCC CTCCAATCAAACCTGATCCATTGTACCTACAAAAGCCCGTCCCA CCTCCTAGCCTTTGTTTCACTGGGTCTCTGCTGGATCACCAT CCCTCCACATTTCCAGGTGTCCCTCAAGACTACTCAGCAGCAGC TATCCATACAAGTTCTCAACCCTGGCTTTCTTGCCCTCAAGTA ACCAAGTTCACTCCTCCCAAGTCATATAGCCCTCTATTTACATTC TTTTCTGGAAGCTATCATTTTTTACGTGCCATTGTAGTGAGTGT CCTCGCTAAGACGATATTTTCTTTGAGGGCAGTAACCTTTCTTA TATGCTCTGTATCCCATGAACTTAGCAAAAAACAAGGGACAGA ACAGGTGCAAGTCTACGTGGTTAGTGAATTTAACAGATCTTCC TAACGTGTAAACGTCTGTTGTCCAGGTGAATGGAAGAAGTGAGCT GAGATAGAGGGGACAGACAGAGTCAGTGTCCAGTGCTGACCTCT GAAATGGAAAAACATGGCCAGTCTTAGGAGGCTGCAGAGGGCCA AGACCCCAAGTGAGGTTTGGGGGTTCCACAGCAGAGGAGGAGCTG TGGACCACAGCAGGACCCCGATGCCATCAGCAGGGGAGGAAGTA ATCAGAGAGGTGGAGGAAGGAAGCCAAGGGAAGTCAAGTAAACA CCAAATATTCCCTCCCGGTCCAATGCTGTGACCTGCATAAGCCA CCACTCCCCCAGTCTAGACTCTACCCATGGAAGAAGGAAGA TAGAACTCTGGATTTGAATATAATTCTAAAATAACCAATTTAT CTGAAAATGACTAGGCTGAGTTTTCTGCTTCAACCAGAAATGGA GCTTGGAGTCAGAAATTATGTGAAATTATAGAAGAGAAAGTCAC CATCTTCCATCTCTGAGTCGTATGATCATTTTAGACATAAAAT GTGCACTTACGATGTACCAAGTGCTTAATATA [C/T] GTGATCT CATTTCAACCAGGGAAGTGTATAATTCAATTGCTTTAACTGACAA AATTCTGCAACTGAAGAAGGTGCTGTTAATAATTGCATTGGGAC GCAGGCCTGAGCAGGCCATGATTTGTGGCTGTCTACATCTGAC CCTCACAGTATCCATGGGAGAAGGCAGCATGTTTATGCCCCCTG	SEQ ID NO. 128

	ACAGCTGGGGAAACCAACACTTAAAGTGATTAAGTCACAAGTCC AAAATAAATGACAGAGCTGCAGTTCAAGCCCAGGTGGTCATTTA CCAAAGGCCATGCTCTTTTCACTTTGCATGGGACTGTGACCGCT GGCTCTACCCAGCTTCCCAGTGGGACCCCTTCCCCGCCACTGTT TCTCTTCTCTGGCCAACGGAAACACAATGAGACCACATATGTAA CATTACATTTTTTTCATAGCCACATTGAAAAAGAAAGGAACCAG GTAAATCCATTTTAATATGATATTTTATTTAACCCAATACAGT TGAGGCTTGAACAACACAGGTTTGAAGTGTGTGGGTCCGCTTAC ACATGGCTTTTGTTCAGTCTCTGCCACCCCTGAGACAGCAGGGC CAGCCCTCCTCTTCCGCTCCTCCTCAGCCCACTTACATGAA AACAAAGAGGATGATGATCTTTTGTATGATCCACTTTCACTTAA TAAATAGCAAATATATGTTCTCTTCTTTATGATTTCTCGTAATA ACATTTTCTTTTCTCTAGCCTCATTTACTGTAAGAATACAGCAT ATTTCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAAC CTGGGAGGCCGAGTTTGCAGTGAGCCAAAATCGCACCATTGCAC TCCAGCCTGGGCAACAAGAGCGAACTCCAACCAAAAAAAAAA AAAATAAAAAGAATACAGCGTATAATGCATGTAACATATAAAAT ATGTGTTAATCAACTGTCTATGTTATGGGTAAGTCTTCCAGTCA ACAGCAGGCTATTAGGAGTTAAGTT	
rs103285 6	CGCTCAGCAGCCATTAAAAGGATATCATCCAGTCACTTAGTTTC TCAATTTAACTTTAAAGGAAAGTTGCCTTATTAGAGAAGTGGCC TCTATTTCAATGTAATGGTCTTTGTACATCTTCCAATGTGCTG GCTTAGTGCTGAAGGATGGGGAAAGGCAGTTTTTCACATATTGCA GCCACCATAACCACAAAGAAAACAGGTGCACCTCCAGGCATCAT TTAGCGGGGTACCA [C/G] ATTCCTGGTTCCAGTTTCCTTTTTTA GAAAATCTGAAAGTAACTTTGGGGCATATCTTTTAAGGAGTACT CCAACACGACTAGTGGACAGACCCCTAAATTAATTGCCAATCAGC TCTGCCTTCTGGTATTTACACCTTTATGTAATAACCTCCACTTG AAGGTAGATGAGATCTGTGACTTGCTTCTAACCAGTGGAATATG GCGGAGGTGGTGGGACGTTACTCCTGTGATTACATTACATCATG TGGCTCCTTTTATGATGGAAGATTGCTAGAGATTCTCCTTGC TGACTTGACAAAGTATGTAACCATGATGAAGACTTCCACGTGGC AAGGAGCTGTGGGAAGCCCAGGTGCTGAGACTGGCATCCAGCAA ACCCCCAGCAAGAAACAGACGTCCTTGGTTCTACACATACAGGA AATGAATTCTGCCAACATCCTGAGTAAGGCTGGAACCTAGATTCT CCCCAAGTTGAGCCTGACAAGTAAATAACAGACCAGCCAACACC TTGATTGCAGTCTTGTGAGACCTGGGGAAAAGGACACAGCTGAA CCGTGTCCATTCTTCTGACCCACAGAACTGTCACATCATAAAG GTATGTTAGTTGTTACACAGTTTAGAAAATATTACAGCTGCTC AAGAAGGTTAGCTAGCTCCAGATTTCAATCCATTACAGGAAAG CAAGCTTTATTCCTAGAAGAATAATTCATGCTTTGCAAAAAGAG GAAAACGTCCTGCAGTTTTAGAAGGTCTTTCTTTCTCAACACA CCCAAATTTCTTTAAATCCTCAAGAAGTGCAATTGTTTTTCATG GTTGACTCGAAGAAGTGAGTATAATTAACCAAAAAGGTGGGA GGAAGGGACAAATTAATTTTGGT	SEQ ID NO. 129
KCP_rs88 8934	CACTCAAAGGGCTGGGGACCCCTGTCCCTCCCATGTGCATCCAT CTCTCCTATCTCTGAGTCCCCAGTGAAGTCTGCCTCCCTAGAG AAACAGTGCTAGAAGTCAGTGGCAAGAGCAGCAGGAGGACTTGG AGCTACATGCAGAGTGTGAGCTCCGGAGTCAGACCAGCTGAGTT CAAGGCCAGCTCCACCATCTATTCACTGTGACTTCAGGAAGGTT GCTTAACCTCTCTGTGCCTTAGCTGCCTCATCTATAAAACAGGA AACAAATGAGAGTCTTTCCTTATGGGGCTATTGAAATGATTAAGT GAGATCAGGCATGTGATGGCACACAGTAAGAACTCCATAAACAG AGGTCAACCACTGCTAATGCAATTATTCTATCACCTCAGGAGACT AAAGCAGGGGAGGAAACACCATTGACTCCTGGACATTTACCCAA GGAGATTATGGATCCATGTTTTGCACACACTTTAGAAAGACAAG	SEQ ID NO. 130

	GAATTCTAACCACAGC [A/G] TCTGTCTCCACTGCCCCGTCAT TTCAGTCTCACCCGTCCACCCTCAACCTCACCAGTGTGGCCCGG AAATGCGGTTGCCAGGGCCACTCTCACCCACCTCAGCCCTGC TCTGCTCAAGTCTCACTTCCACTCCTTCCAGCTCCCATCCCTTT CTACCCAGCTCCACCCTGATTTCTCCACCATGACCTTTACCCCTC CTAGTCTGATCTAGACCCCTGATCTTGCCGAGTATCTAGGACTT TGGTGCCCTTTGACCCTCAGCAGCAGAGGTAGAGAGGGATCTCGG TGAAGTCTGGGATGTTATAGTGACTTGTTTATCTAAGTGCCCTG AGACTGTGAGTTCCCTAATGCAGGGAGCATCAACCTCTGCAGAG AGCCCCAGAGCCCTGCTCAGGTGTGATGAACAGGAGGCACAC TTGATGCCCTCACAAAGTTGTGAGTGAATGAATGAATGAGTGAA TGAATGATTGAATGAAGATTAGTGATTATGTTAATGA	
rs905823	GGTGGGGGGGAGAGGGGAGGGGAGGAGAGGGGAGGGGAGTGGG GGAGAAGGGGAGAAAAGCGCAGCTGGCTTCCCTCACTCTCCTTTT CTTCCTCACCATCCTTACCCTGGCCAGGGCAGGAGGAGGATTG GCAGAGTAGAGGCAGGGTCTTCTGTCTTAGCTGGGCCGTGTGGT GACTTTCTGTTGGCCAACATGGGCTGACTGGAATGTTCTCCAGC ATGGCAGATGGTCATCCAGATGCAGGCTCTTCCCTGGGGCATA TAGCAGAGAGGGCTCTCTTCCAGTCTATTGCAGATGGATGCCCT CGTGAGCTGAGTTTTGATGAACATCCCATGTCCCCAGCCACCCC ATTGAGAGCCTCTTTCTACTCTGGTCTCTGGTCCCAGCAGCAG CCCTCTGGGTACTGAGGGGAGGGCATCTCACCCAGCCCTTAA ACCTGCTCACCTTCTTCCAGAGCCACGTGGCCGAGGAAAGTCA CAAACCCCTTGTCCTCCACAGGGCACACGTGTGCACACGTGTGC AGCTACCTTCTCTCTAGTTGGTACCTGAGGCTGCCTCCTGGATT TTCCAGTCTCTGTGTTCCAGACA [A/C] CCCCAGCCCAAGA ATACAAGAGCTCTGTTCACCAAGCATCGGGCTGTGGCTGCACTA CACGTCTGCAGCTCAGGACCCCTGGCTGCGGCGTAAGCTACCAG CATCCCCCTTCTCATGGGCACCCCTCATCTCCGGCTCCCCATCGCT GGGCTGTGACCTGCGGGGGCGCCCTCTATGGAAGGGAAGGAGA AAAATTCACAGTGCTATCTACTCCTCTGAATGCACTCCACCAA TTTCCTTGGAATTTCTAGCTTTCACTGACATATCTGGGATGGG GCGGTGGTCACAAAATCA	SEQ ID NO. 131
rs883849	CTGGCTGGGGACCATGGGTGAGGGCTGCCACCCCTGGCTCTG TGCCCTTACCTGTGTAAACGAATGGGGCACTCACAGCCCTCTCA AGTGGTCCTGGGGATGAAGTGAGAAGGTGACATATACAAGTGAG TTATACACGTTCTGTTCTGTCACTCACCAGTGCTCACTGGGTG GGTCACTGAACTCCCCTCAGCGTTTCTTCTCCATCTGTAAACC ACCAGTGCAAACCTTTCCAGATAGTGCTGACCCGAAGCAGGAA CCAGTGCCCCCTCTGCCCTCAGTAAGTCTGCCAGCAG [A/G] GGA AGCCCATAGAGGGTCTTGGGAAATGAAGCCAACAGAGTCAAGAG GGTCAGATGATGAGGGACTTCAAGTGCCACCTTCATCCCATTCT TTCTGCAAATATTACACACACCTACGTGACCTCAGGCTCTGT GTCAGGTCTTGGGGATGTAATGGTGTCCATGAAGAAACAAGGTG CCTGCCCTCATAGAGTGGCCTGACATATGCCCCGAGGCAGTCAGC AGCCGAGTGCGGGAGACTCTTGAGCAGAGATTGAGTGTGTTGAT ATCTGTAGGCATCAGCCTGGCTTTGCTGAGTGAGCTATATCAGA GTGGAGGAAGCCAGAGGCAAAGTCCAGACTCCACTGATCCTGGA TTGAGGGGAGAAGGGGCTTGGCGGAAGAGCAGCCTGAGCACCTG CATCTCACTCCAACCTGGTGCTGATTGTTCCCAT	SEQ ID NO. 132
rs213504 6	TCCACAGGTTTGATTATAAATGTGTGATTGAATTGGAATTTCT GTTGAAATTTCTGATCCCTTCTAGACAAAGAGGTAAATGAA ACATGTCAATGGATATCTAAATATCATTACTCACTGGCTTTATT TGCAAATGGCTTTCCATTGACAACAGTTACATTTTGTTCAAAGC AACAAATGATTGGCGCTGACAATCCACAGGAACATGGTGCAGTC ATTAATGAATGTGCTCATTAATTCCTCCCTGCCGGGAGGCATCGA CTCCCGTTCTCCAGCCTGTTTTAAGCAGACAGACCTACATCTGC	SEQ ID NO. 133

	ACCTGTCAGCTTGGAAACCCTAGTAGGGGAGGGGGATGCTGATGT GATGGAGAATGAAGAATGGGCCCTGCAGGCTGACATTTTGGGAG AGTAGGTTCTGAAATTTATCCCAAAGGACATGGAATCCTGGAAG CAGGGTTCAAGATCCTCCCAAATTTGATCTCCAGGATGCTTGG AATGATTGTTT [C/T] GAGGGTTTTGTAAATGCCAGGGGAAAA CCAGGAAGCTTCTCTCCAGTTGTCTTGCCTCCTTCTCTCCAGT CTCCATGGAGCTGACTTTGAGAATTAACCTCCTGAGGGACAGAGA CCCTGGGATGGAGAGCCAGCCCTGCTGGATTCCACAAGGTGCTG CTTAAAGCACAAACACCTCTTCCCAATGACAGGTTCTGAAAGAAG GCCTTGTAGCTAGATGCACAGAGGGTTTTGTTTTGTTTTTTTTT TTTTAACCTTTTCAGCATCTGTCTAAAATTGCTCTGGGCTGGGTA CAGTGGCTCCACCTGTAATCCCAACACTTTGAGAGCTGAGGCA GGAGGATCGCTTGAAGCCAGGCGTTCTAGACCAGCCTGGGCAAT ATAGTGAGATCTCTATGTCTAG	
rs50057	GGATCTGTGCCTGAAGCTGAGCTGCTGCAATGAACTGACATTT CTGCCTTGCAGCCTGGCCATGGGCTTAGCTGGACTAAAATGCTG CTGCAGTGGTGAGGGCAGTGAGAGTCCCTAATGTACATGGCCT TGCTCCTTGTCTGACACATCTTTTAGGGCTGCTGCTTTCTCTA GTGCTGGAATCTAGATAATTCTTTCCAGCCGTTTGTCTTCTTC AATCTTGGAAAATATCTGGATGAATGTAACACTGTACACAC [A /G] AACAGAATTATGACTTACGTCACATTCTATGTCGTGATTTT GTGGACTTTTAATAATTGCATTACATTTGTGACCATTAATTTCC ACCATCGCCCTGCTCCTGAGAATCTGTAAGGGACATTTGACACT CCTCTCCCCACCCACCTCAACATTTGTGCTGACCTGAAGGTCAC ATTAAAAA	SEQ ID NO. 134
KCP_4976	GCAACTTTCCCTGGCCTGCAGGAACCTCAGGGACTCAGGGGACTA ATAACAACAGTGTATGAGCTTCCGGGCACACTGCTTCCAGTGG CAGCCCCGTACTTAGGGCTTTGTATGTATTAATTCATTTACTC CAATTTCCACAATAACCCTATAGGGTAGGGTTTTATTATTGATT ACCTTTTTACAGAAGAGGAGAGTAAGGCAAAGAGAGATAGAGTA GTTTTCCCAAGGTCAAAGAGCACATAAATGATAAAGGATGGATT TGAATGTAGGCAGAATGACCCTCAATACAGACTGTTCCCTACAGT CCACGTCCTCAGCCACTAGACCATACGGCCACTGGGATGATAGA CAGACCACTGCAGCCATGGATAAGGCAAAACAGGGCTGGCTGT GTTGATCTGTGCTCTCTCAGAGCTCCATTCTTCTCAAGGGGGCA CCTTGCAAAAAAACAACAAAAAATGGGGCAGGGTAGGGAACTGA AGGCAGGAGCTCTTCA [C/T] AGAGCATAGCCACATCCTCCAGG CAGACAAGAGGACGCAGGAGGCACCATTCTGTGAGAGTATCACA GTCTGACCCAAAGACACAGCTTCACACTGTCTGATGGCTTGATG GTTAATGTCACTCTGCCTTTTCCCCCTTCTCAGGACTTTGTAACC GCTCTGTGCGATTTTATTGAGAGGAACTGTCCACGAGAACTAAG GTGGACATTTAATTTGTATGACATCAACAAGGACGGATACATAA ACAAAGAGGTAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCTCC AGTGAAGGTAACCTAACCAACAGAAAACAGCCCCAGGCATGAGG ATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTGGGGCTAACAG AGCTGGTCCCTGGCAAAATAAAGAAGGCCTCCCTCATTGCCCTA CCCTGCCCTGTTCCCAAGCGCCAGAAAGGATTAACAGATTCA TTCTCACTGGGTACCTAGATTTCAGTAGATATTACAC	SEQ ID NO. 135
KCP_5077	TAGGGCTTTGTATGTATTAATTCATTTACTCCAATTCCCACAAT AACCCTATAGGGTAGGGTTTTATTATTGATTACCTTTTTTACAGA AGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTCCCAAGGT CAAAGAGCACATAAATGATAAAGGATGGATTGAATGTAGGCAG AATGACCCTCAATACAGACTGTTCTACAGTCCACGTCCTCAGC CACTAGACCATACGGCCACTGGGATGATAGACAGACCCTGCAG CCATGGATAAGGCAAAACAGGGCTGGCTGTGTTGATCTGTGTC TCTCAGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAA AACAAAAAATGGGGCAGGGTAGGGAAGTGAAGGCAGGAGCTCT	SEQ ID NO. 136

	TCACAGAGCATAGCCACATCCTCCAGGCAGACAAGAGGACGCAG GAGGCACCATTCTGTGAGAGTATCACAGTCTGACCCAAAGACAC AGCTTCACACTGTCTG [A/T] TGGCTTGATGGTTAATGTCACCTC TGCCTTTTCCCCCTTCTCAGGACTTTGTAACCGCTCTGTGATT TATTGAGAGGAACCTGTCCACGAGAACTAAGGTGGACATTTAAT TTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGGTAAG TGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGTAAC AACCCAAACAGAAAACAGCCCCAGGCATGAGGATAGCACTGTCTG AATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCCCTGG CAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCTGTTT CCAAGCGCCCAGAAAGGATTAAACAGATTCACTTCTACTGGGTC ACCTAGATTCACTAGATATTACACAGTGGATAAAAATGACTTGT TTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATTTGGG AAGGTTAGGAGCCACAAGCTCAAAGCTAAAAGTTGAAA	
KCP_2410 99	TTGAAAGAGAGCGCTTTGGGGGGTTTTCTTACTGTATGTCTCTA TTGCATGTTCTGTATTTTACATTTTCTATTATTTCTTCTCTGA GGTATAGTATTGAATGTAGAAAAATCCTCAAATGTTCCGGTATTA AGCAATACACTTCTAATTCATGGTTTCAGAGAAGAAAATATCTCG AATAAAAAATAAAAAATAAAAAATGACTTATCAAAATTTGTAGGAT CTAAAGCAGTATTCCAGGAATGCAAGGTTGGTTTAAACATTCAAT AATTGGTCAGTGAATTAATCACATTAATAGAATAAAAAGAGAA AAAATATAATCATTTTCAGTGGATGTAATTGTTTCAGAGCTTCTTA AAAGAAGCAACTCACTATTTTACTAGATGATTTGTTTCTTCTGA ATTCTCTTTAAGGCTACAGGTGGTGCTTCTTACTTTGAACTGA TCACTTTCTAGGTCCCCACCCTTACTTCTTGTTTTTCATACCCT TGTAAGTTTTCTCCA [C/T] ATAGGAAACCCATGCTTGACATT TGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGACTCAGAGTT CTAACCCCTCTTGCCCTCCTTTTTTCCCAGGACGACAACATCATG AGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGTGGTGACACT CAGCCATTCACTCTCAGAGACATTGTACTAAACAACCACCTTA ACACCCTGATCTGCCCTTGTCTGATTTTACACACCAACTCTTG GGACAGAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAG ACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGC CAACTCTTCTCTTTCTTCTTCTTCTGAGAGAGACAAGATGAAAT TGAGTTTGTGTTTGGGAAGCATGCTCATCTCCTCACACTGCTGCC TATGGAAGGTCCCTCTGCTTAAGCTTAAACAGTAGTGCAAAAA TATGCTGCTTACGTGCCCCCAGCCCACTGCCTCCAAG	SEQ ID NO. 137
rs189530 1	TTTTTTTTTCCCCAATCATGCTGTATTCTTAGCGTAATTTTAAAA TACTTAAACAAGATCATGAGAAAATAAATGCCAGATTCTAGC ACCAAATTTCAGAAGGGGGGGCTATGAGAATGAGGGGGCGGGGAG AAGCCTTCCTGAGAGTTTCTAAGAGGCATGGAGGCAGTGGGGAT AGTGATTAGCTCTGGGGGAAGAAGAGGCTACTGGCTGGAAAAGG GCATGAGGTAGGGTTGGTAATCACCTA [C/T] TGTGTTATCTGA GTGCTGGTCACACAGATGTGTTCACTTTAGGAAAATGTATTGAG ATTACACTTGTGATTTCTGCATTTTACATACGCACATTAACCTc agtcatatgctgataaatgtttaacaatgggtttgctggagaaa aaaggggtcccccgatttgtaatgtctgcccatttccgtgggtgt aaatactcccttcacaactgatttcaagcttcccatgcactgta actgaagacagagttgggaagatacgtgcagtagcacacaatta aatcatatttccaccatatacacacaataggtgtaataaacacc cagagcatagaaaa	SEQ ID NO. 138
rs142275 2	GGTTGGCAGCTTTTAATAACTTAGAAATGGCTGGGGGTGGGGGG GAGGAAGTACTGAATCATTTACTCATTAGCAAATAACCAGGGA ATACCTACTCTACACTGGTCACTGATGGAGATA [C/T] AGACTT GGGCAAAGCCGCGTCATCTGGTTGTGTTCAAGCTGAACATTCC CTTGACCCAGTCACTGATGGAGATATAGACAGGCAAAGCCACG TCATCTGGCTGTGTTCAAGCTGAACAGTCCCTTGACCCAGGGCC	SEQ ID NO. 139

	CATGACAGGGCAGAGGGCAtattattatccccattttacaaagg aaagagctgtcagacacagTGTACACAGGAAGGTAGACGATAA TGTCAATATCCCTCATCTTAGTATAAAGTTGTCTTAAAACTC TCCATTATTTATTAATTTATTGACTCACTTATTCATGTTTTCTG CACAGTGATACTTATCCTGCACGAGACTCTCACACCAGTGCTTT GGGTGTAAGAACACCCCAAGGATTGTGTTCCCTTTTCTCGAAGA GTCTGTGGTCTAAGGGGATTCAATGGGGTCCACTTTCCAAACCA AGACAGCAAAGGAACACTAGGAGAGAAGTATTCTGTGCAGAGAT TCAGTTAT	
rs142275 4	GGATTAAcaggcatgcaccaccgcacctggctaatttttgtatt tttagtagagatgggtgtttcaccatgttggccag [A/G] atggt catgatctcttgaccttgggttctacccacctcagcctcccaaa gtgctgagattacaggtgtgagccgctgcaccgCGCAACTGGT TTCCTTTTACTGCCACTTTCACTAACCGTGGTATTTCTCCATGG GCAGCATTCTTGGCATTGTTGGGTGTGTAGGACTGTCCCTCACATA GTGACCTCTTACTCATGAATTGCCAGTGTACATTGAGATTCTT ATGGCAACCAGAAGCTCCCTGCTCCCAGCATTTCTGCAGCTCAG CCTGGGCTGGGGAGGTTAGCTCAGACCAAATATCTCCTTTCTGC CAGTTGCTCTGCTAGGCCCAGGTCATGCTGAGCAGAGCAAGATG TAGCTGAAAACCAAATAAGTCACGTGTTCCAGCTTGCTGGGGTT TTGTGAAGAAAGCAGCCACCCCTCCAGTCATATAGTTTGCAGGT TGGGATTGTCATT	SEQ ID NO. 140
rs205560 6	tggctattgtcttaagctactattaccttcttggcttgtcaagtt gcgcatcttacttttcaaggcttgctacgtgcctggaatttctag atcttcctttatttccatgcttggggagaggagtgcctggcagg ctcctaagaggggtctgtgctccatctcGCCCCCTATCTTGAAC TATCGGTTGGGTGCTCTAGAATCTGTATGGGGTGGAAGTGTTCA TTCATTTTCTGTACAAAAGCAATCAATGCTTATTGTGGAAAACC CAAATAAGAGAGTTGCTCTAAACAACACCCTCCCCAGTCCCAAT ACCTTGCTCCAGAAGAAACCACTGTTTGGTGAGTATATTAGT [C/ T] AATGCTCTGCAGACCAGATCGGATGACCAAGTTTTCCATAAAT GGATGGCCATCCACTTCCCTTCAAGGGCGAGGGTAGTFTGTTCT GATCCATCTCCCTGTTTACAGCTCAGGGAGGGAGGAAGACCCA GGAAGGAGAGCTGCCACAGTTACTAGTGGCCAGCTGGGATTTA AAGTCCGCCGTGACTGAAGCTTGGCTCCACATGCCAGTCTGCAA GGCCCTGAGTGGCCTCAGCAGTAATTCCAAGCAAAGCAGGGAAG CAGCGGGCCAGGTGCTGAAGTGAAGTCTGCTCAGGGCTCCTG	SEQ ID NO. 141
rs933656	CTGCATATGTTCCCCAGGTATTTGCCCCCGAAGCACAGTCATC TCACTGCTTGCATAGTGGAATGCTAATCAGCAGAAGACCCTTC TATGGGAGGCAGCTTGGAACCTGGAGGAAGCCCTGGCTGAGGA GGCTAGTGGTCAGGGAGCCTATCCTGGCCAGGTCATTTTCCCC ACTGGGGCCTCGGTTTCTTCTTTGTAAAGGGAGAACTTACATT AGGCATTTCTCAGGTTCCATTTGGTTCTCAAATCTTAATATTT TTATGGTTGATGCTCTCACCAGAGCTGCTGCTATGATCTCAGAG ACGTGAGGCTCAGATCTAATTAGAAGCAACCGGAAGAGAGCAGT TGGGATTTTTTCAactcaggaatcagtctccctgctgggttcaaa ttcaggctctgccacttacagctgtatgacTAAGCCTTGTTTTTC CTCAACTATAAAACAG [A/G] GATAGTAGTAGTTACCATCTTAA AATAGCTGTTGTGTTGTGTGGATTTCAAGGATCATGCAAGTCAA GCATTTAGCACAGTCTCTGCTACATAAGTGGTCAGCAAATTTGA GGTACTATTC	SEQ ID NO. 142
rs233909 1	AGACCCTTCTATGGGAGGCAGCTTGGAACCTGGAGGAAGCCCT GGCTGAGGAGGCTAGTGGTCAGGGAGCCTATCCTGGCCAGGTCA CTTTTCCCCACTGGGGCCTCGGTTTCTTCTTTGTAAAGGGAGAA ACTTACATTAGGCATTTCTCAGGTTCCATTTGGTTCTCAAATT CTAATATTTTTATGGTTGATGCTCTCACCAGAGCTGCTGCTATG	SEQ ID NO. 143

	<p>ATCTCAGAGACGTGAGGCTCAGATCTAATTAGAAGCAACCGGAA GAGAGCAGTTGGGATTTTCAactcaggaatcagtcctccctgct gggttcaaattcaggctctgccacttactagctgtatgactAAG CCTTGTTTTCTCAACTATAAAACAGAGATAGTAGTTACCA TCTTAAAATAGCTGTTGTGTGTGGATTTCAGGATCATGCA AGTCAAGCATTTAGCACAGTCTCTGCTACATAAGTGGTCAGCAA ATTT [G/T] AGGTACTATTCAATTTATGGCTCTATTGTTGGGG CTTCCAAATGTCCAGAGTAAGGCCATTTTCGAAGTAGGCAGTAC ATCTGAGAGCCTTAACAGCTCATTCTGGAACCTTATCCAGCC CTATCCAGATAACTAGGACCAAAAACCCAGCACACAGATGCTC GTCCCTTGCTTCAACCTCACTGACCTCTACTCTGTGGCTGTG CTGAAAACATCAAAGCCTGCTCAATTAAAATCCTGAATGCCTTG ATAATACAATTTAGAAACATACATAGTTTTTAAATAGGGCAAAA ACTCTGCATGATTAGTGCTGCAAGAAGATATCCAGCCCAACTG GGTGTTCAGGGAGCGCTCTCTAAAGGCAACAGAAATCTAAAGTA ATTTAAGAGCCATGCCACTGAATAAAAATATTAGGTTTCATTTT CTGTCCTTCTCTCTGTTTGGGATCTTTGTGTGTCTTTAATTAAA AGTAGGAGAGCCCTGCTTTT</p>	
rs186233 1	<p>ACTACTTCTAAAGCCTCTTAGACCCTGGTAATCTTCCTCCTAAC ACCATCGGGTGACTGCAAAGCACTGCAGGCCAGACTTCAGTTCT GCTGTGTAATTTGCAAGCTGGGTGACCTTCCTTATCTATAGAAT GGGCTCT [C/T] CTGCTGGCTGGCATGAGGAATAAACAAAAATG GTTGTGTCCAGTGCTGGGGCATAGCACAGCTCAAAAACTTAG TTCATCCTCCTGAGGGATCAAGAAGATACTTGGAAAACAAATGTC CAAGGGCGTAATCTTGAAGGGCTTGTGCCAGGCATATATGGAG AGAAGGGTTTTGTGGGATGTCAGACTTAATAGTGCCCTTTACTC CCCACCCCGTCTCTCTGTTTCATAGACAGGAAATCTGTGGCCTA TTCTGGGACCTCAAAGTGCCACAGGGTTAAAGATACCAAGTCAG AAATCTAAGGTTCTAAATGGACTTTAGACCATTTTTCATTTGGG AAGGAAGAATCTTTAAGGGGTTGTGCTGGCGCTGTCTCTGTAT GCATGTGCAGAAATGTGCTTCCAGATGGGGTAATGGTCTGAGTTT GAGGACAGAAGTCCACTCCACTGCATT</p>	SEQ ID NO. 144
rs233913 9	<p>GGGTGTGGCCTTTGGACAGCACCTTAGCAGGAATGTGGTGGAGA GCAGCCCCATTCACTCCAGAGGAGAGCCTCAAACCTCTCAGGCA GATCTAGCCTAGGTAGAATCTTGGCCTGGCCCCCTCCGGGATGAC AGGTGCCATTGCCCAAGAATGGGGAAAAGGCTGAAGTGCTCCAG CCAAAGACCCCAATTTATCTTCAGGACAATTTTCACTGGAAACC TTGCCTCACCACTGCCACTTTTTTCAAGTAATTAGAATGCTA ATCTATAAGAAAGATGACTattataaaataaattaataaGATA ATACATTTTGGCTTACAATTTTGAATAATATAGCCATCCCATCT TAAAGTAAAAATTCATATATTTTAAATAAGCCTGAGACATGTTT TCCAATGAACCACAGATGGTTTCAATTTTATTATCTATAAAGAG ACATTATGGGCAAGTGTTTTTTAAATGGTAAAACAGAACCTTA GAGCAGCTCTCTTTTG [A/G] AGATCTCTAAGCACTTTCTAAGC ATCAGGACCCCTTCTGTCTATCAGAGACTGAAATGAGGAGAT GGTCTCTGTCAACCCCTCACTCACCAGTGAGCCCCAGACCTTCA TCCCTGATCAGATGGAAGCAGTGTTGGCATGATTACAGTTTCATAT TTCAACTCTGCCACTCAATGACTAATAGCCAAGCACTAATAATG CAGAAAATGTAAATTTAAAAAATAATCTTCTGAGATTGGTTAT GAAATGCACTCAACACAGCACCATCCACAGAGAGGTTCTTTTAA ATTGCTCTTTTCTTCTCTCGACACCCAGAATCAAAAGCATG CCTGAAAGCGTCACACATATATGTCTGTGACCATAACATGGCAT TGCACATGCAAAGGAAATAAATAGGTGTTACCCATGTGACAAAG GTCCATGAGCTCTGTCCGCAAAAAGCTGTTGAGTTTAAAGAACA AATAATTCTGAAAAATCTTCCAG</p>	SEQ ID NO. 145
rs872435	<p>CTGCCATTCTGATCACTGCAAGACCCCAACCCCAATACTCCCA ATTGTACCACCCCAACCCCACTCACCAGTGCTCAGAAATGCCTC</p>	SEQ ID NO. 146

	CTCCAGAAGGAAGGCATCCTGTCTAACCCTGCTTCTAGCCAA GCTGTCTTTCTTCAGAAGGTAGAAAAA [G/T] ATTGTTAGTCAT TGTTTAATCTTTATTGAGTATATACCGCCACACCAATTGCACTG CCATTCAATTATCTCATTAAATCTGACAAGAGCCTTGTAAGTA GGGATTATTTCCACCATTTCAGATGTTGAAACTGAAATGAT AAACACGACATGTTGCCATGGCTACATGAAGATCTCCAAGCCGG AGGATCTCCACCCTCACCTGCCTAGCTTCCCAGACCTCTCTGCA GAAAAGGGACTGACCCCAAGACAGCCCTGGCCTCTGGGCTCCA CCCCCTCCACATCCATCCCAGGGCCGCTGAGGACTGAAGAGTTC TCCACGTTTGCCCTTTAAAGTGAAGTAAATAATCTTTATGAA TTTCTTCATATACAAAATTTGTAAGTACTCATTGCAGCAAAATTT AGAAAATACACATAAGCAAAAAAGAACGTAACAGCCATCCATAA CCCTAACTCTCAGAGATCACCCTATTAAATGTTTATTATCTA AGAGAGAGATGATATAGACAAAGATGAGACAGATTGACACAGAC AAGATGGGTACATGATAGATATTTTCTGTGTTATAACCCCTTGCT TTTTCTTGCACTTCTAGAATTTTTCTGAGAACTAATCTGAAAT CTGCACAGGGTCCCCACGTTTGGATCCTCTATCCCATTGCCTTC CA	
rs329468	AGCTGAGCCCCAGGGCTCCCCATGAGTGGGGAGGAAACTCATG AGTGCCTTCTATATGCCAGCGCTCTATCTGCAGGGGTTCTTTTG ATAGCAGCAGACTGAGAGATGATGTTACTGTCCCCTTTTCTCTG TTGTTGGCAACTGAGACTCAGAGGATGGAAGTGAAGTGTCTCAGG TCCACCACCTCTTCAGCTGTGGAGCTGCGACAGGAGCCTTTGTT TGAAGTCAAAGCTCACCATCACTCCTCTCTCACTGATGCTCAAG TGGGCTATCACCTCGCTTTCTCTGAGCCTTCTCTCGCTATCCTA AAACAGCGCCTCCCGaaatcaccactaaagaacttattcatgta accaaaccaccagcgggttcccctaaaaaacctatggaaataaaAAT TAAAAATAAAAAACAGTgcctcccatgacccatgtctctccagtc ccataactctgctctatttccattcacagctccatccccacott tatgtcttttgttcaactgctttatccccagtgcttagaagagtg cttggcaccttagtagacactcagtaagtatttgcgaatgagtt aatAAGGTTGTGAAAAGAACGTTAGATTACTGGAAGGATTTCATC TGAGTTTAATTCTGCTATGCTGGGAATCCAGTGTGCGGCCTTGG ATGA [A/G] GCCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCT GTACATTTAGAGGGCAGGAGAAAAGCCACACGCTCTGTCACTTA TACAACCTGTTGCCAGAGTGGAGGCTGCTTTGATGCTCAGAAA AAAGAAACAAACATGGAAATGCTAAATGGGTGGCAGAGAGCTTG AGGGAGGAAGGAGATGGGGAGGGTACTCTTGAAACTGTTTGGTG TCTTCCCTCCTGCCCCCTCAGTACCAA	SEQ ID NO. 147
rs50364	GCCTGACAGATTTTACTGAAGGGTGACATTGGAATAAAAAAT GTGTTACCTATCTGGTTGAGTCTTCAGCTTCAGAAAGGTAATAG AGCAAAGGCAGATAAATCCAAACAGGGACTGAGCTGTTTTCATG CAGGCTGCCTTGGTAGCTCTCCAAAGCCTTCAAAATGATGAGA TTTTTTTTTAAATCCTTTTATCC [A/G] GTTGTCTCAAGGGA TTCCACCCCTGCATAGGAGAGCTCACCATTCTGGGATCTTCAG CTTCTATGCCTTTGCATATGCTCTTCCCTTGTTCCctcattctt caacactcaactgaattatcacctcccttgaagccttctctgac atcccTTCTAGTCCCATGCCACCCAGGAGGCACTAAGAGCTTCC TCCCTCAGCTCCCAGTTCTTAAACATGTCAACACTGTTTTGAA ATGATTTGCCAATGAAAAATCTAGACCAGCAACCAACAacatc cttcccaaagggtgtgttatatatggtacatgctctatgtgctaa acaccaaattcattgataacagctaagaaccaggaaacaaacca tcgttaattatggcatctcttgaaaaatctaagatctggactc actgggcttaaatgactgcatgataacaactgggttagtaacaa ctgtttccctttcatggagcagttactctccagttctcagttcc taccactctctatagttgtacactcatcatctgtcctcatctga attacctgccaatgactactggcatttgagtttctaatacatgG	SEQ ID NO. 148

	TCTATGTGTATGCCTCCTCACCAGTGTGAGAACTCATGTAAACA GGTATTATGTCTTTTCATCTCTCTCCTAA	
rs155158 3	ATAATGGTCACGTTGGAGCAATTGCCATTTCAAATCATTAGGAA CACTCAGGTCACCTTTGGCATGGAGCTATTTTGTAAAAGACGTAG AAGCCATTTATAAACTTTGGTTTGTCTTTTAAAAAATTTATTTCA TTC TGAGGCTTATCCGTGTAAAATTACCAAATGATTGTGGTTA GACTCTACATTGTACAGTATTTAAATGTGCACAATATTCCACT TAGAAATAATGTCAGTACTAAAAGTAGTAGAGGGCTTTGATAGC AATATTAATACATCGTTAAGCCCTTCTCATTAAACAGTGTAAATA GTCTTGTTGAAGTTTGT TAGGCATTTTAACCCTACTAATTAAA AATAGACCTACTGACTAGTCTGTTTACTGTGCTTTATTGTGTC TTGGATGTTTCATTAGATACTTTTGCTGTTGAGAAATCAAATCG TCTCTTATGGTTTTAATTACAAAATACATATTAGAGGGATACAG TTC TTAGGGCTGTGATTTTTAATTTGTGTAACCTTTTTTTTATTT TGGAAAGGAAATTT CAGATTTTTTCTAGTAATTTTTCATTTGTG AGTGTGTTTTCTAGATACAGAAAATGTACCTAGATAGATGATC ACATTTT TAGGATATTTTGCTTACGTGTTATTTTATATTTATATA CTATAATACCATTGTATAGTT CAGAACAAGAAAATATCTTGATA AATCATCTGCTACTGTGAGGCAGTTAAAAAAATTTGAGGCTCAC TGAAAATGTGTGACTTGCCCACTGTCTCATATTGCTAGTATTGG AGAGAAAAC TAGAATCTAGGCCTTTATTTTCCTGATGTAATGAT TTTAGCTAATTATTATTTATTTTCTTAAATCATTGCATTAATT [C/G] ATTTTT CACAAGTAGAGCCTATATCAGTGTTTGCAataat taaattttaagtatatatttctataattgtaataaaaatCCTGACA TTTGTTACAGGATGGGGTTTTCTTTTCATCatatttttataataa aaatttaaGCAGTTATAAAAATAAATAGCCTAGTTTTTCAATTGG TATAAGCTGGCTTTATTTTATACTGCTAATAAAGGCACATTATG TTCAAGCA	SEQ ID NO. 149
rs145769 2	CttatatattcattaattaataatttatattCACACAATGATTG TAGAAATGTGAGTGTCTTCTTAGATTACCAAACATCTGTGAAATC GTGAAGGAGTATTGAAATTTAGTAATTTGGTTTGGATCTTTGAA GATATTCGTAGAAATTGTTTTCCAAAAGTTACAACCTGGTTTACA ATTTTTTTCTTAATTGCCATTAACAAGTTTGGACCCTGAGATGA GAAATTATT CACAAATTTCAATTAAATACTGGAATGCTTCATAT TTTCTGTACTTTAGGAcagggatccccaacccccagggccacagg ttggtactggtttgtgacctgttaggacctggactacatggcag gaggtgagcgggtgcgtgagaa [A/G] cattactgcctgagctcc acctcctgtcagcgacagcattagattctcataggaggacggac cttattgggaacacacacaagagatctaggttgcggaactcctca tgagactctaataatgcctatgatctgaggtgggacagttttatcct gaagctccccactatccgtccagngaaaaatttggtccctgtg gccaaaaacactggggacctctgCTT	SEQ ID NO. 150
KCP_1035 5	AGGGCTGGGCGTCCCCCGCCCCCACCCTGCAGCCCTCGCCCCG CCCCGCCCCCTCCGTAGTTGCCCGCCCCGCCCCCCCTCCGCCGCC CCCTCCGCGCTCCGACTCTCGCCCCGAGCGCTGGCAGCAGGCA GCAGGCAGCAGGCGGGCGCGCTGTGGCTCCGCGCCGCGCGGTCC GGGCTCTGTTTCATTATGATTGGTACTCGGCCCTCCGAGACCCA GCCCCGAGCGCAGGGAGGGGAGCCGAGTGTGCGGCAGGAGGGGCG GGCGGACGGCGGCTCCCGCACCGCACGCGGCGCTGGCTCGGCAG CCTCGGCCGGGCGGCGCTCTGGCCCCGTGTCCAGTGCCAGGCA GGCTTCAGGGCACCGTCTCGGCCCTGGGCGAGGGAAACCGCG GCCGGGTCTCGCGCGGGGAAGCGGTTCCGAAGGCTCGCGGGGA GCGGCTAGCCCTGAGTCCCTGCATGTGCGGGGCTGAAGAAGGAA GCCAGAAGCCTCTAGCCTCGCCTCCACGCTTGCTGAATACCAA GCTGCAGGCGAGCTGCCGGGCGCTTTCTCTCTCCAATTCAGA GTAGACAAACCAGGGGATTCTTTCCAGGGTAGGGGAGGGGCC GGGCCCCGGGTCCCAACTCGCACTCAAGTCTTCGCTGCCATGGG	SEQ ID NO. 151

	<p>GGCCGTCATGGGCACCTTCTCATCTCTGCAAACCAAACAAAGGC GACCCCTCGAAAGGTAAGCCACCTTCTTCTTTTGTTCCTGTC TGGGCTTGGGGGTGCTAGGCGCCGAGGTGGGCTGTGCCACCTGC CTCCCTTAGTCCGACTCTCCTCTCCACGAGGAGCCCGACAGG TGCTTGTATCCAAAGGAGAGAGAAATCGGCGGGAGGGCTGGTGT GAACACCCAGAGGAGGGAGCCGGAGTGGACGTCTGCCCCAGCGG CAACTGGACCCCTCTGGGGCACCAGGTGTGGGACTCTCCTCCT GGGGAATCTCTGAGAGCCGAAGGAAGCGGCA [A/T] GTTCACA GGTGGGGGTGACCGATTCTCTGGTGGAAGTGTGGTGAAGCTCT TCCCATTCCCATGACAGCTGGCGTTTGAGCACTCAGTGAGGGTG CTGCCACACTCCACACTCCTCCTAGGCGGCTATGCCAGGTGCA GACCTGCGAGTCCCTTCATCAGGAAGAGTGTCTGTCTGCACCC CCAAAACCTCTGCAAGCCAAAAGGAATCAGCTGCTGCCAGGGGT AAAACCTCCAGGCCTCATGTCTGGTGGCTCCGGGAGTCAGGAG GAGCAACCGTGAAGGGCTGGCTGCGAGCTGAGCTTACATCAAGG ATTAAAAAGCATAATATCGTGGAGTCTCTTCTGCCTGGACGCTG TTCCTTCACCACCTGTCCCCAGCCGAGGCATGGCTGATCTCACC ATCCGTGGGAGAGTCTCAAATGGGTCCAGGTGAAGTTGGAACC AGTGTGTTGGGCCCTGGAGGACAATGCAGGTCTCCTTACCAGCA GTTCAAAAGTTAGTGGTTGGAATAAAGAGACTGGAAGCAGTTAG GAAACGGGAAATGATGGGTTTTGTTTTGTTTAAATGTTCAAATGT CACTACGAGTGGTAAGATTTTAAGCAGCTTGACACTTAAACATT CAAATTCTACCATCAGAGCCCCCATCCTGGATACAGGTGGGAGT TAAGCTCCTACCCTACAGGCCTGATAGTGAGTAGAAGTGTAATG GGTAAGGGACCCCAAGTGAACAATAAGTCTCCTCTTAGAACTT GGTTGGTCTCACCTGTTTAGAACCACAGAGATCTCCATAAGTA AGCTGTCCTTGAAACCCCTGGAAGAAGGGGTCCAGCTTCTGG CCCAGCTCCAGGGGCATCAGGCTGGCTGAGCCCCGAGGAAAGA GATCTCTGGGTGCAGATCTTAGGTGCTGAAGCTGGGTGGCATT TACATCCTAGAACATAGGAAGAGGCTTTGGCCCATTTGTCCAGC TGAGTTACATGTCTCTGCTGGCAAGG</p>	
KCP_1044 6	<p>TGGGGGTGCTAGGCGCCGAGGTGGGCTGTGCCACCTGCCTCCCT TAGTCCGACTCTCCTCTCCACGAGGAGCCCGACAGGTGCTTG TATCCAAAGGAGAGAGAAATCGGCGGGAGGGCTGGTGTGAACAC CCAGAGGAGGGAGCCGGAGTGGACGTCTGCCCCAGCGGCAACTG GACCCCTCTGGGGCACCAGGTGTGGGACTCTCCTCTGGGGAA ATCTCTGAGAGCCGAAGGAAGCGGCATGTTACAGGTGGGGGTG ACCGGATTCTCTGGTGGAAAGTGTGGTGAAGCTCTTCCATTCCC ATGACAGCTGGCGTTTGAGCACTCAGTGA [C/G] GGTGCTGCCA CACTCCCACACTCCTCCTAGGCGGCTATGCCAGGTGCAGACCTG CGAGTCCCTTCATCAGGAAGAGTGTCTGTCTGCACCCCCAAAA CCTCTGCAAGCCAAAAGGAATCAGCTGCTGCCAGGGGTAAACT CCCAGGCCTCATGTCTGGTGGCTCCGGGAGTCAGGAGGAGCAA CCGTGAAGGGCTGGCTGCGAGCTGAGCTTACATCAAGGATTAAA AAGCATAATATCGTGGAGTCTCTTCTGCCTGGACGCTGTTCCCT CACCACCTGTCCCCAGCCGAGGCATGGCTGATCTCACCATCCGT GGGAGAGTCTCAAATGGGTCCAGGTGAAGTTGGAACCACTGT</p>	SEQ ID NO. 152
KCP_3858 9	<p>TCAAACCTTTTCATTGCTCAAAGCCTACAGCAAACTCAGTCCAC ACACTTGGCTATACAAGAAAGGTTGCTTTCTTTGTTGTTCTATA ACTGACTTTAATTTCAACTTCAAGTCCCCATTCTTGCCAAGGGG TAGAAATGGAATCTTGGTCAACTTAGGTTCCCTCCCTACTCTC TGGGGTTGCATTTCCAGGCCAGGCAGTTTCTGCTGGTGCTTTTG TTCCTTGGTCTCTCAGTCTTCTTTCTGTGTTGACATCCATTGACA TGTCTCGACTCCCTCATCTCAGATCACAGGCCCATGCTGACT CCAGGAGTATTCTTGTATTCTCTTCATCTGAACCTCAACACTTT TTGAGACCACGCATGCATGTGCTCTCTCTTCTCTCTCTCTA ACACTTCTGGAACACTCTTGGACATGAGGAGATATTGGTCTTTT</p>	SEQ ID NO. 153

	<p> TAGGATGGGGTCAACTGGCCCTGCCTCAGATCCATTGGCCTGTA CATATCTTGTAGCCATTGTGGTGCCATGGATCACAGGTCACGAT GCTGTGTGGCTGCCTCTGCTCTTAGACCTGCCCCCATGCCACC AGAGGGAGTGTCTGCCTCCCCCTGCCCTGGACACTCAGCTGGAG GGGAGGGTCACAGTCCCTCACAGTCCCTTCTCCAGTGACAAGCA ACAAACCTCCAGTCTTCCTTTCTTTCTGATCCTCCTCCTCTT CCTCCTTCTCCTCTTCTCCTCCTCCTCCTCCTCCTCCTCCTTAT GCAAAGGCCAGAGGAGGAATAATGAGGTGGAGGTCTCTCTGAC CAAGCATGTAGCCTTCCGGATCTGTTGTGCTTTCCAGGAGTCCT TCAAAGCTCTAAGCTTTTGGAAATTCTGCAAGCTCAGGAAATTGA AAACCTTTTCTCTCACAACTGCAGGTCTTTGTCTGCAGTTGTAA AAGTCTGTTTAGAAACTCAGGAGACAAGCAGCATCTTCTTTGTT CCTGCTTTCTGGAGGCAGTCAGCGTGGAACA [A/C] CCTGCCT GCAGTCTGACTCAGGGAAAGGGTCACTGAGTGTGTGTGTGTGTG TTGAGGGGTGGATAATAAGCAAGGAGAACTCAGACAGAGAGC TCACAGAGGGGCACCCAGCACCTCCCTCACCTCTATATTTCCC GCCTGGGCATAGTGGAGGGAGGGTTAATGCCAGCCAAGTTTAAC AGGCATTTCTGATTGCGGGCATTGTTGTTGCGCTATCCTGCAAT CCTACGCTGCGGGTACTGTTTTTATCCTGATCCTTCAGCTCTGG AAATAATATAGAGAGCTGAGTAAGTCTTGAGGCCATGATGC CAGGATCCACGGTGCCCCCAGGCTGAAGAGCCTTAACCACTGGG CTGTACCACCTCACAGGAGGGCAGGTGGCACAGTGCCTGGAAC TGGGAGGGTCCAGCACGTGGAACATGCTCTGTCAATTTACTTAC TGTGTGTCACTGGATCAGTCACTCAACACCGCTAAGCCTCATTT TCCACCTCTTCAAAGGGATCTAATAAACCTGTTAGCAAGAGGC TGCTGTGAACACTAAATGAGGTGGCTTAGGTGAGAGCTCTGGTC TGAAGATGCTCACACTTTGAATCTCAAGACTTGTGTGAACCAAT ATCAGATTTCTCCTATTAGATTGCAATTCTCAGGGAGTCACATT CCGTCTCAAATGCCATCTCCTGATCCACAAAATGAGCACAAAC ATCTCTGATAAACGGTAAGTAGATGGTTCAGTGCGGCAGCGGGA GTGGGAGGGCGGTTGACTGGGCCAGAACCTCAAATGTATTCCTG TGAGTTTCTCATGCATTATTAGTTTGGCACCAGAAGGTGCC CAGACTCACTTTGCAGCCAGTCTGTCCCCATAGAGGTGATAAAG GAAAAACATATGCACATTTAACTTTTAAAAAGTTTATTTGAACA TTCAGCGATTACAAACGGTATAGCACAGACAGCAAGCAACTAG CACTCCTCTAGGAGGGGCCAAACAG </p>	
KCP_6519 9	<p> ACAGAAATCCTTAAGAGCATCAGCCGTGACACAGAAATCTAATA CAATAAAACAAAGTGCTTATAAACCCCAAGAGTTGTTTAAACCC AGAAATTGCCAATTGACATATGGGACTATATCTTCTTAGCCCT AGTAACTGAGTGGCTTCAAACAAGTCCCTATCACCTCCCAGGG CCTCAGTTTCTTACCTGTGAAATAAGAGGATCAAAAAAGATA ATGTTCTCTCTGTTCTTCTTCCAACCGAGGCAGGCATCTCAAGTA TTTCTTAGTCAGTTCTACTCTAGGCTACACAGTATCTGTATCTG GCAGCTGTATGAACTACTGTTGAAAATCCTCTTCCCAATCCCAG TTTCAACATCACTCCTCAAGGCAGCATCCACCTTCACTCTAGAC TGAATTAATTCCTCTGTCTTACCACCTAAACTCCTCTAGAAAAC TTGATAGAGGTAAAGATAAATGCATTTTTTCAAATAATCTACTT TTCTAGTCCCAAGGCATTGTGTATATCATTCTTATGTAAGTTAT CACAATAAACCCATAATTAGTTACTTCCATTTATGTCAAATCGC CTACAAAGCAGAAACATGTATTATTATTTGTTGCTTCCCTCCC AGTATCTAGCATACGAACTGTTTGCAAACATGCCAGTTCTTCA AACTTTGTAACCTTCATGCCTTTTCTATCTACTACTTGGGATGGG CCCACCTCCCTTTGTCTCTAAGCACACTCCTATTATCCTTC AAAGTCCAGCACAAAATCCCTCCTCTGTTAACTTCAACTGC TCCAGGCTGAGTCTTATGTTTGGGTCTTCATACGTACCCCTCT TCTATTGTTTGGGGTATTGTGTGCTGTGGGATCTGTTTACTCTC AGTTCTCCCTCTAGGCTGGGTTCCTTGAAAAACACCTCTGGA </p>	SEQ ID NO. 154

	<p> CATTTCACCTCTACATCCTCTGCATTCTTGGCCAGGCTCTGAGA GGGCATTGGTAAATGTTAACTGCCTGGCAATG [A/G] TGATGCT GTTAACCTGATGTGTCAGGGGTCTGAATAAAGCTGCCTCAAGGT AGGCAGATGCCCCACAACCAAGCAAGAACTCAAAGCTGCAGGCTC CTCAGCCTGAACCTTAGACAGCGTCTTGGTCACCATTTCAACAC CTTGACCACATTTCTCACTCTCCCAAATTTCTCCTGCTTATTC CTCATCCACATACATAAGGCTGTGTCTCCAGGGGAAATTCAAC TACTTGGTAATTATCCTGCTTCTTAAGTTTGGGGCTAGGGGATT CATAGATGATGTTTCAGTATTATGCTGTGCAATGTAGATGCTTCC TAAACCTTCTCAGGAGCTACCACTGAGTGGCACCTGGGGACCTC TCAGGAAGAGCCAGTTTTCTGGGCAGTGTGGGGCAGGACAGAGC TCATTAAACCAGCCTACCACCTGTCTTCCAGCTCCTCCTCTCAG CCTCTGGGCTTCCAGCAGAAAGCACACGAGAGCATTCTTGTGG TTTTCTTATGACTTGAGCCAGCGAGACGTACATGCCCAGCACCT GTTACCTGGGCTGGCTCTTGGCTGAGAGCATAATGCTTGGGT CAGGTTTCAGATCTGCTGGAGGAACACAGCCAGAATGTCTTGAC AGGCAGCCCTGGCAAAGCCCCAGAAAATATAAGATCTGAGTCTT ATGATGGACTCTGTGACCTTGAGCCTCTCACCTCGTGACCTTGG GCATCTCATGTTCTCTCCACAGGTCTCGGTTCTGGACTCCTTCA TGGGAGCTGTATGCCCCTGTACACAGCAGTGTGTGCCCCCG GGGATCAGGGACCAGGATGGTCCTTTCTTGGTGGTGAAGGGGGC ATTTTGCATATTCCAGAGATTCAAGTTTCCAGACCTATCTAGAA AGAAACATTTGAGTTTACAGGTTGGCGCTTCTCAGCCTCTGTCT CTCTTCTCTCTGTTTCATCTCCCTCTGTCCCCTCTATGTATGTT TGGTCTCTTTCTGTCTCTCTGCG </p>	
KCP_8246 8	<p> CTCACTGCCTGCAGTTTATTACAGGCATTGGATGAGACAGCTTCT TCCTGCTCCATGTGGAGTCAGCTGGGTACTTGAAGTGGGACATG GATGATCTACTTTCAAGATGGCTTATTCTCAGGGCTGCCAATG GATACCGGCTATCAGTTGAAAGCTATAAGCAGGGGCACTCTGCA TAAGCATGGCTCATCTCTACAAAAGCTCCTCCCCAGTCTCCTTG TTTGGGCCTCACAGTGTATGGTAACCTCAGGGCAGTCAGAATGT GACAACTAAAGACTTCAGGAGTAAGTATTCCAGGAAGCAAGATA TAAGCTATGTGGCCTTCTAAGACCTAGCCTCAGAGGTCACATAG TGTAACCTCTATCACACCCTATTGGTAGATATTGTAACAGAAGC CCACCCAGTTTCACAGATGGGGACATAGACTCCATTTCTTAATA GGTAACTGGCCAGAGTTGTAAAGAGCATGTGGGATGGAAGATA TTGTTGCAAGCATCTTTAGCAAATACAAGTGGACATACCCAATG CAAGCACAGGATTGATCCTCCACTCTGCCCCCATACCCCATGAT TTATTAGCCACTCGGACAAGTGACTTCAACTCTCCAAGCCTCTG TCTCCTCCACTAAAGTGGGGACAAATGAGTATTACAAATGAGAC CATTAATAAGATAATACATTTTAAAAATTAACCTGGTACCTGT CACAAAGTACATGCCTAACAAATGTTTGCTTCTGTCTCACTTCC TCAATTTTCATCTCAGTCAACCTGGACTGACTCAAAATGGCATTCT TTCTTGGCTGCCCCCTTTGAAGTATTTCTGCTGAGAAAATAGTT TCTGTGTATTTGTAAATTTACAGGTTGAACATAGATCATTATTC AAGCATTGCTGGTCGATTCTGCTTTTCAAAGGCGGGAGCTGCTG GCTGTGGGAAGGGACCCAGCAGGGGTCTCTTGCAACCCTGCTCT ATGGGTGGGGGAAATCTGGACCTCCCTCTGGT [A/G] GGGTTGA TTGAAGTGAAGGGTCACCATATGTCTTTCCCAAGAGGGTGACTG ACTTCCTGCTTTGGTCCCAGTTTCCCTGAGATTTTCTGAAAGC CCTTCCGGCTAGCCAGTTGGGAGTGTTAGTACATCAGATCCCA TGCTTTGGTGAAAAATGTAAACACAGACCTGATTTTTCATTTTA AATGAAGCCAAGCATATTGCTCCAGCAGATGCCGAGTGACTCA ATCTGTCTCTCGGTTCTGAAGGGAAGTGAAGAACAACATGGTA AAATAAAGCAAACAGCACATTTATTGGTTGATAAAATGCTGTTT TAGTCTACCCTGGCATTATATGGTGATTGCTATGTGGCGAACAT CTGTTATTAAATCCAGACTTCTGTTGCTGGATACATTGAGTCA </p>	SEQ ID NO. 155

	AAAGCTGGAGCGGATGAGAAATCCATTTATGCGTCTGTTGCGTG TGAATGTCAGAGCTCATATGATGCCTTTGTCTTCATTCTAACTG AATCTTTTAATATGGACCGTCTCACTTGTTAATTCGACTCAGG GGCAATAATGTTTTTCATTTGATTAATAAAGGTTAAAGAAACAAA GAAACAGTGTTTTCTCAGGTGCTCTAAGTAATTCGTGAATGAA TTTTCGGAGACAGCGTGTGAATTTGAAAAGAGTAGGACTTTTTA AAGAGTTCATCTATGAACCAATAATTCAGATCCTAGGGCCTT ATCCTAAGGACATAATAGAAATGAGCACATTTATAAGAACAAAG ATGTTCAATGAAGTGTTACTTACAACAGCAAAAAAAGCTTGAAAG TCACCTAAATGTTTGTAAGTCAAGAGCTTCATTGATATTGACTG CAAAGTCCATGTTATTCCATGTGACGAATTTTTTAATCAATCAC CTCTTGATGGATTTTAAATTTTTTACAATTTTTTGCTATCCTAA AAAAAATGTGTCAATGAACAACCTTTGAACTACCTTGACTACCAC TTTAGGATAGATTGCTAGACGTGGA	
KCP_8579 3	ATCACCCCAAATAGTTATGATGAAGGTGATCTATGTACGACACT TAGAGAATCAGTGATGGAAAATTCACCAAGAACAGCCACAGGCA GGCCAGAAGAAATGGCCCTGCCCTCTACTTTTAGGATTAAGCAG AAGCTGGCCCTAGATCTCACCAGTTACCAGTGATCTTGCGCAT TTTAGCATCATGTGCATTGCTTCACTGTGATACCATCTTGCTGG CACAGCCATGGAAAGCCATGAGTTAATGCATCTCCCATGTAAC AAACCTCCCCTAGGACTCTGGTCCACACCTATCTCTGCTAGATT CTCTGGCATTGCAAGAAATTTTCAGACTGCCCAAGAGATTCTG TTCCAATCTAGGGGCTCCTTATCCCCAGCTCAGAGCTGGATTTG GCTCTTGCTTGAGGCGGGAAGCCCTGCTGGGCCAGGGCTTAGA GGGGCTCACAGAAATCAAAGCAAGCATTCTCCGCTCTCTCCCT ACAGCCCTGCATGCATCTTCTCTGATCCCTTGCTGAGTGCGGG GTGGCATTCAAAAGCTCATTACTGGCTTACATACTTTGCCCTTA AATCAGCTCTTAAATGCCCTGGGATGAACAGCCCTAAATAGGAA AGAAAAAACAAGTTTCTTGCAAGTTACAGATATGCTT GGTGCTTTCTGTGCTAGGGTGTAGCCTTCTCTGTTCTAAAT TTGATTTTCTGAGTCTTTAAGGAAAAATGGCTACTGGTCCCCCTG GACGCTGATTGCTTCAGCATCTGAATCTGCTCCATCACTTCTAC CTCCACCCACTGGTCCACGTCCAGTGGGTAGAGGTAAAGGGGAT GGAGATATCATTATCTTCAAAGGATAAACTGCTCTGAGAGAT CTTTGCTTTCTTAGAAACACTGCTGGAAAGTTGTTTCTTTAGAC TACATTAACAGAAGTACCATCTCTAGGAAGACAAGGTGGTAATA ACTAACATCAAATGAGCAGTTCTATGTACCC [C/T] GTACATG TCTTAGCCAACTTCATCCTTGTAACAAACCTGGAAGGCAGGCAC TGTTATCACTCTTATTTCCAGGTGAACCAGTTGAGGTTCCAAGA AGTCTTTTGTCGAAGGTCATGCAGAGTTGAGGCCCCCAAGTCGG TAGACTTCAGGAGCCAGACCCTCAACCCCTCACTGCCTCCCCG CTCATGCTGCACTGAGCAGACCATAACCCGGATGGTCATGTTTCA GTTGGCTATCAATGCAGACCACGCTGGGCATATTGAGGGGACGG ATACTCAGAACTATATAACATAAGGAATAGAGGAAGGACTGGAG GATGTATTAACATGAAGAAAAGGTAGACTCATGGCAGGAGATGA GCAGGGTAAAGAGGTGCAAGACATAAAAAGCCAATTTCAATATAC ATGAAGATTTATCAAGAGCCAGAAGGCCCTCTATGGGTCCAAGA GTTACAAGGCCATAATGAGGTGAATTAATGCCAGCATATAAGGAA AAGCTTTTGAATACTCAGAAGTGTCCAAAAGGGGTCAGGCTGC CTTGGAAGTAGTAAGCTCTCCATCAGAGGCTTGCCCACTTCTT ATTAGGGATGGTATGAGTATCTCAAGTACAGATACAGATGACCC AAATAACCACTGAGGCACTTCTGACCCCAAGTATAAGAGATTCT ATTGTAACGCACAGGAGTCCATCTCAAGCAGCACACTGAGCCAT CTCCTTGATAAACCTAAAGGTAGGTATTATCTCCCTCCAGATGCT GTCTTCTTAGCCTGGGATGCAAAAGCCATAGGATCACTTCACGT CCAACCCCATCAGGTGATCTGTCTATGAATCACAAGTTATTGGA GCCAGATGGAACCTACAGAGCTAAAAGATACATGAAGACACCGAG	SEQ ID NO. 156

	GCCTGCAGACAGGGACTAAGTTTCCAAGGTCACAGAGCTAACAAGTGTACAGAGTCAGGCTAGACCCAGGACTCACAAGTTGAGCTCACAAATTAGTTCCACTTCCTACACCACC	
KCP_9354 5	CCTGAGCCTCTGCCTCCTTCTGAGAAAGACCCTTGTGATTACATCAGGTTACCTGGATAATTCAGGATAATCTCTTCATCTCAAAATCCTTAAGTTGATCACATCTGCAAAATCTCTTACCATGTAAGGTAACATATTCACAGCTTCTGGGGATTAGGACATGCATCCCTAGGGAACCATGATTCAACCTAGCATGGGGGAACCCACTACAGGCAGGTGTTGTCTTGGCCATCGCCAGCTCAGTGCTTGGCACAGTAGAGCCATGGATATTCATTAGAGAGAGCATGCCTGAGGCAAGCCTGACCTCAAGATCAAGACAGGAAATTGGCTTTTCATGGGTAAAGACCTGTTACTTTGCTCATCAATGTATCCTTAATCATCAGAGGTCAGATCTGCTGGAGAGTGCAATCTTTCAG [G/T] TTCCAAAAGTAAGACTGGATGCCTTAGAACTTAAAGTCAGGGAGGTACCCAAGAAAGCAATCATAGACTGAGTCCCCATGCAGTGCACCTTCTCGGATGGACAATTTCTCTGTTCTGACAGTCACTGTTGACTCCATTTCTCAGATGAGGGACCGAGGCACAGAGAGGTGCAGTCAGTCACCTGAGGCCACACAGTCAGGAAGTGGAAATCCATGGAACTCATCATCAGCTGCCCTCGCATCAGGGCCAGTGCTCTTTATCTCCACCCACACATTATAAAGCCACTCAGCTTTTACACTCAAGGGAACTTCCTATTTCCCTACTGGATTATATGTATAATTTGTAGTATTGCAAGATTTGAACAGAAGCGAGCAGCAGCTTGTAGTTGTGTGTCTCACTCACTCCTGCCGTGTTGGGATGCCACGTGATTGTTTAAAGGGTTGGAATCAGGAGAAGGCAGGCTCAGAGCAGGACCAAGAGAGAGCCCAACCCCTCGCTCCC	SEQ ID NO. 157
KCP_9784 4	ATTATAAGTATATACCACACTTTGTTTATCCATTCACTTGTGCGATGGAAATTTGGGTTGCATCCACCTTTTTTTTGCTATTGTGCATAATGCTGCTATACACATGGCTGTGCAAAATATCTAATATTAGTCCCTGCTTTTCAGTTCTTTTGGATATGTATCCAGAAGCAGAATTCTTGGATCATATGGTAATCCTATTTTTTAATTCCTTTTAGGAACTGCCATATGTTTTCACAGCAGCTGCAGCATTTTACATTCTACCAGCAGTGCACAAGAGTTCCAATTTCTCCATATCCTCACCAACACTTGTATTTTCTGTTGCTGCTGTTTGTGTTTTTTTATTAATAGTCATCCTATGGGTGTGAAGTTGTTTCTCATTTGTGGTTTGTCTTGCAGGTTTGTATTTGTAGATTTTCTGATGATTAGTGATGGGTGCATCTTTTCTGTTCTTACTGACCTTTTATATATCTTTCTTGGAGAAATGCTGTGTTAACTCTACTCATACTTTTGTAAATAGTATCCCAATCCTCTAACTCCCCAATGAGGTGGATATTAGTATGTTTCGTGTTACAGTAAAGCCAACTAAACCTTAGAAAGACTAGGTT [A/T] ATTATCCAAGGTCACACAGCTAGAAAATGACACAGCTTGTATTGAAACATCAGTTTTTCTCTTTCCAAACCTAACGCACATTTATGAAACCTACATTATTGCACCATAACATCATGTTGATTACTTATCTGCTCTCCTGCCTGTCCCATCTACTACATAAAATTGAGTGTGGTTTGAATCAGAGACTACTTCTCATCTTTGGGCACAGTGGCAGCCATGGATCAGAACTCTTACATGCTGGATAAGTGGATGCAAGCTCAAGGCCACACCTAAAGTCCCCAGGTGACTTGATCACTTGAGTTAGCTGCTGGAAACCTGGGCTTCCTCTTCTGCAAAATGGGGAGAGAAAATAAATTCCTCAGTGGATTGTTTAGAAGATTTGAGCAAAGACCTCTGCAAAGTGCTAAGCATGTGGCTAGCATGTGGCAGGTGCTGCCTAAATAGTAGAAATTAACACTGCCATGCTTATAAGCTCCGGACAAACACAAGAAAGCCGAAACATAATCTGTGCCCTTCTGCTTGCATTCTCCTGATTGGGGATGTAAATAGCCCAGCTACAATCAAAGAAGAAAATCAAAAGTCAGCACAGACTATGGATATGCTTCTATATGTGTAGATTATTTCCAGACTCATTCGGAAGAATCTGGACATACTGGTTGCCTCAGAGGTCAAGAAAATTGGCTCATTACTTCTGTAACCTTAATTTGACTCTCTATGCTTTTACATAGTTGGAATTTGCCATGCACATATACTACATTTAAAGAGCGGTGACGCG	SEQ ID NO. 158

KCP_1028 82	<p>CACAATTATGCTGTAGGTGAGTTTACCTTGGGAAACCAAGGCA CAGAATTTAAGTAACATATTGAAGCTCATGCAGCTGCTAACAGG GAAGGCCAGGGTCTGAACCCAGCTGATCCGGCTCCAGCATCCGA GCTCTGAACCACTGGTCTATCTGCCTCTGTTAGGACTTGGTCC AATGTCATCATCTAGAAAGGAACATTTAGGCCCGCACGGTGGGT GGCTGGTTCAATCCAGTTTAAAGGCCAGGAGCAGGACAGTGACT TGCAGCTGCAGCAATCCTATGACTCAAACCAAGCAGCTGTGAC AAATAAAGGGACTGACTCTCATTCTCCCGTGCTAGGGAAGGATG AGCTATCAGGCCCTTGTGTCAGGCTGAGTCAGTCATCCCAACAAC CACCTAAGTGAAACCTCTTCACTGAGCCTTATTTCTGAGCGCT CTCCCTTTATCTGTGCTTGCAAAGAGG [C/T] GTCTCCCTCCAT GCCAGCCAACCCACCCACCCCGCACACACATACCCTCTGGC TGGAAC TGACGACCATGGGTTTTAGAAATGAGATAAATCTGGGA GATGAATGTATTTCATGAGCCATAAAGGGGTTCATGAATCACTGG CCCCAATTACTGCCCTTCAATCCTGACAGGATGAATTCCTCAAG CAGATTCTCCTTGTGTCAGACAACACGGGAGGCAGTGCTGGCTG ATCTAGAGCCACAGATAACATCATTATTCCATAACCAGGCTGGTT TCGGTTTCCCAAGCCACCTCCACTTGATTTACAGCTCACTTCTG ATGCTGGAGAGAGAGATAAATATATATATATATATATATATA TATATATATATATATATATATGAAAGAAAGAAAGAAAAGAGAGA GAGAGAAAGACACAAAGGGGAAGCTTTCATGCC</p>	SEQ ID NO. 159
KCP_1073 80	<p>ATCCCAATAGGACACATGTTGTATTAAAAAGCCATGCGAGACGG AAGAAGGAAATTGAATGAAATTTGAGGGCAGGTAGGAGCAGAGA CAATAAATAATTTCAGCAGTGAAGGAAGCAGAAAAAAGATTGCAC TCATTTTCGCCCTTCAACAATTATACATAACACCTGTCTGGGCC ACAGAAGGGCCAGATCCCATTCCTGTGCTCAGGAAGCCACAGG CCGGCAGGGAGAGGCTGGTTGGAATGTGTGCTTTGCACTGTAAC GGAGGCATCGAGCATGGTAAGGGACTGGCGGTGGCTGCTGCCTG CGGACGTGAGCAGGGGCCCTTTGAAGAGGCAGGACCTGTCTGGA GTCTTACCTGGGCCTTGGCCCTGGCAATGGGGAATGGAGCAGGC AGCAGGGGACAGATGCTGCCAGA [A/G] ACCGAGATGGTGCCGG AGGACTGGGCTGAGTCTGGGTCAAATGACACCGCCCAAGGCTCT CTGCCCTCTGGGGTGAGGCAGGAGGCTGCCTCTGTGTGTGATT AGAGACCCTAGAATCCCAGTGGCCATCACCCACAGCACATGCC AACCTTTCTGTGATAACTTCTCTTGTGGAAGTGTGAAAGTGTA AGACCAGCTCCTGTATAGTGCATGGCCATCCTTTGCTTTGGGGA CAGTAAGTCAGTCAACACATACTTATAAATGGGGTCTGGGCCG TGGCACTGATCTGGTCTCCACCTTGCCCTCACACTGCCCTTCC CACTCACCCTTCCCTCCTCTGCATCTTAGCCGCAAGGGACTTT CAGACCAAGCAGACCTGGAATCAAATCCCACCGCTGGGCCTCAA TGCCAGTGGAGACAGGAACAGCTGATCCCTGGAGCCCTCAGGAG GAAGAGGACGGGATGCCTGGC</p>	SEQ ID NO. 160
KCP_1087 03	<p>CCCACTCACCCTTCCCTCCTCTGCATCTTAGCCGCAAGGGACT TTCAGACCAAGCAGACCTGGAATCAAATCCCACCGCTGGGCCTC AATGCCAGTGGAGACAGGAACAGCTGATCCCTGGAGCCCTCAGG AGGAAGAGGACGGGATGCCTGGCTTGGCTGCTGGTCTGGGGCAG GTGCCCAGTTACAGCAGTTGGAATAATCCTCAGTGTGGAAGGA AATTTGGAAGTGAGCATCTACCTGCCTGCCGTGCAGTTTGTGAC TTTAAAGATGGTTGACAGAACATTCCCAAAGGACCACAGCGGTG ACCACTGTTCTCGTTTCCCTTTGGTGGCTCACTCACTCAGTGCT GGACACAGTGGTCTTGACAAGACAGTGCTGTGGCTTCCATGAAC CTAGGACAGGGATAGACTCAAGGACTAAGAACAACCAGGAAGA AGCATCACCACAGGCTCCTTGCCAGTCACCTCATCTCACCCTCC TGGCCCTGGCGGATGGGTCTCCATATTTACAGGGGCCAGATGAA AAAACCAGAGGAGCCAGGAAAAGGAGCTTCCCTTCCCAAGGGC GCAAGGTGAGGTGCCAGTCATGAGATGCAAGCCCTGAGCTTTCT GATTCCACTGCATGTGGTCCCAAGGTTCCGGCGCCGCATCACACA</p>	SEQ ID NO. 161

	<p>GTTAGTGAGCACACTCTCCTCCCCTGGCCCCGAGTGAGCCAGCT GGATGGCAGATCAGAAAGAGAAGTCCCGGGTGCCCCAACATGG CTAGCTCCTTCCAGGACCAGGGGCTAGGCCCCAGCTAAGGCTGG TGCACACAGCAGGGCAGGGGGCGAAGGAGTGGGATCCCACCCAG GGATCCCACCCACCCCAAACCTGCTTTCGGACATCTTTCCAATG CATAATGTGCAGATGAGGCCCTTTGATAAGGACCAAATCCCTTT CCGTTGCTTGGCAACCTGGCTCACAAGTCATAGCAGGGAAGTAA TTTACAGGAATTCAAAGTGTGCTGAGGTTTC [G/T] GCTGAGC TGAATTGCTGCAAAGAGGAACCTCAATGGTCCAAATCACACCTC TGGCGGGGAGGAGGGGCTGAAGGAAAAGCTTCCACTTCCGTAC TTGAGAGTACAGAGCCCTGAGCTCAGACTCAGCGATCGTTTTCC ATTAACGGATTACTGGTTCCATGTTGAGCTCCTGCTGTGTGGC AGGCCCTGTGCTGGGAGCCAGGGACACAGTGACAAACGAGACAG ATGCCAACCCCGGATGCACAGAGCTCAAAGAGACAGAGGAGTAA ACAGGGCTACACATGTGACAAGATAGGCTGTGCACAGGGGCTG AGCAGGACCCTTGGGGCAGGAGGAGGCAGTGGAGGATGGGAGG GTAGGGACGCAGTGGTGACCAGCTAGCCAGATAGAGAACAGAGG GTGTCCCAGCACAGGGCCACACAAGCAAAGGCAGAGGTGGGGAG AGAAGAGCCTGCCACACTCTCAGATCACCATGTGGTTGGGCCAG GGCCCCAGCTGAGGCTGAGGACACATGGAGCCCAGATCCGGCAG GGCCTTGAATGCCAAGTCAGAAAGCATCTGAAATTTAGTCTACA GATGATGTGGGTTATTGACAGCCAGGACAGGGAATGACATTTGT GTTTCAGGAAAACCACTGTCTTCACTGTTAGGGGGTAGATTGAG GGAGAAAACAGGAGGTGGAGGGGAAGAACTGTGAGTAAAGGAGT CTCTGGGGTACAGGTGAAGTTTCTGTGAACTGGAGAAAGAAAC TGTGAGGCAAGAGTTGACAAAACCTGAAGTAGGATGGAGAGGA AGGGACAAGTTCCCTTGGCATGGTGACGGCCCGGTGGTGGGAAC CAGGGAAGAGGAGGGGCTTTGCAGGTGTCTGACTTGCCCAACAG GTGGCGCCATTTACCAAGATGGGAAGGGCCGGGGAGAAGGGAGG GTTCCATTCTAGGGAAATCTCAGGTCTCGCTATTAGGATTCTT TCGGTTGCCAGTGACTGAAACCCAG</p>	
KCP_1248 77	<p>ACTGTCTAGATCTGGGGACCCTCCCAAGCTCTCAGAGCTTTGGA AGGAAGGTCCCTGCAGGGAAACTGTGTGTTTCTTCAACAGTG TATCCTCAGTGCCTAGCACATGGTAAGTGTTCATAAACAGCTG TTGAAGAGACGGATGGATAACTGAATGAATGGATGCTTCCATGG GCAATGACACACTAATCTGAAAAGCCCTGTATCAATGAAAGAAT CACTTAATAGTTTAACTTTTCCCTCATCCTTCAGAACACAGATG GCATGCCATCTTCCCTTCAAATCTCTTCCAGTGCCCCACACAG AAGAGGCACACTTGGACACTGGTGTCTGATGGACCCAAGTTCAC AGCCTGTCTCTGGTCATCAGGTATCATGACCTTGGGCAAGAAGC TTAACTCTCTGAGCCTCAGTTTCCCTTCTGTCCCCCAGGGAAA ATGAGTCTTGGCCCTCCTAAGGGAGGTATGAGATGTAAGACCCC GAAGGACACAAAGGTT [C/T] GCCAGGAGCCTTCAGGTAGGAGG CAGGTAAGGAGGTCTGCTAGATTGGAATGAGTTTCTGGAAGGCC CCAAGGAGCTCAAATCAGACCTGGGGTGAAGGTGTCTTGACCA AAATGAGACCCATCAAAGAAGCCTGGATGAAGGTGCCACAGCA TCCATCAGTGCCAAAAACAGAAACACTTTAGCCCAGGATACAAG GAACATTTTAAAGCAACAGAGATAAGAGATAGTTAGAACTCAGG CCTCCTGGCTCTTGCTGTTCTTGGCCCATAAATTAGTTGTTATGG GACCTTAATAAACTTCTTGCTTCTTGGTACCTTTGCCAAACAA TCTGATGAGGAGAATATTGAGTCATGGTGCCAGGGAATAATGAGC ATATTCTGCAAATTCCTGGCACTGTTAAACACTGGATTCTGTCCA CCTTTAGAAATCCTCAGATCACTATGTCAGCATCCCCAATCAC AGCTCTCCAACCTCAAGGAGGGTTGAGGGGTCTGAAG</p>	SEQ ID NO. 162
KCP_1260 86	<p>AAGAATATCAGTTCCACTTCCCTTGTCCCTAGAGAGCCTTGATG TGGATGTTGATGTGCTTCCAACACATGCACCAACCTTTCCCTG TCCTGTAGCAGTTGAGATGGAATCATCCCACTCCCAGCTCCAGG</p>	SEQ ID NO. 163

	AATAGGCTCTGATGGGCTTGAACCCAGCAGCTTAATTCCATTGG TTCTCTAGGCCCTTCATCATTAGTACAGGAAAGGCACCTTGACCTA AATTAGTTCGATAAGATTTAAGCTCAGAAAATCTGGTTTGTTGGA TGGAGAAAGAGATGCTTTCTTTCTCTCTGGAAGGAGTTTATTGC AAAAGTAAGGGCTGGGGCTGCTACAGCCATTGTGCTACCATGAG GGAAGTAGCCATGATAACAAAACCTTGCCCTGGGGAGGGGCTACGC ATCACAGAAAATGATGCAAGTCCTGCTCAAACCTGTGCCTGAT GCCTGCCTGATCTATGGACTTCTTAGTTCCATGTAATGGATTCT CTCTATTTTAAAGCC [A/G] TATCAGGTGAATTTTGGAGAA ATAAAACAAAAGCATCTTGACTAATTTAAAAAATCTTCTTTGG GTATTCAACCCCTCCTAAACTCACCCCAAATCCACTGGGAGCAT GTCAAGATTTTTGTGAGCCGATTTAGGAGATGCAAATTCATTTG CCTTAATTGGATCTCCAGGAAATGACTTCTGCCCCCTCTTAAAT CATTTAAAGCTCAAAGAGGCATGAGGGCCCTCCCCAAGGATGCA GGTATCCTCTTGACTGACAGCCTGTATGCTCTGCTTCCAGGATC CTTCCATCTCCTCCCTTTACTGAGGGAGTCTGCTATGTGTTAGA GGTGTCCATCACTGGTCACACTGGGAAGCTGTGGCAGGGAAGCT GGAGAAAAAGCAAGATAGGCCCCAGAAAGAACCAACTCCAGA CTCAGGGAGACTCAGGCCAGAATCCTAGCTCAACTTCTTCCAAG CTCCCAAAGTCACACTCTTTTCTCTGAGCCTCGATTT	
KCP_1262 08	ATCCCACTCCCAGCTCCAGGAATAGGCTCTGATGGGCTTGAACC CAGCAGCTTAATTCATTGGTTCTCTAGGCCCTTCATCATTAGTA CAGGAAAGGCACCTTGACCTAAATTAGTTTCGATAAGATTTAAGCT CAGAAATCTGGTTTGTTGGATGGAGAAAGAGATGCTTTCTTTCT CTCTGGAAGGAGTTTATTGCAAAAGTAAGGGCTGGGGCTGTCTAC AGCCATTGTGCTACCATGAGGGAACTAGCCATGATAACAAAACCT TGCCCTGGGGAGGGGCTACGCATCACAGAAAATGATGCCAAAGTC CTGCTCAAACCTGTGCCTGATGCCTGCCTGATCTATGGACTTCTT AGTTCCATGTAATGGATTCTCTCTATTTTAAAGCCGTATCAGG TTGAATTTTGGAGAAATAAAACAAAAGCATCTTGACTAATTT AAAAAATCTTCTTTGGGTATTCAACCCCTCCTAAACTCACCCCA AATCCACTGGGAGCATGTCAAGATTT [T/C] TGTGAGCCGATTT AGGAGATGCAAATTCATTTGCCTTAATTGGATCTCCAGGAAATG ACTTCTGCCCCCTCTTAAATCATTTAAAGCTCAAAGAGGCATGA GGGCCCTCCCCAAGGATGCAGGTATCCTCTTGACTGACAGCCTG TATGCTCTGCTTCCAGGATCCTTCCATCTCCTCCCTTTACTGAG GGAGTCTGCTATGTGTTAGAGGTGTCCATCACTGGTCACACTGG GAAGCTGTGGCAGGGAAGCTGGAGAAAAAGCAAGATAGGCCCA GAAAGAACACCAACTCCAGACTCAGGGAGACTCAGGCCAGAATC CTAGCTCAACTTCTTCCAAGCTCCCAAAGTCACACTCTTTTCTC TGAGCCTCGATTTTCCCATCTGCAAAATGGGGATACTAAGGGTC ACCTAGCTGGGCTGCCCTGGAGATTCCAAGACATTA	SEQ ID NO. 164
KCP_1290 93	GGGTCCTAACAGGCCACAGACCCATCCGTGGCCAGGGGATTGG CGACCCCTGTCTTTTTTTTTTTCTTTTTTTTGAGATGGAGTTTC GCTCTTGTTGCCAGGCTGGAGTGCAATGGCACGATCTCGACTC TTCAACCTCCGCCTCCTGGGTTCAAGCCATTCTCCTCCCTCAGC CTCCCAAGTAGCTGGGATTACAGGCACCCGCCACCATACCTGGC TAATTTTTGTATTTTTAGTAGAGATGGGGTTTCTCCATGTTGGT CAGGCTGGTCTTGAACCTCCGACCTCAAGTGATCCGCCACCTC AGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACACGACC TGCCCGGGGACCCCTGTCTTAAACCACCCAGCCTGTGATACTT TGTTATGGTGACCCTAAGAGGCAAATACACCCTCCTTTCCCCAA CCTCTCCCTCAGACGAAACCGATGCGAAAAGTGCTTCATGAAG TTTCAGGTAAAGAAGT [C/G] TGGGACGAAAAGGGATAGTGAGG ATGGCGGGAGGGGCTGAACTCCAAATGGGCTTATCAAGGCTCTG CAAAATGGCGTGACGGCGCTGCCCCCTTCTGGTGCCCTGAAGAC TAACGCACATGATGTCAAGTGCGGGGCCCAAGTACTCAGGAAA	SEQ ID NO. 165

	GGTTCTCATTGACACTGGGAGGTCTTACATTGGGGGGCCCTGA GCCTCCAGCCCTTCCAAATCTATTCTCAGCAGGAGCTCAGCCAC ACCTGTGTCCCAGAACTGAGGCCAGGCCAGCCTTCACTCCACG CCCAGCCAGCCCCAAGGAACCGACTCCCTGAGGCTCTATGCTCC CTGCCTCCAGTGGCCCCGTGTCTGGGAAATAGTGGCCCTGGCCCT GATGCCCTGACCTGGGCAATCCATCCCCTGGTCTCTCAGCTCC CGGGCCAGGTTTTCTGGGCTACTTTAACCAGGGCAAACCTCATT CCTCGAGTACAAAATAAAAGATTGCAACAGCATAATC	
KCP_1291 27	GGTTAGTGGGATGCAGCGCAGGCTAAGGAGTGTCTGGGGCCAC CAGAAGCCAGGGAAGCCTAGGAAGGGTTTTCTAGAGCCTTTGG AGGGAGCACAGCCCTGCTGACACCCTGACTTCAGACTCCCAGCC TCCAGAGCTGGGAAGGGATAAGTAGCTGTTGCTTTAAACCAGTG GTCCCCAACCCTTTTGGCACCAGAAACCGGTTTTGGTTCAGTGG AAGACAATTTTTCCACGGACAGGGTGTGTGGGGTGGGAGATGGT TTCAGGATGAAACTGTTCCGCCTCTGATCATCAGGCATTAGCAT TAGTTAGATTCTCATAAGGAGTGAGCAACCTAGATCCTTCGCAT GCGCAGTTCGCAATAGGGTTCATGCTCCTATGAGAACCTAATGC GGCGGCTGATCTGACAGGAGCGGAGCTCAGGCGGTAATGCTTGC TCGCCAGCTCACCTGCTGTGCAGCCGGGGTCTAACAGGCCACA GACCCATCCGTGGCCAGGGGATTGGCGACCCCTGTCTTTTTTT TTTTCTTTTTTTGAGATGGAGTTTTGCTCTTGTGGCCAGGCT GGAGTGCAATGGCACGATCTCGACTCTTCAACCTCCGCCTCCTG GGTTCAAGCCATTCTCCTCCCTCAGCCTCCCAAGTAGCTGGGAT TACAGGCACCCGCCACCATACTGGCTAATTTTTGTATTTTTAG TAGAGATGGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTC CCGACCTCAAGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGG GATTACAGGCGTGAGCCACCACGACCTGCCCCGGGGACCCCTGTC TTAAACCACCCAGCCTGTGATACTTTGTTATGGTGACCCTAAG AGGCAAATACACCCTCCTTTCCCAACCTCTCCCCTCAGACGAA ACCGATGCGAAAAGTGCTTCATGAAGTTTCAGGTAAAGAAGTCT GGGACGAAAAGGGATAGTGAGGATGGCGGGAG [A/G] GGCTGAA CTCCAAATGGGCTTATCAAGGCTCTGCAAAATGGCGTGACGGCG CTGCCCCCTTCTGGTGGCCTGAAGACTAACGCACATGATGTCAA GTGCGGGGGCCCAAGTACTCAGGAAAAGGTTCTCATTGTGACACT GGGAGGTCTTACATTGGGGGCCCTGAGCCTCCAGCCCTTCCAAA TCTATTCTCAGCAGGAGCTCAGCCACACCTGTGTCCAGAAGTG AGGCCAGGCCAGCCTTCACTCCAGCCCAGCCAGCCCCAAGGA ACCGACTCCCTGAGGCTCTATGCTCCCTGCCTCCAGTGGCCCCG TGTCTGGGAAATAGTGGCCCTGGCCTGATGCCCTGACCTGGGCA ATCCATCCCCTGGTCTCTCAGCTCCCGGGCCAGGTTTTCTGG GCTACTTTAACCAGGGCAAACCTCATTCTCGAGTACAAAATAAA AGATTGGAACAGCATAATCAAATAGGTCATACCCATAAATCAAC ACATTTGAGCACCTATTTTGTGTTCTTTCACTAATCCAAACCA TATTTATTGAGCATCTACTATGTGCCATTCTCCAGTAGCCATTC TAGGTGCAGGGGATACAGCAGAGACCTTGAAAAAAGGAACAGTC TCTGATCTTGCTGAGCTTAGAGTCAAGTGGAGGTGAGGAGGAAG GAAATGAATTAACAACCTAAGTGAAGCAGAAGGTAACCAATTGAT TGACTGACGAAGGGGTACAAACAACAAACACCTTCCTTTCTCCA AACTCTATCTTTAACTGTATTCTCTCGTTTTCTTCTCCTCTCCAT TTTACAATCATTTTACAACATCTCTGGCTATTCTCCTATATTTCT TGATCACTTCGGTTCTCATCAATAATAATTTCAGTTTTTCAAG CATTGGAAAGTCCCATCCAATTAATAATGTCAATCTCACACGCAG TTTAAACGTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGC CTCAGTTCTGTGTGGAGGGGAGGA	SEQ ID NO. 166
KCP_1296 90	TGGTGGCCTGAAGACTAACGCACATGATGTCAAGTGCGGGGCCC AAGTACTCAGGAAAAGGTTCTCATTGGACACTGGGAGGTCTTA CATTGGGGGCCCTGAGCCTCCAGCCCTTCCAAATCTATTCTCAG	SEQ ID NO. 167

	<p>CAGGAGCTCAGCCACACCTGTGTCCAGAACTGAGGCCAGGCCC AGCCTTCACTCCACGCCCAGCCAGCCCCAAGGAACCGACTCCCT GAGGCTCTATGCTCCCTGCCTCCAGTGGCCCCGTGTCTGGGAAA TAGTGGCCCTGGCCTGATGCCCTGACCTGGGCAATCCATCCCCT GGTCTCTCAGCTCCCGGGCCAGGTTTTCTGGGCTACTTTAAC CAGGGCAAACCTATTCCTCGAGTACAAAATAAAAGATTGGAACA GCATAATCAAATAGGTCATACCCATAAATCAACACATTTGAGCA CCTATTTTGTGTCTTTTCTACTAATCCAAACCATATTTATTGAG CATCTACTATGTGCCA [G/T] TCTCCAGTAGCCATTCTAGGTGC AGGGGATACAGCAGAGACCTTGAAAAAAGGAACAGTCTCTGATC TTGCTGAGCTTAGAGTCAAGTGGAGGTGAGGAGGAAGGAAATGA ATTAACAACCTAAGTGAAGCAGAAGGTAACCAATTGATTGACTGA CGAAGGGGTACAAACAACAACACCTTCCTTTCTCCAAACTCTA TCTTTAACTGTATTCTCTCGTTTTCTTCTCTCCATTTTACAA TCATTTTACAACATCTCTGGCTATTCTCCTATATTTCTGATCAC TTCGGTTCTCATCACAATAATAATTTTCAGTTTCAAGCATTTGA AAGTCCCATCCAATTAAAAATGTCAATCTCACACGCAGTTTAAAC GTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGCCTCAGTT CTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGAGGAGAGGAA AGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGGGA</p>	
KCP_1303 09	<p>CTATCTTTAACTGTATTCTCTCGTTTTCTTCTCTCCATTTTA CAATCATTTTACAACATCTCTGGCTATTCTCCTATATTTCTGAT CACTTCGGTTCTCATCACAATAATAATTTTCAGTTTCAAGCATT GGAAAGTCCCATCCAATTAAAAATGTCAATCTCACACGCAGTTTA AACGTTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGCCTCA GTTCTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGAGGAGAG GAAAGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGGGAGGAG AGGGGAGGGGAGTGGGGGAGAAGGGGAGAAAAGCGCAGCTGGCT TCCTCACTCTCCTTTCTTCTCCTCACCATCCTTACCCTGGCCCAG GGCAGGAGGAGGATTGGCAGAGTAGA [A/G] GCAGGGTCTTCTG TCTTAGCTGGGCCCTGTGGTGACTTTCTGTTGGCCAACATGGGC TGACTGGAATGTTCTCCAGCATGGCACATGGTCATCCAGATGCA GGCTCTTCCCTGGGGCACTATAGCAGAGAGGGCTCTCTTCCAGT CTATTGCAGATGGATGCCCTCGTGAGCTGAGTTTGTGATGAACAT CCCATGTCCCCAGCCACCCCATTCAGAGCCTCTTTCTACTCTGG TCCTCTGGTCCCAGCAGCAGCCCTCTGGGTAAGGAGGGGAGGGC ATCTCACCCAAGCCCCCTTAAACCTGCTCACCTTCTTCAGAGCCC ACGTGGCCCGCAGGAAAGTCACAAACCTTGTGCTCCACAGGGC ACACGTGTGCACACGTGTGCAGCTACCTTCTCTCTAGTTGGTAC CTGAGGCTGCCCTCCTGGATTTTCCAGTCTCTGTGTTCACAGACA ACCCAAGCCCCAAGAATACAA</p>	SEQ ID NO. 168
KCP_1305 57	<p>AGTTTAAACGTTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGT GCCTCAGTTCTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGA GGAGAGGAAAGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGG GAGGAGAGGGGAGGGGAGTGGGGGAGAAGGGGAGAAAAGCGCAG CTGGCTTCTCACTCTCCTTTCTTCTCCTCACCATCCTTACCCTG GCCCAGGGCAGGAGGAGGATTGGCAGAGTAGAGGCAGGGTCTTC TGTCTTAGCTGGGCCCTGTGGTGACTTTCTGTTGGCCAACATGG GCTGACTGGAATGTTCTCCAGCATGGCACATGGTCATCCAGATG CAGGCTCTTCCCTGGGGCACTATAGCAGAGAGGGCTCTCTTCCA GTCTATTGCAGATGGATGCCCTCGTGAGCTGAGTTTGTGATGAAC ATCCCATGTCCCCAGCCACCCCATTCAGAGCCTCTTTCTACTCT GGTCTCTGGTCCCAG [C/G] AGCAGCCCTCTGGGTAAGGAGGG GAGGGCATCTCACCCAAGCCCCCTTAAACCTGCTCACCTTCTTCA GAGCCACGTGGCCCGCAGGAAAGTCACAAACCTTGTGCTCCCA CAGGGCACACGTGTGCACACGTGTGCAGCTACCTTCTCTCTAGT TGGTACCTGAGGCTGCCTCCTGGATTTTCCAGTCTCTGTGTTC</p>	SEQ ID NO. 169

	CAGACAACCCCAAGCCCCAAGAATACAAGAGCTCTGTACCAAG CATCGGGCCTGTGGCTGCACTACACGTCTGCAGCTCAGGACCCC TGGCTGCGGCGTAAGCTACCAGCATCCCCTTCTCATGGGCACCC TCATCTCCGGCTCCCCATCGCTGGGCTGTGACCTGCGGGGCGC CCCTCTATGGAAGGGAAGGAGAAAAATTACAGTGCTATCTACT CCTCTGAATGCACTCCCAACCAATTTCTTGGAAATTTCTAGCTT TCACTGACATATCTGGGATGGGGCGGTGGTCACAAAA	
KCP_1312 44	GTCTCTGTGTTCCAGACAACCCCAAGCCCCAAGAATACAAGAG CTCTGTACCAAGCATCGGGCCTGTGGCTGCACTACACGTCTGC AGCTCAGGACCCCTGGCTGCGGCGTAAGCTACCAGCATCCCCTT CTCATGGGCACCCCTCATCTCCGGCTCCCCATCGCTGGGCTGTGA CCTGCGGGGGCGCCCCCTCTATGGAAGGGAAGGAGAAAAATTCAC AGTGCTATCTACTCCTCTGAATGCACTCCCAACCAATTTCTTGG AAATTTCTAGCTTTCAGTGACATATCTGGGATGGGGCGGTGGTC ACAAAATCAATCCCACTTTCCTCGGCTAGTCTTACAAGCACCC AACAGCTCTATTGAGAATACAGGGCTGCCCAGCTACTTCCCAT CATTATCCCCAGGTTGCAAGCTTTAGTCAAAACCCAGAGGCAGC AGGGTGCTGTGGTTCACCTGCTGTTAGGATGATTTAGGAGTGC AAAGTGTTAGAAACGC [A/G] GTAAAACATGATGCTTAGAGATT AAGTGGGATGGGGACTGGGCAGATGATGCTGCTTTGGACCCAGC GAGTGAGGTGAGACTGCGACAAGACAGAGCCACTGAGCAGTGAC CTGGGGGATGGGCATTGCAGGCAAGGCAGAACCCCAAGTGGGAA CAACCTCACTGGGCTTAGCAAACTAAAGAGGCCCAAGTATAC TGAGCGATGAGGTGAGTGGCGTGGGATAAGGTTGGAGAGGAGGC TGGAACCAGACCCTGCAGGGCCTTGCAGGTGATGGGAAGGAGTT TGGAAGGTGCTGGAAGGTTTGAAGCAGAGGAGGGATATGATCAT GCCTGTAGCTGCTATGTAGAACAACCTGTATGCATGCCAGGCCTG TGCCACGCATGCTCTAATCATTACTGGCTTTAACCCCTGCACTA ACGTTGTATGCAGGTAGGAGCATCTGCACCCAGCAAATGGAAA CTGAAGCTCAGGAATATTGAGTCACTTGTCCAAGGCT	SEQ ID NO. 170
KCP_1318 54	ACCTGGGGGATGGGCATTGCAGGCAAGGCAGAACCCCAAGTGGG AACAACTCACTGGGCTTAGCAAACTAAAGAGGCCCAAGTAT ACTGAGCGATGAGGTGAGTGGCGTGGGATAAGGTTGGAGAGGAG GCTGGAACCAGACCCTGCAGGGCCTTGCAGGTGATGGGAAGGAG TTTGGAAGGTGCTGGAAGGTTTGAAGCAGAGGAGGGATATGATC ATGCCTGTAGCTGCTATGTAGAACAACCTGTATGCATGCCAGGCC TGTGCCACGCATGCTCTAATCATTACTGGCTTTAACCCCTTGAC TAACGTTGTATGCAGGTAGGAGCATCTGCACCCAGCAAATGGA AACTGAAGCTCAGGAATATTGAGTCACTTGTCCAAGGCTCCCCA GCTGTTAGGTGCTAAGGCTGGATTCAATCCAGGACTTGCAGACT CCAGTATCTTGGCTTTTCTAACGAGAGTGTGCTAGCTTTCTAAT GGGGGTGGGGAAGGCA [G/T] TCTGCCCCCTCCCATGGCACCG TGAGCAGGTGTCACTGCTCCAGCCAGTACGCCCTGGACACCGACT AGGAAGGAGTATGTGCTACTAGGAGGGATGGTCTGGGCTGACTC TTTGAAGTTGACAAGGAGTTGCATAATCCCAGCTAATAATTATG CTGGACCAGGGGCAGAGACATTACTCCAAGGTTGACCAGGTGTG GAGAAGAGGCTGCTGACTCCGGGGCCCCAGGACCTGGCCCCCAG GTCTCATTGCCCCAGTGCTGCCCCAGAAGGAGTAGAAGCTGGAG CTGTCCGGGCCACAGCCGAGGCTGGGTGAATGCTGCAGTGAGGC TGCCGCACAAGTTGCGTGTGTGACATTTGTCTTCTGGAGGGGA TTGGGATGGGCTACTTCAGCATTTAAAAACCCCTACTAGGTCTG AGAAATCCCCTCAGCTTATGAGCCTGGGTGGGCAGCAGGCCTTC TCAAGAAGCCCAGAAGGCCAGATGCTCACTTCCAGG	SEQ ID NO. 171
KCP_1326 77	CAGTGAGGCTGCCGCACAAGTTGCGTGTGTGACATTTGTCTTC TGGAGGGGATTGGGATGGGCTACTTCAGCATTTAAAAACCCCTA CTAGGTCTGAGAAATCCCCTCAGCTTATGAGCCTGGGTGGGCAG CAGGCCTTCTCAAGAAGCCCAGAAGGCCAGATGCTCACTTCCCA	SEQ ID NO. 172

	GGCTCTCTTGCGGCTGAGCTGAGAGCAGGCACCTGAGGCCTGGC AAGTGTGACAGCTGGTGACACAGACAGACAGGGACAGGGAGATG GGACTGTGCCTGCAGCGGTAGCCCTGGCCGGTGTTCAGTGGGGC CAGCATCCGTGTCTTTCTGCGGGCCAGTGGGGGCCGTGGCTCT GACGATGCATCCCTCCCCCACGTTTTTCTCTTCTTGTCTTGGA CTTTGACAGGGAGCACTCTGCTTTTGGGAACAGGAGCTGGGTCTC TGGCCATTCTCCGCAGCCCCCTACCATTCACTCAGTGGCTCTCA AAAAATAGAACCTGGG [A/G] CAAAGCTGTTCTTGGCCCCAAAC AACATGAGGAAAAATAAATAAATAATGTACCTGGTAACCTGAGAG AGTTCCCTCTGCATCTTGGGCTCTTTCAATGAGATGTCTCTGTC CTGCAGCAAGCCCCAAGGGCTTCCCTCACCAGGACCAGCACCT GGTTTGCTGACCCACACCTGCCAATGCCGGGGCAAGAATGTC CCAGGCTGCCCTGGTTCCCAGAGCTGATGCTTCCCACAGTGCCC AGCTGTGCTGGCATGGAGCTAAGGACAGGGCCAGTCCCAAGAAA ACAACAAGGCTCCAGGGCCACCGGCCACTGCTCAGGACCCCTGGC TGACCCACAGATGCGGAGTGCCTGAGATGGCTCATGGGTGACC CCCAGGCATCTGGCAAAGGTCACAATGGCTGTTTGGCTTGAAGA CAGCCCTTGCAAGATCTGTTTTGAGCCAACCTGTGGCATTTAGC CCTCCCTGGGTGACAAATAAAAAGGCTGAGGCTTGTA	
KCP_1340 45	ATTGGAAGATAAGAATGCAGCCAAAGAGGTCTTCAGGGTAGCGT GTGGCCTGGGCGCTGAGACTATTGGGCCTAGCAACTTCTCAAGC AGTCTATTAACACAGCCGGTAGCCAGCTTTTCCCCGCCCTTCT CCCAGGCACACACAGCCACCTCCATCACCAAAGGTGAGGCGAAC CACCTCCCATGGCTACCCCCAGCCTGACTTGCTTTATAGAAATC ATGGCATCTCATCTCACAACAGCCCCACACTCAGTGAATCTT GGCCATTATGACAACTGGGGACACTGAGGCTCGGAGTGGTGGA ATTCTCAGAAATCACATAACAATAAGTGTTAAAGTCAGAAATTTCA ACTTCATCTCTTAACCTCAAAGGGCGTGTGTGTGTGTGCGT TTCTGGCCATAATCATATTGTGCCCTACAAGCCCCAGTGAGGAA TCTGCTAGGAACACTGGTTTGGGGAAAAAATGTAATAAAATATG TGATCCAGAAGGCGGC [C/T] TTGGTACCTGTCATAAACCGCAG CATGGGGTACTCACTATGCCTGGGGTCTGGGCTCTGAAGGCATG ATTGAATGATCTCACTGCAGGCCTGGTTGTCTGCGAAGACACC CGTCAATACATGAATATTGACACACAACGCTGCAGTGACGCGC TTCTGGCAGGGGAGCTGCTGCACTCGAGGGCAGCTCAAGGTTAA TTTGCAGGGTTTCATGTTTGGAGTTTCTGAGCAAGTGTGTCAGCT TTGGCCCCCAGCCCCCTGAGGGGAGCTCTGCCCCGTGCATGAGGG TCAGACAGAAAATCTCCTTTCTCCATCCAGGCCTGCAGTCTGC AGCACTGAGGTGAGCGCTGGCCACAAGCCCACCCTGTGCCTCGT CAGCCCCACTGAGCCTCTCCATCTATCATGCCACAGGCTGACCC TGAAATGCAAAATCATTCTGTCTCCCGCCCTCCACTCCCACCT CGCACATCTATGGATTGTGCTGTTTCAGAAAACATCTGT	SEQ ID NO. 173
KCP_1355 18	AGTTAGATTGAGCTGGGTCCCCTCTTGGGCCTTTGCTGGTCCCT CCCTAGAAAGTCTGCCCCCTCCCCCTGCAGGGTGGCATCAGCAT TCAGGCCTGGCCCTGACGCCCTCCTCTCTGGGCCACCTTCACCT CCACAACCCCGGCACCAGCACCCATCCCCACCACATCCCCAGCA CGCAGCATCTAGTAAGGGCACCAAATGCATGCCAGACATATGA GTGAAATGAATTAACCTGAACCTGAAAAAGGGCAACCACCACA CAAGATTCTCTAGAAACAATGTGAATTGTGCAGAAGGAAATTA CCCTACTCCATCCAGCCCATCCTAAGGCAGGGACTTGGACCTGT TCCTCTTGATGGGGCTGGGGCTGAGGCGGGCAAGGCAGGCAAGT GCTGAACAGTTGGCAACATTGCCCATCCCGTCTCCCTGCACCAG GCTGGGCCTGGGGTGAGGGGGTGGGGGCCGGGGTAGCTGGGCTC CTCCAGCAAAGAGCAG [G/T] ACTGAGTCCCTGGTGAATATTAG GTAAAAGGTCCCTGACAATTTTGAAGGGCCAGATGCCAACTCGA GGGATACAGAGAAGATCTAGGCACAGTCTTTCCCCACCATGTCA GACAAAAGGTTAGATACAGGACCTGATATGTTATAAAACTCAA	SEQ ID NO. 174

	TCAATATTTACTTAGTGAATAAATGGACGGATGGATGGATGGAT GCATTAGGCAGCCAAGTGGGCAGCACCGATGACTTAATGTACTG AGTGCTCCGACTCCAGCAACATGCATTTCATTGTTCTACTGTGT GCCAGTGAACAAGAGCAATGAACTCAATGACTTCTGCCCAGGGT GGGCCAGGGAACCAGGGAAGACTCTCCAAAAGGCAGCATTG GCTGGGACGTACAGATGAGTAGGGGGTCGAGTGTGTCTGTTATGT CGCTGGAGCCCAGAGGCGTCCATCAGGACTTGGGGGAGGGCAGA TGAAAGGGCCTTACTGCCTAACTTGGAGCCACTGTAT	
KCP_1360 36	CCCATCTTGGGCCTTGTCTGGTCCCTCCCTAGAAAGTCTGCCCC CTCCCCCTGCAGGGTGGCATCAGCAATTCAGGCCTGGCCCTGACG CCCTCCTCTCTGGGCCACCTTCACCTCCACAACCCCGGCACCAG CACCCATCCCCACCACATCCCCAGCACGCAGCATCTAGTAAGGG CACCAAATGCATGCCAGACATATGAGTGAAATGAATTAACCCT GAACCTGAAAAGGGCAACCACCACACAAGATTCTCTAGAAACA ATGTGAATTGTGCAGAAGGAAATTAACCCCTACTCCATCCAGCCC ATCCTAAGGCAGGGACTTGGACCTGTTCTCTTGATGGGGCTGG GGCTGAGGCGGGCAAGGCAGGCAAGTGCTGAACAGTTGGCAACA TTGCCCATCCCGTCTCCCTGCACCAAGGCTGGGCCTGGGGTGAGG GGGTGGGGGCGGGGTAGCTGGGCTCCTCCAGCAAAGAGCAGGA CTGAGTCCCTGGTGACTATTAGGTAAAAGGTCCCTGACAATTTT GAGGGGCCAGATGCCAACTCGAGGGATACAGAGAAGATCTAGGC ACAGTCTTTCCCCACCATGTGAGACAAAAGGTTAGATACAGGA CCTGATATGTTATAAACTCAATCAATATTTACTTAGTGAATAA ATGGACGGATGGATGGATGGATGCATTAGGCAGCCAAGTGGGCA GCACCGATGACTTAATGTACTGAGTGCTCCGACTCCAGCAACAT GCATTTCATTGTTCTACTGTGTGCCAGTGAACAAGAGCAATGAA CTCAATGACTTCTGCCCAGGGTGGGCCAGGGAACCGGGAAGAC TCTCCAAAAGGCAGCATTGTTGGGCTGGGACGTACAGATGAGTAG GGGGTCGAGTGTGTCTGTTATGTGCTGGAGCCCAGAGGCGTCCA TCAGGACTTGGGGGAGGGCAGATGAAAGGGCCTTACTGCCTAAC TTGGAGCCACTGTATGTTTCAAACAAAGGAG [A/C] GAGAGGA TCCTGGGAAAGAGAAAGGGTACTCTAGGCAGAGGATGTGAATGG GCACAGCACAGGTGAGAACATCAAGACCAGGGGTCAGGGAATCT ACTGGTAAACAATTGTATCCCAAGGGAGCAATCACAGCCTCTCC ATCCACAGGGAAATGCCTGGTGGGGAGGAATGGGAGGAAAGAAA CAGATTGCATGACTGTGTCTTGAAGGTCTAATTCCAGAGTACAG CATCACCCCTATCTTCCAGGTCCAGAACTGAGGCTCAGAGGGA GACTTTCTGATGAGTGCAGCGTGCAGATAAGAGCATCTCCAAAG CTACCTCCTTCCCCAGTCACACCAGGGCATAAGCAACTGATAAC AGCTGTGACACGGGACAGTGGAGGGAACTAGGTTAGGAATA AGGGTACGAGGCTTGAGTACAGATTGTCAATGACTCAGTGTGTG AACTTGGTCAGGTGACTCCAACCAGATGACTTCCTTCTCTGAGC TTCTGTTCCCTCCTCTATGAATGGGGACAATCACTCAGCTTCAC AAAACAATGGCTGCGAAATTGCCTGGTACAAGAGAGAGAACTTC CAGTGTGTAGGGGCTGTTGTCTTAAGTCCCAGCCCCCTAGATA GGTAGTTATGTCATCTGTGAAATGGGTGTTAGAATTCCTACCTC CCAGGACAGCTGTGGGCAGAAAACCAAGAATGTGTGTGAGAGC CCAAGCACCATGCCTGGCACATAGTAGGTGCTCAGGAAAGGCTG AGGGTGCAGCTGCTGTCCACACACATGGTACCACTGCCCCAGGA AGGGGCTTCAGGAACCAAGAGCAATTCTGAGCACTGGTGACTGG ACTCTGCCATTCTCCATTTCAAACGCTTTTTGAAAGCAGCTCCA GACCAAGCAGGAGAGCAGGAGGCAAAAGAACGCAGGGGCTTT CCCGAATGGAATTTTAGAAACACACAGAATTGTCTCCTGCACAG AAGGGAAGCTGTCTCCACAGCACA	SEQ ID NO. 175
KCP_1376 60	CACTGGAGCTGAGACTCCCAGGTCCCCTAGGGCTTCTCTCCAG GGGCCTCTGGGCTCCCCAAGGCCACGTGCTGCCCCACTAGAGA CCTGGGCCAGTCCTGACCAGGGGAAAGAGTAGCGCCGACAACAG	SEQ ID NO. 176

	<p>CCCCAGATGGTATGTGCACTGGCACATACTGGCAGCTGCCTTCA TGACAGCAAGCCATAGGTCCAAATCCCGCCCTTCACAGGGACA TCCCCAAGTGGTCAGGGGTGGACCTCCCTTCCCGGCTGTCTTT GGTGTCCAGGACGATTTGCCACAGACAGGGGGAGCTAAAGGGGC CCACGCTTGAGGCCGCTCAGCTCTGAGTCCTCGCCGGCCACAGA GGACCTTCGTGCCTGTCTCTGTCTCTGCCCAGTCCCCAGGC CAGGCTCAGCTGGAGTTGGGGAGCAGAAAAACACGCATCTGAAT CAAGGCTCTCGGAGCCTTTGCTTCTGCCTCCAAGAGGCGAGGGA AAATGAATAACCCAGGC [A/G] AGCGAGCAAGAGAGACCCCTCAGA AAACCCAGATGCCCCTGGAATCAAGCCCTGTCCACCAACGCC ACGTGGATTGACAGGCTATTAGTCTTCTGTAAATTAGGATTCTC GCCTCAAATCTTGTATCTTTTTCCCCAGAAGATTCTCCTCCAG CCTTCACCACTGCCCCCTGGCGCTTCTTGCAAGGCTTTTGAAG AATCCTTTGCAGAGAAGCAGCCTCCTTTGGCAGGGGCTGCAGAG CACTCTGCCTCCCTAGGCCAGGGCGAACCAACAGAGGCGGGAGA TGAGGAGGAGCAGCGCGCTCTGCTGCGTGGCCCTGGGCAAGCA CCACAACCTCTCTGGGCGCTTTGCACATTCTTACCGCCAGGGAT GTGGGCGGTAAATGAAAGAGACCAGCACAACAGGTGTGAGCTC CCTTCCTCGATTCTTAAATGTGATGCCAAAGATGGGCCAGCC TCCTGCTGTGCCTTCTCTGGGGGGACATTAAATAAGT</p>	
KCP_1436 12	<p>TGGCCGCCTCTTCCAGATAACAACCTCTCCTCTCCTTCCCTGCCC TCCTGCTCCTCCTGTTTCGCGCTACATAACAGACTCTGTGGGGCC TTGGTTTATGTATTTCTTCTCTCCCCTACTGAAATACATGTGA GCGATGCTGGGGCAGGCCGACTAGAAGAAGCAGACTATCTGCTT CTTCTCCACCTTAGAATGGTGCTGGGCCAGAGAGGCATGCA GTGATATTTGCTGAATAAATGAATGTGAGATAAAGTGGTGTGG GGAATCCAGGGGAAAGATTTGTCAATTCTCCACCCTCCCAGTTCA GCTTAAAGCAGAGAAGTGAGAGGTGCCAAAAAGGGGTGTGTCT GGGGGGTGGGGGTGGGGATGTTCCAAGATCTCCAAGGCCTGGA TTTTAAGCAAGGTTTGAGATGCCAGCAAGAGGGCCTGGCATTGC CAGATTGATAGTCTGCATTTCCAGAGAAGGACAACCCACCTCTG ACCTTAGCCC [A/G] AGCCTCAACAGCCTGCTCAAGGAGATCCA CCCTTAGTAGGAGGAGGCAGCCAGGCCAGGTTCCAGTCCCTGCC ACCGCTTGCCAGGTGTCTTTGGGCAGCAGTTGCCCTTTGCTCGG TGGTCTTCAGCTTTGCCCCCTGCCAGGCAGTGCTGGCCTCCTG CCTGCATCGTAGCTCATGGAGTCTCTCAGTCACCTCTGTATGC CCTGCAGCATCCCCAGTTCTCAGTGAGAAGAGTGTGCTCTGAAA GTAAAGTAACTTACCCAAGGTCACACAAGGTCTGAGTCTCAAAT GCATACAATTTGACCCCATAGTCTAAGGTCTTGACCGCAATGGA ATAAGAAATTATTTTACCATTCTGAGTGGCAGTCTCTGAAGACT ACAGCAATAATTGATGCCTCTCAGGGGATAGGTGTGTCACTTA CAGGTGATAGTGAGGTTGTCTCAGCCTCCCTGCTCTTCGTTAG ACCTCCCTCCTCCTCTCTACCCGGGCCAAGCGT</p>	SEQ ID NO. 177
KCP_1449 60	<p>GCGGAACACCTCTGCCGCACCTGCAGCAGCCTTGCTCTATTTCT TCACAAGCTTCCCCATGACACTGACCCAAGGCTGTCTGGCCACT ACAGCTGCTGATGATGATTAGCAATAATAATAATAAAACGAA ATGCCTTCTGCTTAGATCATCTTTAATTTCCCCTCCAGAATGAC ATTCGACTCTGCTTAGAGTTACAGGCAGCCCAGCAATTACTGAG CGCAAATACCGTGTTCAACCGCCTCACCTCATCCAGCCCCCAC AACACCCAGCCCTGAGACTGGCTCCACGATCACCTCCACTTTAT AAAATAAGATATCAAACCTCTGAACAGAACGGACGTCTCAAAAA TGGGCATATTACATTTAAACCCCTCAATCTGTTGGGTATTTGAGT GAAATGGACATACCTCCAGGGAGTCGGTGGCGAGGGCCGGCTCT GAGGACTTCTGGGTGGGATCCTGGCTCTGCAGGACTGCGTGA CCTTGGTGAGTTACTT [C/T] ATCCCTCAAACGCGCTGTTCTC CTTCATAGAATGGAGATGACCACAGGGCCAGATTCATAAGGTTG TTCCTTGTAATACAGGTGAATATCCATACCCAGCAACTGCTGGA</p>	SEQ ID NO. 178

	CCACCTGTGGTTTTCAAGGATAATTTCCCTCCCACGTCCCCGTGG CCCTTGGAACCTTCCTCTCCTCCTGTCTCCCCCTGCCCCCATCA CTTTGTAATTGAAAAGTCATGATTGCTCTCCCAGGTGTAGCACT GCTCACAGGTCAGATTGCCTGCTCTGACGTAGTGA CTGACTCAGTTGG ATGCGGTTTCAGCTGTGTATGATCAACTCCCTCCCCCTGACAAAA ACATTATTTTGCATCACAGAGAAGTTGATTCTTTTCACACATAA AAGAAGGCAAAAAGTGGTGCCTAAAGGGCTGGTACAGCAGCTTC AAGAAATCAGGAAGAACCTGGGCTCCTTCTGCCTTCTTGTTCTG CCAATATCACCCCATGGCTGCCACTTCATGGCCCAAG	
KCP_1467 46	TTGTGAGTAGGGCACGCAGGGAAGAAACCTGTTCAACCCAGCCCC CGTGCTAGAAAGACATCAGCAGGGCCTGCAAAAGCCCTGATTAA ATCTCACAAGTTTGCACCTGGAGCCGCCATCTTGAATTGCAGGT GAATATCAGCCTTTGGTTTGGGCTGTGTGCCCCAGATGATGGTG GTCCCAAATTACATAGGCCAATATCCAGAGCTGGGTTAAAATGA AGCATTTCGAGGAAAAAATGCAATGAAATTTGTTTAAACCGGTA CTTCAGGCCTTTTGAGCACAGAACAGCGTCCATCCCTCCAAACAC ACACTGAGGATATACACTTAGCCAGGAGGGAACATAAGGAGGGG TGGACAAGCCATGTTTACTAAAATCTCTCAGTGTGTGCCAGGCA TGTTTCATGTATATTAGGAAGAAGTGTGAGTATTTAAGATCCTC GGCCCTTGCCCGAGTCCCAACACGCCTTCTTGTCTGGAGAACT GTAAATCTTGGAACATCTTGCAAGGGGGGACACCTCACAGAAG GCAGGCTTGGCATGGGATAAACAGAATCGACTCCTCTGCTTTCCT TCTGATGCACAGTGAATGGGCAGGTGGAAGCATCGTTGCTTAAA GAGGAACCAAACTCCACCCAGAGCTGCTAATTCCTTTTGGCT TGCAGTTATGCAGAGGGCTAAAAAATCCAACGAATCAAAAATCC CCTGGTTGCTAAGTAGAAAGAATATGTTTTGGCTGCTGCTGTTT CCTTCCCAAGGAAAAGATTCAAGCAGAGGGGTCCTCCACCTCT CAACACAGAAAGCAACATCTCTGATTGCCTCTAGACACACCTTC ATGCTCGTGGCACTTTGGGACCCTCTGCCCCGCTGGCTTATGGGC ATGGCTTCCCCATCACTCTGGGTCTTGGGAAGAGCCTCTTTCC CAGACCCACCTCTGTGCCTCATCACATTTCTCCAGGCTATTG ACTTGTTCAAGGTTAAGGTATGAAGAGAGTCA [C/T] GCAGCAG CCCTACCTGGCTCTGCTCTGCTGGGGGAAGCCTTTTCAGAGCCT GCCTCTTCTCAGCATGAGGGGCTGCTCGGGCCAGTCCCAGAG GCCATGCTGGTCCCAGGGGAAGGTGGCCGTCATCCCCATCTGTG TTTTCTCTTGCAGGTAAGTCATGCTCCAGCAGTCGGGAGGGTTG TGTGATGACACACTTGGCAGTTTGGGAGCAAAAGCCGCCACAGT AAGACACAATTGATTCAATTGCCTCTCAACCTCTGCTGGGGTGG ACTTTTCATGCGTGGACTTCTGTCCCCAAAGAGGCTTCTCTGGGT CTGGAAAGGGCCCTAGCCTTGGTTGGGGGAGGCAAAGGGGTGGC GGCTTCCAGGTACCATCTGGCCAGGAACCGGCTCCATTGTCTGT GCATGTAGCTTGCACCTGGGCTGCCTGCTCCAAGGAGGCATCTC CCCACGATCTACGACATTGGCTTCAAAGAGCTGCTCCTGGCAGC TTCGAATGGCTGAGACCTACTGGCATGGGATGGAGGAGTGCAGG GAGCTTCCCGGGACCTCGCTAGTCTGCTGCTGGATGCTCAGAAGG CCCTCGTCTCGGTGGCATGCAGCCTCGGCCATTTCCAAACTCA CGGCATCTCACCCAGCCATGTACCCACCCCGGCTCTGTGCCC CTTCCCATCACCTTTCTCCCACCCATCACCTCACATCAAGGTTT CAGCCAGCGGGAACCAGGTTTAGACTCCAATTACCTGTGCGTGT GGGAGGTTGGATTGTGACATCTTTGGAGGGCCGGGCTTCTGAAG CGACATTTGATTTCTGGTACTGAAATGTCAAAGGGTCTTGAGGC ACCCGCTAGGGCAGCACGCGGAGCATCCACCTGCGTGCATCCTC TGGGCTCTCTGCGGCACTTGGTGTGCTGGGGACATGCCGGGAGC TGGTGGTCAGCCCTCCTCCTGCCTCCTCAGTGTGCTGCATCTTAC CTTCTGCAGCTGCCTACCAGAAGCA	SEQ ID NO. 179
KCP_1492 16	ACACCTTGACTTTAGCCAGTGCAACTGACTCCACATTTCTGGC TCCAGAAGTGAAGAGAATACATTTGTGTTTTGTGAAGCTAGCA	SEQ ID NO. 180

	AATTTGCAGTAATTTATGACAGCGCTATGAGAAACAAAAACACC AGGATTATGCCCCAAGGATCCTGATGCCCTCCCTCCTCTCTGCT CTGCAGTGTGCTGGAGCTCACAGGGCTCTGCTGCTGGGAGTTAG TATCTAGTCCAACACTTTACCCACTCACCCCCCAAGCTAAGGGA CTCCTGAAATCAGGGACAGATGCATAATAGGTGCCCAGGAAGT GAGACTCGCCTTCCCCAGATTAGAATAAAGAAGACAACTATC CACGGCTGCTGTGAGCCTCTCATCAGACCTCAGCTTCTAGGGCA GGGTCCCTGCCTGTCTCCAGTATGTGGCCTCTGTGTCTTCTTCG CCCTCCATCCCCACAGTGGGACGAGAAGTCATCAGGAAGGCAGG GGATCTGCAGGCAGCC [A/G] TCAGGGCTCTAATTGCAGCTGGC TGGGGGACCATGGGTGAGGGCTGCCACCCCTGGCTCTGTGCCT TCACCTGTGTAACGAATGGGGCACTCACAGCCCCCTCTCAAGTGG TCCTGGGGATGAAGTGAGAAGGTGACATATACAAGTGAGTTATA CACGTTCTGTCTGTCACTCACCAGTGCTCACTGGGTGGGTCA CTGAACTCCCTCAGCGTTTCTTCTCCATCTGTAAACCACCAG TGCAAACCTTTCCAGATAGTGTGACCCGAAGCAGGAACCACT GCCCCCTCTGCCCTCAGTAAGTCTGCCAGCAGAGGAAGCCCATAG AGGGTCTTGGGAAATGAAGCCAACAGAGTCAAGAGGGTCAGATG ATGAGGGACTTCAAGTGCCACCTTCATCCATTCTTTCTGCAAA TATTCACCACACACCTACGTGACCTCAGGCTCTGTGTGTCAGGTCC TGGGGATGTAATGGTGTCCATGAAGAAACAAGGTCCC	
KCP_1495 35	TCCCCAGATTAAGAATAAAGAAGACAACTATCCACGGCTGCTG TGAGCCTCTCATCAGACCTCAGCTTCTAGGGCAGGGTCCCTGCC TGTCTCCAGTATGTGGCCTCTGTGTCTTCTTCGCCCTCCATCCC CACAGTGGGACGAGAAGTCATCAGGAAGGCAGGGGATCTGCAGG CAGCCATCAGGGCTCTAATTGCAGCTGGCTGGGGGACCATGGGT CAGGGCTGCCACCCCTGGCTCTGTGCCTTCACCTGTGTAACGA ATGGGGCACTCACAGCCCCCTCTCAAGTGGTCTTGGGGATGAAGT GAGAAGGTGACATATACAAGTGAGTTATACAGTTCTCTGTCTG TCACTCACCAGTGTCTCACTGGGTGGGTCACTGAACTCCCTCAG CGTTTCTTCTCCATCTGTAAACCACCAGTGCAAACCTTTCCCA GATAGTGTGACCCGAAGCAGGAACCACTGCCCTCTGCCCTCA GTAAGTCTGCCAGCAG [A/G] GGAAGCCCATAGAGGTCTTGGG AAATGAAGCCAACAGAGTCAAGAGGGTCAGATGATGAGGGACTT CAAGTGCCACCTTCATCCATTCTTTCTGCAAAATATTCACCACA CACCTACGTGACCTCAGGCTCTGTGTGTCAGGTCTTGGGGATGTAA TGGTGTCCATGAAGAAACAAGGTCCCTGCCCTCATAGAGTGGCC TGACATATGCCCCGAGGCAGTCAGCAGCCGAGTGCGGGAGACTCT TGAGCAGAGATTGAGTGTGTTGATATCTGTAGGCATCAGCCTGG CTTTGCTGAGTGAGCTATATCAGAGTGGAGGAGCCAGAGGCAA AGTCCAGACTCCACTGGATCCTGGATTGAGGGGAGAAGGGGCTG GGCGGAGGAGCAGCCTGAGCACCTGCATCTCACTCCAAGTGGGT GCTGATTTGTCCCCATGGCCCCAGCACCCAGGCAGGTACCAAG TAAGCTCAAGACAAAATGATGAGTGACTCAACAGTG	SEQ ID NO. 181
KCP_1567 32	ATAAATTGGATTTTCATCAAAAATTTAACTTCTGCTCCAAAAGA CACTCTTAACAAAGGGAAAAAGCAAGCCACAATATGAGAGGAAA TATTTGCAAAGCATCTGATAAAACATGTGGATCTAAAATATGCA AGGAGAATAACAACCTCTATTTTCCACTAAGGAATGAATGACTGT ACAAGGACCACATTCTAATTAGGAGCTTCTGAACCCAAAGGAAT TTCAGATAAGGGGAAATTTAGGCCCAAAGCCAGGAGAAGGGGTG AGTAGGGCTTGATCTCTGCCTCTGAAGGGCAGAGGGCGTGGACT ATTCTTGGCTCTTAGGGGACAGCTAGAGAAATGTGGGTCTCATG GCGACAACCTCTGGACTCCATTGGAAGAACCTTCTAACAGTCAGG GCTCCCAGAGATAAAC TAGACAAGTCACCAAGAGAGGCAGTGGG TACCCCTCACAGGAGGGGTGCAAATCAAAGCCAAGGCTTGGAGT GGACCATATTAAATCC [A/T] TTTCTTATCCTGTGATTCTTAGA GTCCTATCTGTATCAGGGGAAGGCAGGTGGGTCTAGAACTTTC	SEQ ID NO. 182

	TAAATGTGTCCCTGTGGGTTTTCTTTCTCCAGCTACACACAAA CTTGGGCCTAATAAGAAGTCTATGGCATTAAACCAGCAGGAATG CTTAATGCTTATATCTGACCTCAAACCAAGACTGTCTCCACAGT GAACAACCCCGTCTGTCCCCTGGGCGTCTCCTTAGCAAATGCC ATCAGTCAATGGTGCAGCCATCTTGGAGCCCTTGCCATCTATAA TCTTCTACCGCCACCCCCCAGCTGATTGTTTTCTTTGTATGTC TCCTTCCTGGACATTACTTATTCTTTACTTTTAAATATTGCTT CCGTAAAAAAACAAATGAATGCCTCGGACAGATTATATAAAGAAC ATTCTGGAGAGGCGGGTGGATTAATTATTACGCATCCCTCTCCC TTTGTAACATTTATTGTCTCATATGCATTTATATGG	
KCP_1586 17	TTGCCCAAGTGATGTTCCATGTCAGGCTCTAGGGTCCCTGCAGG GACAGAGAGGGACTAACATTTACTTACATGCCTATAGTATGTCA GGCATATACTTGTGCCTTTATATATATCAGCTCTGTTTTTGTCA TTAAAACATCCCTGTAGAAAGATAGGCACTGCTGTCCCATTTTA CAGATGGGGAAACCCAAGCTCTGAGTGGTTCAGCAAACCCCTGGG TGCATACCCCCACCTTGCCCCCTGCAAAACCAAAAAAACGAA GGCCCTGCCTTCCTGGAGCTGACATTTAGGTTGATTCTGAAAGT CAGTAGGCCAGATTTTCACTCTTCATTTTCTTGTTTGGAAATG AGAGAGCACACAGCTGGGTTCGGGGGAAGGAGCGAGGGTCTAGGC CTGCATCCACTCACCCCAAAGGAAAGGAGTAGGGGACCAGTCTG CTGGACATGCAGACAGCGATTGGAGAAAAGTCAGCCAGCTATG AACCCCATTCCTTTCAGTA [C/T] GAGCCAAGAGGGATGGCATC TGTCAGAGTTGCTGGATTGTTGGGATTTTGATCTTGCCAAGTGTC CATGAGGAATTGGGGAAACTCTCCCCCTGGCTGGACTGAGGCTT CAGCAAGCATTGTTGCTGCCCAGTGGTGATCAGCTCAGTGTCTT TGGAAGAGCAGAAAGTGGTATCACGAACATATCTTCTCCTTT GCTTCCTTCTCCTCACTCTTCATCATCATCATCATCATCAT CAAATATGGATCTGTGAGGCTACCTCTGGGGTTGAAACTTGGTT TTGGGCAAAATTTGTGATGTTCTCTCTGCCCAATCCAGCCTCAG GCTACAAATGAATGTAAAAATCTCTAATTTAGTGCCAAGTAACA GAAAACAGCTCTACTTATCTTAAGCCAAAAGAGGGACTTCTCA GAGGCATACTAATGGAGGATGGCAAGAGGGCCTCACGTGGAA	SEQ ID NO. 183
KCP_1601 45	GCTCTTCTGCTGTGGAGGATCCATGCCATTGACCTAGGCACCCG TTTTCCACATATTGAGCATTGCTGAGCACCTATTCTGTGCCAGG CACTGTGCTTCAGGGCCATGGGGGATGCTCCAAGCGGTAAATG CAACCAAAGCCCCGAAGGAGCTCACATTCTAGTCATGTCCACAA AGAGGTAATAAATCCATAAATTTGTATGTACTATTCTAGTCACAA TAAATTTGTGTCGTACTGTAATGCTGGGTATCCATTTTAAACG GGGGGCATCGGCTGAATCTGGGTCAATTACAGTAGGAAATGCATA TATATAATCATTACTCATGAATATTAATGTATTTAATGAGGGT AAAAGATATTACTTAAAGCAAAGTATTCGTTCCAGCTACTGTTG GATTTGTTCACTACTGTTTCCCATGCAGATATTACCTGTGATTT ACCTGCATATCAAGCATCTGGAAGTAGCTCAAATCCACCTGTGG GTAAATTAGGTTAGCC [A/G] TTTGTTGGCAAAATTAACAGTGT TAACTAATTTCCAGGGTATGCTTGCAAGTCAGTAGTTTTCATACTT AGGTACATGACTTGCAATTCACATCATCTGGTTAATGGTGTGAAC AGAGATTTTCTTTATGGTTTTTGGAAATACAGTAAGATAATGTTA AGCTAACGTAAGTCTGTAAACAGTACCTGGTTCTGAACTGTATT TATAAGGTGTATCATAAAACCAATTACTTTGGAGTTTGCCAATCT TAAATTCAGAACAAATTCAAAAATGAGCCAGAATCTAGTTTGCAT CATTACCACTTATAAAAAATAAGGATCTGTAAGTTGGCTGGATAA AATATATTACAAAATAATGACTTAAGTGGCTCTGGAGCCAGCAC AAAAGATAAAAATTTGGGTATACTCAAATTAACCTTCAAATATC TTAAGTCATTCTTAAATACATGTAAATATGCCAACTCAAATA CATCCAACAAAATAATATTTTTCCCAATTTGTTGGA	SEQ ID NO. 184
KCP_1648	TCGACGTTTCCAAAGTCATGGGGCCTATGGTTTGTGAGCTTATT	SEQ ID

97	<p>TAGGTTGTCCCCGGGCCCAGCATCAAAGCATTGAGACACGTAC TGAGGGACTCTTTTCTAGCCTCTCAGTCCTGACTGCTCAAGGA CCAAGTGGTACTTCTTGCTGCGTTCCTTTAATGCTTGCCTAAT ATGAGCTAGTCTTCTCTGATCACTTTTTTTTTTAATCCAAAGTA GGTGGGCATTGTCCCAAGAGCCTTTGGAAAGCAGCTGCCTCTCA CTAGGACTTCACAGCATCATTTTGCTTTGCTCTCTTTGTGGTTA AAATTACCTTCCATTCTGCTGGTGGGTGTATGTCAGGATCCCCACA AGAAACAGAGGGACACCCAAATTAGGGACATACTTCAGAGGGAC TAATGACAAAGGCATGGGTGGGAGTAGAGGGGAATACAAGGGAG ACTTCAAGAATCTTGGCCTTTATTATAAATGCAATGTATGTCCA CTATGGAAAATTTGGG [A/G] AAAAAAGCAAAGTAGAAAGAAGA AAAACACATTCCTGAATTCCTACTGCATGGAGAGAAGCATCA TAAACACCTTTTGGAGGAGTCTCTTCTTCTCTTCTCCCTTTCTC CTTCTTTGTATAGAGAGGTCTTCTCTGAGGACTTCCAGAATCT TGCAGATCCAAAATCTTAAGAATTTGCAGAGGCAGTGAGGAGTT AACATGCACAGCTCAGGGAATATTCTGCTTTTATCTGGAACCA GGCTCGGAACAAGACTCCTTGCTTTTCTGCTCTGTGTTTTCATC TTCTCTCAGAACCCTAATTTGAGATAAGATCTTTGACTATTAT TAGGCGGGTGCAAAGTAATTGTAGTTTTTGGCATTATTTTAA TAGAAGTGTCTCTGTCTCCTCAGATCTCCATCGTTCATCTCCTG ATAAGTCCCTGAAAATTTCTGGCCCCCTTGGAGCTCCTTCCAGG AGTAGAATGATCACAAGAGCTGCCATGTATTGCTTAT</p>	NO. 185
KCP_1692 34	<p>TTGCTTATTCCAACCTTGGACTTGCCGGAGTCCCATAGACAGAGG CTACTCTCCACCGTGCTGAAGCTGGTGCATGCCATGTTTTCAGT AAGAGAAAGGAGGGTGCCTGGGCTTTCGTCTCCACCCAGGTGCCT CTCCCCAGCAGCTGCACCAGGCCAGCTGAGGGGGATTTTAGCC CGAATCCAGGGTTTCTCCTACAGAAGACAAGGAGTTTGGGCACCT GCCAGAATTAGAAGAACAGAAAGAAAATGTTCTGGATTCTTCAT CAAATGCCCCCTAGCCTGAGAAATATAACTAAATTCACCCCTAGG TCATCTTACAATCTGTCTGCCCCAGTGTTCCCCACTCAGGGAA CTGCTCCACCCACATCCTGGTCCCCAAACCAGAGGCCTGGGAGT CACCCCTGACATTTCTCCTCCCTACACCCCTAATCAATCAAATCC TGTTTATCCTGCCCTCTGAGAGTCTGCACCGAAATCTCTCCT CTCCTTCCACCTACC [A/G] TGGCCCAGCAGCTTTACCATCAT GTCTCACGGATCTCTGCACCGCTCCCAACTGGCCTGTGCGTTCA CTCCTGCCCCCTCCTCCAGCCCTGTGTACACTCCCTTCCACCAT CCTTTCTATACTCTCCTCAATCCTATCTGCACCCCTCCTTCAACC CTGTCTGTACTCTCCTCCAATCCTGTCCACACACTCCAAACAAA GTCATATTTCCAAGACAAATTTGACCATGCCACTTTCTCCACA GCTCTCCACCACCTCCAGGATCCCATCCTCAGTGTTAGCCAGAC ACTCCCAAGGCCTTGTGATCTGCCCTGCCTATGTCTCCAGCCTC ATCCTGCAACTCCCCCTACACTCTGTGTTCTGGCCATCAAACCA ATGGGCTCCTCTTCTGACCCCCATCCACTCTTGACATCCTG CACTCTATGTCTGAACAGCTCGGTTTCTCTTCTTTCTTCTGGC ACATGTCTGCTCTACCTGCAGGTCATCTTAGATGTCA</p>	SEQ ID NO. 186
KCP_1738 48	<p>AAAAGGGAATTTATTGGCTCATGTAAGTGAACCTTCAACATTTTA CAGAATCTCATTGGCTCCAATGGGCTCATACGTCCATCCCCAAA CCAATCACAGTGACTGAGGGATTATCCAAGGATCACACTGGCCA CTTTACAGGTTTTATCCCTAAAGGAAATCACAGGTAATAGATG TGGGGCTGCAGAAATGCAACATGCACCTTTTCCCTTGAAACTGCAT CCCTTTTCCCTGAAGATGAAGCTTGAAAGAACTCTAAGAGGTTA AGCATGGAGCTGATGGGCAAGCCACAGGCAGAAAGAGTAGCTGT GCAGCCAGGCTCCTGGCCAGGGAGGGCAGATAAGGAGGGGAGGC AAAGTTTGGTAAACAGGAAGCTAATCTATGGGCAAGAATCATTT TCTTCAGCATCCTGACCTCTCCTAAAAATGTTCTCCACTGGTCCC TGCTAGGACAAAGGAATTACCACCAGACTAGAGTCAGGAGTCTC GGGCTGGTTCTGCTGT [A/G] TGACACAGGACAGGTGGCTTGCC</p>	SEQ ID NO. 187

	<p>TGGTCTGGGGCCACAGCCTCCTCCCCCTGTTGATGAGCATGTTGGT TGTTCAGCACCATGTCAGCCCTAGAAATCTCTGAATTCTTGAC CAGATCAGTAATTGCTCTCTTGCGTTTACTTTTCCTTCAAATAA AGAGATTGGCATAACAGGGGAGGAGCCAGTACAGACGGCATGCT TGGCTCAGGTTCCAGAACCAGAAACCAGACAAGAGTTGGGAAA CCATGATGGTGGAGGAGGGTGTGCCACTCCTTACTAGTGCCTAA TCTCTTCGAGACACTAATGTTTCAGTATTATCCACAGATTCTGA TGCCAGGCAGCCAGATGACTGGGGTCAGTTATTAGCATGCTTC CTGGAGGTGGTTCCAGGTGCAGGCTACCTGCAGTCTGGCTGGA TGGGCCCTGCACCACACTTGCTTCTGGGAAGCTGGTTTTGGGGT TGCCACAATCTCTGAAAGAATCACTAGGCCACCCTCT</p>	
KCP_1739 82	<p>TTCACAGGTTTTATCCCTAAAGGAAATCACAGGTAATAGATGTG GGGCTGCAGAAATGCAACATGCACCTTTTCCTTGAAACTGCATCC CTTTTCCCTGAAGATGAAGCTTGAAAGAACTCTAAGAGGTTAAG CATGGAGCTGATGGGCAAGCCACAGGCAGAAAGAGTAGCTGTGC AGCCAGGCTCCTGGCCAGGGAGGGCAGATAAGGAGGGGAGGGCAA AGTTTGGTAAACAGGAAGCTAATCTATGGGCAAGAATCATTTTC TTCAGCATCCTGACCTCTCCTAAAATGTTCTCCACTGGTCCCTG CTAGGACAAAGGAATTACCACCAGACTAGAGTCAGGAGTCCTGG GCTGGTTCTGCTGTATGACACAGGACAGGTGGCTTGCCCTGGTCT GGGCCACAGCCTCCTCCCCCTGTTGATGAGCATGTTGGTTGTTCC AGCACCATGTCAGCCCTAGAAATCTCTGAATTCTTGACCAGATC AGTAATTGCTCTCTTG [A/C] GTTACTTTTCCTTCAAATAAAG AGATTGGCATAACAGGGGAGGAGCCAGTACAGACGGCATGCTTG GCTCAGGTTCCAGAACCAGAAACCAGACAAGAGTTGGGAAACC ATGATGGTGGAGGAGGGTGTGCCACTCCTTACTAGTGCCTAATC TCTTCGAGACACTAATGTTTCAGTATTATCCACAGATTCTGATG CCAGGCAGCCAGATGACTGGGGTCAGTTATTAGCATGCTTCCT GGAGGTGGTTCCAGGTGCAGGCTACCTGCAGTCTGGCTGGATG GGCCCTGCACCACACTTGCTTCTGGGAAGCTGGTTTTGGGGTTG CCACAATCTCTGAAAGAATCACTAGGCCACCCTCTGAGTGGGTG CTTCTGTAGGAATTATGGATAAAAATTGTTCCACTAGTCTTACCT TCTTGGGGAACCCTTCTTGATTTCCAGGCTGGGCTGGGTGTCC CTGCAGCCTAGCCCCACAGCCCTCCTGCTTCTCTTTCT</p>	SEQ ID NO. 188
KCP_1742 43	<p>TGACCTCTCCTAAAATGTTCTCCACTGGTCCCTGCTAGGACAAA GGAATTACCACCAGACTAGAGTCAGGAGTCCTGGGCTGGTTCTG CTGTATGACACAGGACAGGTGGCTTGCCCTGGTCTGGGCCACAGC CTCCTCCCCCTGTTGATGAGCATGTTGGTTGTTCCAGCACCATGT CAGCCCTAGAAATCTCTGAATTCTTGACCAGATCAGTAATTGCT CTCTTGCGTTTACTTTTCCTTCAAATAAAGAGATTGGCATAACAG GGGAGGAGCCCAGTACAGACGGCATGCTTGGCTCAGGTTCCAGA ACCCAGAAACCAGACAAGAGTTGGGAAACCATGATGGTGGAGGA GGGTGTGCCACTCCTTACTAGTGCTAATCTCTTCGAGACACTA ATGTTTCAGTATTATCCACAGATTCTGATGCCAGGCAGCCAGA TGACTGGGGTCAGTTATTAGCATGCTTCTGGAGGTGGTTCCCA GGT [A/G] CAGGCTACCTGCAGTCTGGCTGGATGGGCCCTGCAC CACACTTGCTTCTGGGAAGCTGGTTTTGGGGTTGCCACAATCTC TGAAAGAATCACTAGGCCACCCTCTGAGTGGGTCTTCTGTAGG AATTATGGATAAAAATTGTTCCACTAGTCTTACCTTCTTGGGGAA CCCTTCTGGATTCCCAGGCTGGGCTGGGTGTCCCTGCAGCCTA GCCCCACAGCCCTCCTGCTTCTCTTCTCATCACAGTCTGTTA TCTCTACCAACTGTAGGCCTGCCCCACTGATGGTGTGAATAAAG GGACTGGGTCTCTCTAGCACCTAGCATAGATCTGATACATAGTG GGTGATCTCTATTGAATGAACGATGAATGAATGAATGAATGAAT ACATTTAGATAATTCAGATTACTCTTTCTAGCTCAGCAGTGTA AGCAGGAAGACATGCTGTCAATATGATTTAGGGCAAGTTT</p>	SEQ ID NO. 189
KCP_1751	AACGATGAATGAATGAATGAATGAATACATTTAGATAATTCAGA	SEQ ID

06	TTACTCTTTCTAGCTCAGCAGTGTAAGCAGGAAGACATGCTGT CAATATGATTTAGGGCAAGTTTTCAAATCTCTCTGGACCTCAGT TTTACCTCTTGAAAAATAAATAATAAATTTGTCCTTACTTCAT GAGACTATTTTGAAGATTAAATGAGATAATGTATACACTACTAC TCACTGTCCTTACTTGAATATTCCTAGGTCCTTGGTGCTACATT AGGCTACATAGAATGTATTTAAAGTAATAGAGTGGTATTTAATA AATATTCATTTTCTTTCCCCAGAACTACCTTAAATTAATTTGTT GAAAGGACAGATGGATGGATGGTGTGATGGAAGTAGCAGGCTTCC AGCAGCAGGGGATGGAGTGAGTGTGTGGATACCGCTGGATCAGC AGAAGGTTATACCATTTTAGAGTAACATCTCGGACTTCGGAGA GTTCTGCGGTATGAAG [C/G] TTTGGCTTTAATTAAAGTCTCAG CACAGTGTTAAATGCCATTTTATTTTAGGTCATAATTAACACTA ATGAGATGAGTGGATTACAAAGAGCACACATTTTGAGAAAGTGA AAAACAACATCTGAGCTTGGTGGTTTCCATTTTCGCTTTTCCCC CTCCCATGCTCTGTTCAATTAAAAGTTTTTGAGAAAATATTACAA CCATACTCCTTGTCTTTGTGGTAATGAAGCATATTAATTTGAAT GTGATGAATACAATATTCCTGACTTTTTTATTCCCTTATCTA CAAAAGTTTAAATAATGGACCAATTAAACCAGGAGAGAAGAAT GCAGGGTTTGCCTGGGGATCCAATTCAGCAACCAGAGAAGTGAA AGAACAAAATTTTGTGACGGAGTCTGGGCCAGACTTCATCCCTT ACCTATAGCTGACAAACAGTAAGTCAAATTTGGGCAGATGTGGAC CAGCGCAGAACACATACTATATTGAGGATCGAAAGGC	NO. 190
KCP_1751 70	GTGTAAAGCAGGAAGACATGCTGTCAATATGATTTAGGGCAAGT TTTCAAATCTCTCTGGACCTCAGTTTTTACCTCTTGAAAAATAAA TATAATAATTTGTCCTTACTTCATGAGACTATTTTGAAGATTAA ATGAGATAATGTATACACTACTACTCACTGTCCTTACTTGAATA TTCCTAGGTCCTTGGTGCTACATTAGGCTACATAGAATGTATTT AAAGTAATAGAGTGGTATTTAATAAATATTCAATTTCTTTCCCC AGAACTACCTTAAATTAATTTGTTGAAAGGACAGATGGATGGAT GGTTGATGGAAGTAGCAGGCTTCCAGCAGCAGGGGATGGAGTGA GTGTGTGGATACCGCTGGATCAGCAGAAGGTTATACCATTTTAG AGTAACATCTCGGACTTCGGAGAGTTCCTGGGTATGAAGGTTT GGCTTTAATTAAAGTCTCAGCACAGTGTTAAATGCCATTTTATT TTAGGTCATAATTAAC [A/G] CTAATGAGATGAGTGGATTACAA AGAGCACACATTTTGAGAAAGTGAAAAACAACATCTGAGCTTGG TGGTTTCCATTTTCGCTTTTCCCCCTCCCATGCTCTGTTCAATT AAAAGTTTTGAGAAAATATTACAACCATACTCCTTGTCTTTGTG GTAATGAAGCATATTAATTTGAATGTGATGAATACAATATTTCCA CTGACTTTTTTATTCCCTTATCTACAAAAGTTTAAATAATGGA CCAATTAAACCAGGAGAGAAGAATGCAGGGTTTGCCTGGGGATC CAATTCAGCAACCAGAGAAGTGAAGAACAATAATTTTGTGACGG AGTCTGGGCCAGACTTCATCCCTTACCTATAGCTGACAAACAGT AAGTCAAATTTGGGCAGATGTGGACCAGCGCAGAACACATACTAT ATTGAGGATCGAAAGGCCAGGTTCCAGACCGTCTCTAATATTT TCTTAGTGAATATTTGTTGGATGAATGCATGGATGGG	SEQ ID NO. 191
KCP_1752 52	CTTACTTCATGAGACTATTTTGAAGATTAAATGAGATAATGTAT ACACTACTACTCACTGTCCTTACTTGAATATTCCTAGGTCCTTG GTGCTACATTAGGCTACATAGAATGTATTTAAAGTAATAGAGTG GTATTTAATAAATATTCAATTTTCTTTCCCCAGAACTACCTTAAA TTAATTTGTTGAAAGGACAGATGGATGGATGGTGTGATGGAAGTA GCAGGCTTCCAGCAGCAGGGGATGGAGTGAGTGTGTGGATACCG CTGGATCAGCAGAAGGTTATACCATTTTAGAGTAACATCTCGG ACTTCGGAGAGTTCTGCGGTATGAAGGTTTGGCTTTAATTAAAG TCTCAGCACAGTGTTAAATGCCATTTTATTTAGGTCATAATTA ACACTAATGAGATGAGTGGATTACAAAGAGCACACATTTTGAGA AAGTGAAAAACAACATCTGAGCTTGGTGGTTTCCATTTTC [A/G]] CTTTTCCCCCTCCCATGCTCTGTTCAATTAAAAGTTTTGAGAA	SEQ ID NO. 192

	AATATTACAACCATACTCCTTGTCTTTGTGGTAATGAAGCATAT TAATTTGAATGTGATGAATACAATATCCACTGACTTTTTTATT CCCTTATCTACAAAAGTTTAAATAATGGACCAATTAAACCAGG AGAGAAGAATGCAGGGTTTGCCTGGGGATCCAATTCAGCAACCA GAGAACTGAAAGAACAAAATTTTTTGACGGAGTCTGGGCCAGAC TTCATCCCTTACCTATAGCTGACAAACAGTAAGTCAAATTGGGC AGATGTGGACCAGCGCAGAACACATACTATATTGAGGATCGAAA GGCCAGGTTCCAGACCGTCTCTAATATTTCTTAGTGAATATT TGTTGGATGAATGCATGGATGGGTGGATGAATAGATGGATGGAT GGACAGATGGACGGAGAGAGATGGATGAATGGATTGTTGG	
KCP_1768 36	GCAGGCCTGTGAACCTGACACATGGTCCAGGTGTCTCCCTGAGG ACTTCTGGAAGTCTCCCCACCTCTCTGTGGTCTTTAGGCATTA ACACCACCTTGTCACTGTGTCTCTGAGGCAGTCTGGAAGTTCA TACCCCACAATCTCTGTGTACCTTGTCCCCATTCTGTTCTCTG CATTCAGATGGTTTAAACACACACACATACACGCGCAAAATG TTGTTCTTTTCTTAAACCCATTGTGGCCAGGCTAGACAAATC CTTAACACGGTCTACAATATTCTGCATGGCATGGCCCCCTGGGTG CCTCCCAACCTGATCTGTCAACACACCACCTCCACCTTTGCGTGT TCCCTGGGCCCCTAGCACTAACCTTTGGTTTCATTCCTAGACACCT TTTCAGCACTTAGGCCCCACAGCCCTCAGAACCTTTACACTTG CTGTCTCTTTTGCTTTAA [A/G] TGTTCTTGCCCCACCTACCAC CTAGTTAATGCCTTTTCTCCTTCAGCTCTTAGTTGAAGCATCA CTTCCTCAAGGAGGGCAGCCCTGATGAACTCATATGCAAACCT CCAGCCTGGGTGGGCCCTTATCTTTATGCTGTGATGGCCCTGAG TATCTTCCTTTATGGCACCAATCACGGCTTATATGATATACTT ATGCTATTATTTGAGTTATGTCTGTCTCCCCAGTAGGCCACTA GTATTAGAATCATTGATTTTTAATCATTGTATCCCTAGTGCTTA GCACAGAGCCTGGCTCATAATAGATGCTTAATAAATATTTGTTG AATAAATGAATGAGTGAATGAATAAATGCCTCATTCAAGAGCTT TGGCTCTTTCTGTACTACTACATTACTTCTATTTTTTAGCTCTT AATTCTCAAAGCACTTTCTTTGTGCTGGGCTTATGCTGGGAGCT TAGACAGTAAAGCTTAGA	SEQ ID NO. 193
KCP_1801 73	TTACATCCACAGGTTTGATTATAAATGTGTGATTGAATTGGAA TTTCTGTTGAAATTCTGATCCCTTCTAGACAAAGAAGGTAAAAA TTGAAACATGTCAATGGATATCTAAATATCATTACTACTGGCT TTATTTGCAAAATGGCTTTCCATTGACAACAGTTACATTTGTTC AAAGCAACAAATGATTGGCGCTGACAATCCACAGGAACATGGTG CAGTCATTAATGAATGTGCTCATTATTCCTCCCTGCCGGGAGGC ATCGACTCCCGTTCTCCAGCCTGTTTTAAGCAGACAGACCTACA TCTGCACCTGTGAGCTTGGAACCCTAGTAGGGGAGGGGGATGCT GATGTGATGGAGAATGAAGAATGGGCCCTGCAGGCTGACATTTT GGGAGAGTAGGTTCTGAAATTTATCCCAAAGGACATGGAATCCT GGAAGCAGGGTTCAAGATCCTCCCAAATTGATCTCCAGGATG CTTGGAATGATTGTTT [C/T] GAGGGTTTTGTAAATGCCAGGG GAAAACCAGGAAGCTTCTCTCCAGTTGTCTTGCCCTCCTTCTCT CCAGTCTCCATGGAGCTGACTTTGAGAATTAACCTCTGAGGGAC AGAGACCCTGGGATGGAGAGCCAGCCCTGCTGGATTCCACAAGG TGCTGCTTAAAGCACACACCTCTTCCCAATGACAGGTTCTGAA AGAAGGCCTTGTAGCTAGATGCACAGAGGGTTTTGTTTTGTTTT TTTTTTTTTAACCTTTTCAGCATCTGTCTAAAATGCTCTGGGCT GGGTACAGTGGCTCCACCTGTAATCCCAACACTTTGAGAGCTG AGGCAGGAGGATCGCTTGAGCCCAGGCGTTCTAGACCAGCCTGG GCAATATAGTGAGATCTCTATGTCTAGAATGTTTTTTAATTAGC TGGGCTTGCTGCCTGCACCTGTAATTCAGCTACTTGGGAGGCT AAGGTGGGGGATCACTCGAGCCCAGGGGGCTGAGGC	SEQ ID NO. 194
KCP_1802 37	CCTTCTAGACAAAGAAGGTAAAAATTGAAACATGTCAATGGATA TCTAAATATCATTACTACTGGCTTTATTGCAAATGGCTTTCC	SEQ ID NO. 195

	<p>ATTGACAACAGTTACATTTTGTTCAAAGCAACAAATGATTGGCG CTGACAATCCACAGGAACATGGTGCAGTCATTAATGAATGTGCT CATTTATTCCTCCCTGCCGGGAGGCATCGACTCCCGTTCTCCAGC CTGTTTTAAGCAGACAGACCTACATCTGCACCTGTGAGCTTGGGA ACCCTAGTAGGGGAGGGGATGCTGATGTGATGGAGAATGAAGA ATGGGCCCTGCAGGCTGACATTTTGGGAGAGTAGGTTCTGAAAT TTATCCCAAAGGACATGGAATCCTGGAAGCAGGGTTCAAGATCC TCCCAAAATTGATCTCCAGGATGCTTGGAAATGATTGTTCCGAG GGTTTTGTAAAATGCCAGGGGAAAACCAGGAAGCTTCTCTCCAG TTGTCTTGCCCTCCTTC [C/G] TCTCCAGTCTCCATGGAGCTGAC TTTGAGAAATTAACCTCCTGAGGGACAGAGACCCTGGGATGGAGAG CCAGCCCTGCTGGATTCCACAAGGTGCTGCTTAAAGCACAAACAC CTCTTCCCAATGACAGGTTCTGAAAGAAGGCCTTGTAGCTAGAT GCACAGAGGGTTTTGTTTTGTTTTTTTTTTTTTAACCTTTCAGC ATCTGTCTAAAATTGCTCTGGGCTGGGTACAGTGGCTCCACCT GTAATCCCAACACTTTGAGAGCTGAGGCAGGAGGATCGCTTGAG CCCAGGCGTTCTAGACCAGCCTGGGCAATATAGTGAGATCTCTA TGTCTAGAATGTTTTTTAATTAGCTGGGCTTGCTGCCTGCACCT GTAATTCAGCTACTTGGGAGGCTAAGGTGGGGGGATCACTCGA GCCCAGGGGGCTGAGGCTGCAGTGAACCATGATTACACCACTGA ACTCCAGCCTGGGCAACAGAGTGAGACCCTGTCTCAA</p>	
KCP_1840 80	<p>CTGATGGAACCTGGGATGTGAGAAGAAGGCAGGTTTTCTGATAAA CAATTCCTGTATCTTTCACAAATGCCAAATCACAGACTCAGCTT GGGACATATGAGGACAGCACAGACTTTGGAGGCAGGTAGATTTT GGGTTGTACGCAGACACCCACTACTATGAGACCTGGATTTCTT TCTGACGTTATTGGGGATAAGAAGTGGCACCTCACCATTCTTAG GAAATAGTAGGTAAGTCTTTCTGGTTGCCACTGAGGTGACTCAC CTGAGACACAGTTGCTCCTAAAGTTCAAGGTTAGGAGACAATCC AGAAGGGGAGCTGTCTGTGAAGTCAGAATTCTTGGAAGAATGTA AGTCTTTACACAGTAACAGCAAAGCAGACAGTGGGAACCACTAC TCTGCCTTCTTGATCATCTTTCTCTAGAAATACCAGAAAGCAG TGAGGGATTAAAGTCTAATTCTGGCACCTGACCTTATATCTAAC AGATGCTCAGTATTAC [C/G] TGTTGATGGGACCTCACTGGGAA TGTTTTGTGTGCAGTACAAAAGGGCAATAGATGAAACTTTGGGA CGGGAGCCCAGGAAAATGGCTGAGAGGAGAGCTTATGCCCTAGCT TATGCATGAGCTTGCAAAAGGGAGAATACACGGGAGGGAAGAT CAGCAACAGCATGAGTTTTATAAGGCAGAGAGTTGTTGGGAAGG AAGCAGCAGGGAGAGGGGAAGGAGTAAGTAGAAACCTAGAAGAG ATACAGCTAAGATAAGCCAAGAGAACAAAGTATTGACTTACCAG AAACATGGAAGTCTTCTGCTTCTAATTTAGTTCCGCATATCTG GATATGTGAATGCCTAAAATCCCATTAAGCCCAGTGGGTTAATT ATTACACTTGCTAGGGCCCCAGAGGAGAGGAAAACACAGTAAGTC AGAAAAACCTCTGGGCAGGTGAATTTCTCAGGTTTTCTTCTGGG CAGATGGGATCTGGAATGGTAGCGTGGCATCCTGGTA</p>	SEQ ID NO. 196
KCP_1855 79	<p>CCTTTCCAATATTAAATAATATTAACATTGGTAATAGTGGTAC TAAACAACCTAGGGTGTTTTTTTTTTTCATTTAATAGTATATTTT TAGTATCTTTCCAGGAAAAGATACATGGATGTGCCACATTATTT TTAATGGCTCACATGGTACTCCTTTTATGTATGCACTATAATTT ATGGAACCAGTTTTCTCACCGATGAGCATGTAAGTTCTTTTCAGT CTTTTACTGTTATAAACGAATGATGCAATGAATATCCTTGTA TATATATTTGTGCGCATATGTAGGTATCCTTACAAGTGGAATTT CTGAATAAATGGATATATACAATTTATTTATGAATTTACCTTCC TACAAGTGATTCAAGAGAGTGTCTTTGCTCCACAGTGTTGTCAA TATAGTGTATTCTCAAAATCTGACACCAATATGTGTGAAGTGCC TGCTCTGTTCCACACTTTACACAGGTTCTCTTATTTG [C/A] G TTAAGTTTATTTAAGAAGAGGAACTGGGCCTCATGGAGATCTA GGAACCTTGCCCAAGGACAGGTCTCTGTGACTCTAAGAGTGCAAT</p>	SEQ ID NO. 197

	CTTCCCTTTTCCCATGTCAAGCACCTTTCCCCACCAGGCTCAC TGCTGACAATCCAGTGTACGAAGAAGGGAAATTACCCCCACAGA GCCCAAAGTTTAGGACATGCCGACAGCATCACTCTTTTGCCTC CTCATTCTCTCTTTTCAATTTCCAGAACATTTGCTCACTCAGTGCT GCCCAGTGATACTTAGCCAGCCTGATTACCCATCTAATAATTTT TGATACTAATATAAAACCTTTCCCAAAGACAAATATAACTGAGAC GCACTCCAGCTTACCATAGCTTTTCTGGTGGTACAGTTTCCAGG GACATTTCACTGTGTCAAAGCAGGGACCACATATGTTCCAGACC AGCTTGTGGGTTTTTCACTGGGAAGTGAAGACAAATTGTTGTC CCTT	
KCP_1860 48	TTCCACACTTTACACAGGTTCTCTTATTTGCGTTAAGTTTATT TAAGAAGAGGAACTGGGCCTCATGGAGATCTAGGAACCTGCC AAGGACAGGTCTCTGTGACTCTAAGAGTGCAATCTTCCCTTTTC CCCATGTCAAGCACCTTTCCCCACCAGGCTCACTGCTGACAATC CAGTGACGAAGAAGGGAAATTACCCCCACAGAGCCCAAAGTT TAGGACATGCCGACAGCATCACTCTTTTGCCTCCTCATTTCTCTC TTTCATTTCCAGAACATTTGCTCACTCAGTGCTGCCAGTGATA CTTAGCCAGCCTGATTACCCATCTAATAATTTCTGATACTAATA TAAACCTTTCCCAAAGACAAATATAACTGAGACGCACTCCAGCT TACCATAGCTTTTCTGGTGGTACAGTTTCCAGGGACATTTCACT GTGTCAAAGCAGGGACCACATATGTTCCAGACCAGCTTGTGGG TTTTTCACTGGGAAGT [A/G] AAGACAAATTGTTGTCCCTTTGA AAAAGCATCTTTCATCTCTCCATCTATCTGCGATCTAAAGCAAT GGGGCTCTTTCTGTATGTCCTTCAAATGGTCTACACTGACACAC GTTTTCTCTGAGCTGCCGAGAGAATATGCCATGAGATGTTGCCA GTGATGGTTACACTCAGCTAGCAGAAGATTAGGGACTGGTTAAA CCTTTGGAGAAATTGCCCTTGGGAAAAGAGGAAATAAAAGCAAAT ATTACTATGAAACATAGAGATTACCAGGTAGGAGGAGGAGAGAG GTGGAGGGAGGGGTAGGAGTGGAAGGAAGGGAGGGAGGCAGAAA GAGGAAGGCAGACTGGTGGAAAATAAACCGTGCACTTTAGAACA GCAGGAAGGGAGGCTTGGGAAGCCTGGTTTTCTGGCTTTGAATGA CCGCTTAGCGCTTGCCGGTGCGCCAGGGTGCTGTGAGGATGTGG GCAGAGGGCGAGTCCGAAGGGCTCCAGACACTGGGAA	SEQ ID NO. 198
KCP_1866 79	GAGAATATGCCATGAGATGTTGCCAGTGATGGTTACACTCAGCT AGCAGAAGATTAGGGACTGGTTAAACCTTTGGAGAAATTGCCCTT GGGAAAAGAGGAAATAAAAGCAAATATTACTATGAAACATAGAG ATTACCAGGTAGGAGGAGGAGAGAGGTGGAGGGAGGGGTAGGAG TGGAAGGAAGGGAGGGAGGCAGAAAGAGGAAGGCAGACTGGTGG AAAATAAACCGTGCACTTTAGAACAGCAGGAAGGGAGGCTTGGA AGCCTGGTTTTCTGGCTTTGAATGACCGCTTAGCGCTTGCCGGT GCGCCAGGGTGCTGTGAGGATGTGGGCAGAGGGCGAGTCCGAAG GGCTCCAGACACTGGGAATAGTGGTGGTTCGTGTGCTCCTCCCTG AACTTTTTGCACTACCTCGGACTGATTGACTTGTGAGACGGTAA GCGAACCTTGGAGCTTCCCCGTTTTCTGTGAATGTGTTTTTGTG GCTTCGGTTGCTGTGA [C/G] AGTCGTTTCGAAAATGCACGGAA ATGAGGGCGGAGACCCGAGAGATTTGAAAAAGCCGGGTGAAAC AGCGTGGTATTGGTCCCCGCTCCCCAGTCGCGCCCCAGTGCTG CGCTGTCCGTGCTGTGAAATGTGGTGCCTGGGGAGTGCGGG AGCCAGGAAGTTAGGGTCTCCTGCTCCGGCCCTATGAGCATGTG AGTCTTGATGGATTATTAGCTATGGGTGAGGCCAGCACACAACA TCACAATTCTCTCTGAAGCTGTCTGGTAACCTACGTATATTGTTG ATGGAAGCCAGTGACTTTTAAAGCCATTATGTTGATTAACTTT TTTAAAGAAGTTTAGGAGATTATATGAGGTAAACCTTTGTA AAATGCTAATCACAGTGTCTGACAATTAGAACACATTTAATAAA TGTCAGTTTTCTTGTCTCAACCCTTATAAGAACCTTTATCCAAA GCCACCTCCTCAGCTCTGACTTCAGCTCCATTCCTTA	SEQ ID NO. 199
KCP_1871	TGCTGTGACAGTCGTTTTCGAAAATGCACGGAATGAGGGCGGAG	SEQ ID

16	<p>ACCCGAGAGATTTGAAAAAGCCGGGCTGAAACAGCGTGATTG GTCCCCGCCTCCCCAGTCGCGCCCCAGTGCTGCGCTGTCGTCG TGCTGAAATGTGGTGCGCCTGGGGAGTGCGGGAGCCAGGAAGTT AGGGTCTCCTGCTCCGGCCCTATGAGCATGTGAGTCTTGATGGA TTATTAGCTATGGGTGAGGCCAGCACAAACACATCACAATTCTCT CTGAAGCTGTCTGGTAACTACGTATATTGTTGATGGAAGCCAGT GACTTTTAAAAGCCATTATGTTGATTAACTTTTTTAAAGAAGTT TAGGAGATTATATGGAGGTAAAAACCTTTGTAAAATGCTAATCA CAGTGTCTGACAATTAGAACACATTTAATAAATGTCAGTTTCTT TGCTC [A/G] ACCCTTATAAGAACCCTTATTCCAAGCCACCTC CTCAGCTCTGACTTCAGCTCCATTCCCTAGTGAGAATGGGGTTA TAAATCCAGGTTAACCCGATTGTTTAGGATTAGAAAAGTATTG GTTTCCAACGTTGAAGGAGTTCAAGAAACAAAGAGTTTATTTT TCCTCCTTATGAGATATTGTTCCAAATAGAACACAGTTTGTCTA GATGATTTTGTCACTTAAAATTAGGCTCCAGGAAAGATTCCAA ATTTTCATGAGCAATTGGGCTCATAAAACAAGATCAAACCTCCAAT AGTGTATATCCAAAGTATGTATAATGTGTATTCCGGTGTATATTC TTCCACCACTGCATGGTGTAGACAGAATTTCTCTTCCAAGGGGC ACCACATGACAAAACCGTACATAAATGAAATGCATTTGTAGA CAAAGGACTAGCTAAAATACCAACTGAAAGTGGGAAGACCAGAA ACTGAAG</p>	NO. 200
KCP_1872 58	<p>AATTGCCTTGCGAAAAGAGGAAATAAAAGCAAATATTACTATGA AACATAGAGATTACCAGGTAGGAGGAGGAGAGAGGTGGAGGGAG GGGTAGGAGTGGAAGGAAGGGAGGGAGGCAGAAAGAGGAAGGCA GACTGGTGGAAAATAAACCGTGCACTTTAGAACAGCAGGAAGGG AGGCTTGGAAGCCTGGTTTTCTGGCTTTGAATGACCGCCTAGCG CTTGCCGGTGCGCCAGGGTGCTGTGAGGATGTGGGCAGAGGGCG AGTCCGAAGGGCTCCAGACACTGGGAATAGTGGTGGTCTGTC TCCTCCCTGAAACTTTTGCACTACCTCGGACTGATTGACTTGTC AGACGGTAAGCGAACCCTGGAGCTTCCCCGTTTTCTGTGAATGT GTTTTTGTGGCTTCGGTTGCTGTGACAGTCGTTTCGAAAATGCA CGGAAATGAGGGCGGAGACCCGAGAGATTTGAAAAAGCCGGGCT GAAACAGCGTGATTTGGTCCCCCGCTCCCCAGTCGCGCCCCAG TGCTGCGCTGTCCGTCGTGCTGAAATGTGGTGCCTGGGGAGT GCGGGAGCCAGGAAGTTAGGGTCTCCTGCTCCGGCCCTATGAGC ATGTGAGTCTTGATGGATTATTAGCTATGGGTGAGGCCAGCACA ACACATCACAATTCTCTCTGAAGCTGTCTGGTAACCTACGTATAT TGTTGATGGAAGCCAGTGACTTTTAAAAGCCATTATGTTGATTA ACTTTTTTAAAGAAGTTTAGGAGATTATATGGAGGTAAAAACCT TTGTAAAATGCTAATCACAGTGTCTGACAATTAGAACACATTTA ATAAATGTCAGTTTCTTTGCTCAACCCTTATAAGAACCCTTATT CCAAAGCCACCTCCTCAGCTCTGACTTCAGCTCCATTCCCTTAGT GAGAATGGGGTTATAAATCCAGGTTAACCCGATTGTTTAGGATT AGAAAGTGATTTGGTTTCCAACGTTGAAGGAG [G/T] TCAAGAA ACAAAGAGTTTTATTTTTCTCCTTATGAGATATTGTTCCAAT AGAACACAGTTTGTCTAGATGATTTTTGTCACTTAAAATTAGGC TCCAGGAAAGATTCCAAATTCATGAGCAATTGGGCTCATAAAA CAAGATCAAACCTCCAATAGTGATATCCAAAGTATGTATAATGT GTATTCGGTGTATATTCTTCCACCACTGCATGGTGTAGACAGAA TTTCTCTTCCAAGGGGCACCACATGACAAAACCGTACATAATAA TGAAATGCATTTGTAGACAAAGGACTAGCTAAAATACCAACTGA AAGTGGGAAGACCAGAAACTGAAGTGTAAGATGAGGTAAGCCCT GGAGTAAGAGTCAAGAAATCCACTTCTATCCATAATCTGTCTC GGTTTAATGTTGGTCAAGTCATTTTTTAAAAAATTCAGGTCTT GGTTTCCTTATGATGACTTTAGATCTCTGTTTCCTTGGAAATCTA GAGTGATCCAAAGGTTTCTTTGAATTCAGTTTTGTGGGTGAGA CGGGCAGCCAGACTGTGAGTCCCTCAGCTCTGCTTCAACCAGAA</p>	SEQ ID NO. 201

	CAGCTCCACTTTACTGTTTCAGCATGTTAGCCCTGTATGTAAGGA TGTTTTTTAGCTTTAGCTAAAATTTAGTGACTCTATGACCCATA GGCCCTGCTTCCCTGAGATTTTGAAAGCTGAAGCACATTCGGAA AACTTTTTCTTCCCTAAAATCACCTGAAATCTGACAATCTGGA AGACTAGTTCTGTCTGCTCCAGCCCTTGGTCCCTTAGATGTGCT TTTCTGAAGATCCAACTCAACCTGCCAGTCAATATACCAACTG AGCAGAGCCCTGTCTCCACCAGATTTCAAGAGAACATGTTCC ATTCTGTTCAGAGCTTCAGAGCAGCTTCCGCTAAGATTGCACA TTAATGCAACAGCGTCTATTTTCTTTGTTTCTTTTTTTTTTTT TTTTTTTTTTTTTGATGAGACAGGG	
KCP_1876 88	ATTTTTCTCCTTATGAGATATTGTTCCAAATAGAACACAGTTT GTCTAGATGATTTTGTCACTTAAAATTAGGCTCCAGGAAAGAT TCCAAATTTTCATGAGCAATTGGGCTCATAAAACAAGATCAAAC CCAATAGTGATATCCAAAGTATGTATAATGTGTATTTCGGTGTA TATTCTTCCACCCTGCATGGTGTAGACAGAATTTCTCTTCCAA GGGGCACCACATGACAAAACCGTACATAATAATGAAATGCATTT GTAGACAAAGGACTAGCTAAAATACCAACTGAAAGTGGGAAGAC CAGAACTGAAGTGTAAGATGAGGTAAGCCCTGGAGTAAGAGTC AAGAAATCCACTTTCTATCCATAATCTGTCTCGGTTTAAATGTTG GTCAAGTCATTTTT [T/A] AAAAAATCTAGGTCTTGGTTTCCT TATGATGACTTTAGATCTCTGTTCTTGGAAATCTAGAGTGATC CAAAGGTTTCTTTGAATTGAGTTTGTGGGTTGAGACGGGCAGC CAGACTGTGAGTCCCTCAGCTCTGCTTCAACCAGAACAGCTCCA CTTTACTGTTTCAGCATGTTAGCCCTGTATGTAAGGATGTTTTTT AGCTTTAGCTAAAATTTAGTGACTCTATGACCCCTAAGGCCCTGC TTCCCTGAGATTTTGAAAGCTGAAGCACATTCGGAAAACTTTTT CTTCCTTAAAATCACCTGAAATCTGACAATCTGGAAGACTAGT TCTGTCTGCTCCAGCCCTTGGTCCCTTAGATGTGCTTTTCTGAA GATCCAAACTCAACCTGCCAGTCAATATACCAACTGAGCAGAGC CCCTGTTCTCCACCAGATTTCAAGAGAACATGTTCCATTCTCTGT TCAGAGCTTCAGAGCAGC	SEQ ID NO. 202
KCP_1893 31	CTCTAAAATTTACCCTCTGTTCTGTACACCAAGTACCTCAGCA AGTAATCCAGTTCCAGATGGGATCTGCAGTCTGCCATTAAGTCT TTACCACACATAGGCTCTTATGTAGAGCCCTTACCATATGGTC CAAAATGCCATTTTAAATGTGTATTTGATATGGAGACTCTGTTT ACAATTTGAGTACTAAAGAGAGAATACCACCTCTAGTAGATAC ACCAGGACCAATGTAATGCTGTCAATCTAAGGAGAGCAGTGAA CATCTCCAAAGAACCCTCTGTAGTCTTCTTCCGGCCCTGTATC TTATTCTTATTTTATTTTAAAGGTTTTTTTTTTTTTTCTTCGAGA CTAAATCTCACTCTATCACCAAGCTGGAGTGCAGTGGCATGAT ATCAGTTTATTGCAACCTCTGCCTCCCGGACTCAAGCGATTCTC CTCACTCAGCATCCCAAGTATCTGGGACTACAGGCATACACCAC TATGCCCAGCTAGTGT [A/G] TGTGTGTGTGTGTGTGTGTGT GT GCCAGGGTGGTCTTGAACCTCCAGAGCTCAGGCGATCCACCTGC CGAGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACAGCG CCTGGCCAATCTTTTAGGGATAATTTTAGAACAGTATACAGATA TTGAGCCAAGAGTCAAAGAGCTGGGTTGCAATTCTGGTTGTGC CATTTATCAGTTGTGTGAGGTGGGACAAGTCTCTTTTCTCCCT AGCTTTCTCTTTCTCTTTTATAAAATAAAGAAATGAGAATGAT AGTTGTATTAATTTCTGAGGACTGCCAGAACAAATTAACAAA CTGGGTGGCTTAAAACAACAACATTTATTCTCACATAGTTTCA GAGGCTAGCAGTTTGAAATCAAGTTCTTGACAAACTCCCTAGA GTCTAAAGTCTCTAGAGAAGGATTCTCTCTTGCCTCT	SEQ ID NO. 203
KCP_1927 42	GAGCAAGCACTGCAGCCATCTCCTTTATTTCCCTCAAGGCAAT ATCCAAGGATTAAGTCAAGAGCCGTCTGCAGATTCCTCTCT CTACCTTGCCCTGCATTTTTTGTGCCCTTCTCTTCCCCCTCTC	SEQ ID NO. 204

	<p>CAGCCCCAACCTCTCTCCTGATCCACGGTACTCCTCCTGGGAT GTCCACTGGGGCTGATCCTCCCCATTCTCCCCCTGAGTTCCCT GCTGTTAATCTGTCTCCAGCAAAATTAACCTAGCCTATGTCCCA TGCCCTCTGGACTCTGGCTGCTCGTCAATCACTCTTAAAAATCC GGTTTCTCCTTAGGCAATCATTTTGTTTTGATTTTATGTGTA AAAACCTGAGTAAATTTTTTTTTTTTTTGAGATGGAGTCTTGCT CTGTTGCTCAGGCTAGAGTACAGTGGCATGATTTCTGCTCACTG CAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCT C [T/C] TGAGTAGCTGGGACTACAGGTGCCACCACCATGCCTG GCTAATTTTTGTATTTTTGGTAGAGACAGGGTTTCATCATACTG GCCAGGCTGGTCTCAAACCTCTGACCTTGTGATCCACGCACTTC GGCCTCCCAAAGTAATCACTGCTGGGATTACAGAAGTGAGCCAC CGTGCCTGGCCAAACCTAAGTAAATGTTTTAAAAATTATACTACT AACATAGCATACAGGCTTTAGACTGTTGGTTGCTTTTAAAGTTTG CTTACTTTTAAAGCTAGAGAGAAGATGGTTGAGGTGATCTTGTC TCCTTCAGTATTCACCTCTGAGCCATGCCTCCTGAGGAAGTTTGC TTTAGGGGAGGCATTGCTATGTTATACACTCTACGATGCACCAG CCCTTGCTCAGAAAGGCAAGGTTTGAACCCCAACACTGTCTTTT GCAAACCTGTTACCTTAGGAAATAGATTTTATCTCCTTAACTCAC TTTTTA</p>	
KCP_1931 93	<p>GTTCAAGCGATTCTCCTGCCTCAGCCTCTTGAGTAGCTGGGACT ACAGGTGCCCCACCACCATGCCTGGCTAATTTTTGTATTTTTGGT AGAGACAGGGTTTCATCATACTGGCCAGGCTGGTCTCAAACCTCC TGACCTTGTGATCCACGCACTTCGGCTCCCAAAGTAATCACTG CTGGGATTACAGAAGTGAGCCACCCTGCCTGGCCAAACCTAAGT AAATGTTTTTAAATTTATACTACTAATACATAGCATACAGGCTTTAG ACTGTTGGTTGCTTTTAAAGTTTGCTTACTTTTAAAGCTAGAGAG AAGATGGTTGAGGTGATCTTGCTCCTTCAGTATTCACCTCTGAG CCATGCCTCCTGAGGAAGTTTGCTTTAGGGGAGGCATTGCTATG TTATACACTCTACGATGCACCAGCCCTTGCTCAGAAAGGCAAGG TTTGAACCCCAACACTGTCTTTTGCAAACCTGTTACCTTA [G/A] GAAATAGATTTTATCTCCTTAACTCACTTTTTACATTTGCAAAA TGGGTAAATTGTGACTACCTCACATGGATGTCATGAGATGAAAT GTAAGAATGTGTGTCCCTGGCATATAGTAACCACTTTTCGCCAAA GACTGAGTTATCCAACCTACAGACAGAGAACAGCTGGTGGCCTAA TCAAAGGGAGATACAAAATAACAATGCCAAGACTGGAAAAGGAA GTTTCATCTTAGGATTTCGAAGAGAAAAAGAAATATGACTGTATT ATAATAGGTATATTTATTAAGCTCTTACCATGTGCCAAGCAAAG TTCTTTATATACATGATATACTTCATATACATTATTTTCAATTTAG TCCTCATGGCTACCAGGTGAGCACCATTATTTTCCATTTTACA GATGAGGCACAGAGAAGTTAAGCCACTTACCTAGGAAGGGCAGT CCTAGTTAAGAAGCTGGGATTCAAATCCAAGAGGCTGGATTCCA GACCTCAGG</p>	SEQ ID NO. 205
KCP_1939 56	<p>TTATAATAGGTATATTTATTAAGCTCTTACCATGTGCCAAGCAA AGTTCTTTATATACATGATATACTTCATATACATTATTTTCAATTT AGTCCTCATGGCTACCAGGTGAGCACCATTATTTTCCATTTTA CAGATGAGGCACAGAGAAGTTAAGCCACTTACCTAGGAAGGGCA GTCCTAGTTAAGAAGCTGGGATTCAAATCCAAGAGGCTGGATTTC CAGACCTCAGGCTCTATTATGAGAAGTACCTAAATAGAGATTGG TTTAACCAAAGCCTGAGTCCCAACTAAGGGCAAGACTGTGACAC AGAGGTCACTAATCAGAATGAAAGATTGAGCCAGAGTTGAGTTG TTGGAATGTATTTTGGTACATTTAGGTTGTTTTAAGTATATCAA TCTCCATTCCACTCAATGGTTGAGTTCAAGTTTCAAGTTTCCAA ATGCTTTATGGGAAAGTCATATTTTCTCCATTGCAGCAGGGGA TGCCAGCGCAGCCATG [C/T] TTCTCAACCACCAAGTAGAAGCA AAGCCAAACTGACCCAAGAAGATGAACAGAGGGAATCCAGGGAG TTCCAACCTTGGGTTTACAGCTGCAATTCTCAAAGGATGGACTAA</p>	SEQ ID NO. 206

	GCCATGTCACCCCTCCAGATAACACAGTCATATTAATAGTGACC TTTTGGAGGCCTCCCTAAACAGCAGGTGAAGTCCCAAAATCATT AGATTATTCCTGGCCTCAATTGTGGCCCAGAGGGAGAGCCCTAA GATTTTCCATGGGAACAAAGATCTAAATTCTGGGACTATCTGG GCCATGTCCACCCTGCACCATTACTACAAAATGGGCTGATCCT ATGGAAGCACACTACCTGTGTTGTGGTCATATAGATCATCACCT GGCTTCTCCAGGGCTAACCAGTTAGCATGGAAATGGGACACCCA AGAACAAGAGGATAGAAAGAAGGGAAGGGTGGAAAGAAGGAAGG AAGAAAGGGTGGGAGGGGAAGAGTGGTAGTTTTG	
KCP_1946 16	TCCTGGCCTCAATTGTGGCCAGAGGGAGAGCCCTAAGATTTTT CCATGGGAACAAAGATCTAAATTCTGGGACTATCTGGCCATGT CCACCCTGCACCATTACTACAAAATGGGCTGATCCTATGGAAG CACACTACCTGTGTTGTGGTCATATAGATCATCACCTGGCTTCT CCAGGGCTAACCAGTTAGCATGGAAATGGGACACCCAAGAACAA GAGGATAGAAAGAAGGGAAGGGTGGAAAGAAGGAAGGAAGAAAG GGTGGGAGGGAGGGAAGAGTGGTAGTTTTGGAAGGAAGGAGGGA ATCAGAGCTAAAGATAATACATGATATGAGTCAGTGTTCATGT CCCTGAAGATTAGGGGAATCAAGCTTTGCTTCCAGGAGAATTAA CACAGGAGAGCCAACAGAGATGTGGAAATTTAGGAAGTCAGAGG AGACATTCTTTCA [T/C] TCATTCATTCTGTTTATTTCATT GCTCATTTTTACATGAATTGACTCTAGAACAGATGCTGGAGATA CAAAGATGCATGAGACTTGCCCCATCCTCAACAGTCATTCACA GTCTAATCAGAAAGAGAGCCTTGCAATTTGGAATACAATATGGAG TAATAATACCTCTGTGTTTCAGCCTGCACAAAATACTCTGTATGC ATGGTCATATGTCCCTTGAAACAAC'TTATGAGGAAGATACTAC TATAGTCTCCATTTGACAGATAAGGAACTGAGGCTTAGGGAGG TCAAATAACTTGCCCAAGTAAACAAC'TAGTAAGTAGCTGAACC ACAAAACAGAGATTTCATGCAGAAAGCTGTACAACAGAAGAAACC AGGACTACATCTGCCTCAAAGGAACCAGAGAAGGCTTCAAAGA AGGCAGCATTTTAAATGGGTTTTGAAGGATGTATAGCA	SEQ ID NO. 207
KCP_1965 48	CCCAGCCCTCAGGCACATCAGTGCCCTCTCTAGGCTCTCTCTCA CCAAC'TTTAGAATTGAATTACATCAGTTGTTTCCAGATGGTGAT CTGCAGAATTCCTTTAAAGACCACCTGTGGGATTTGAGGGAGGA AACTTACACTCTCCCAATCTCCCTCTTTAACCCAAGCATCTGAT TGCTTTTCATCTGTTTACATACTTAGCTTCTGTGCACAACTTCC TTTGATTAAAGAGTTCCCTTGCCCTTATAGTAGTGGATGATATCT AAGGATGATGTAAATACTGGGTGTTAGCTAAGGTTTTTACCAA CTTAAAGCCTTTATGCTTCATAATTCCACTTTATTGATGTAGGA AGACAAATGATAGACTTACTTTCAAGGTGGATAGAAGGGATGCG ACCTAGCCAAGGCTACAGCATTCTCT [A/G] TGGCACCCTGC CATGACAACCATCAGTTTGAATGCCTTATGGGTGCATCCTATGG GTTATGCACTGGCCCCAAGCCATAACCCCTAGGACTCTAGAGCC AGCAGCAAACACAAAACACTGAATTAATAATGAGTGAGATCTCT GTTCCCATAGCTGCCACAGGCTAAATAAGTTGAGGGGGTATTGT AAAACCCAAGATGAGATCACTGAGCCTCTGGTATCAAAAAGGTG TATTTACAGAAATGTTTAGTTGGACGAGAGCTTGAAGAGCATGG AAACGATCTGGTATCATTCTGGTCAAAGACCAGAAATTTAGACCC CAGTTCTGCCATTTGCTGACTAATGACTTTGGGCAAAATACTTA ACTTTCCCTGAGAGTTAGTTTCCCTCATCTATAAAGTGGGGTAATA TAACCCACCTTGCAGGATACTGGTAGGATTA	SEQ ID NO. 208
KCP_1976 78	AGCAGGGTCCCCTGAGCGTTCCCTCCTCAGCTCCCAACACTTCCC TCCAGGCACAGTATGCAGGGCAAGGTCTGGAGGGGGCGCCGA AACACCACTCGAGATCCTCACTCTCAGGAATTCAATATAGAAAA CACATTAAGACCTGTTTACATGGAACTGCTGTTTATAATTATTG TTCCCTATGGGATATTCCCACTGCTTCCCTCCAATCCTCTTTTA AACTGCTCAACTAATAGAGTTTTCTGGCTTCCCCAGGGAGACA TTCACAGATGCTAATAGAGACATAATTCAAAAATTGCTTGATAT	SEQ ID NO. 209

	ACATGCCCTCAATTTTCCCCAAGAACCACCTAAGTAAAGAGCCC CAGACATGCAACACATTTCATTGGCCAGATGCAATTTAACATGCG TGGGATTAAATATACAGGCTACTACAGCCAGGTTGTCATCAAGC AGCAGCAGGCATGGCATTATCCTAAGGTACCACCA [T/C] GG CCAAATGCAACAGGAAAGAAGCAGGCTGCTGGGTGGGACCCCTG GAAGATCCCCCTCCTCTGTAATTTCCACTGCAAGCTTTTCCCAGG CCTTTTTCAGGCAAAGCGGGGAGTTTGGAAAATAAATCCCCCAGG CTTGGAGAAGCAAAGAATCAATGCTAAGCAGCTCCGGAAATAAT AGCTTCCATCTCTCTGATATATAAAGAGGATAAGGAAGGCAGAA AGAAGGGGCATGATATTATGAGATTGCAACAATACATTGCAACA TTACATTAAAGAATTACAGAAAGCAAGATCTAGCTTCAGATGCC AGTTCATGCACTTACTCCCTGTGTGACCCTGGGAATCACTTAAG CTGTCTGAGACTTAGCTTGTCTAATGACAACTGGGGATACTAA TATCACCTCCCAGGATTGTTGGGAAGGTAAATGGAGATTGACAA ATGTGAACACACTTAGTATGTCTTT	
KCP_1977 75	TGTTTACATGGAAGTCTGTTTATAATTATTGTTCCCTATGGGA TATTCCTCCACTGCTTCTTCCAATCCTCTTTTAACTGCTCAACT AATAGAGTTTTTCTGGCTTCCCCAGGGAGACATTACAGATGCT AATAGAGACATAATTCAAAAAATTGCTTGATATACATGCCCTCAA TTTTCCCCAAGAACCACCTAAGTAAAGAGCCCCAGACATGCAAC ACATTCATTGGCCAGATGCAATTTAACATGCGTGGGATTAAATA TACAGGCTACTACAGCCAGGTTGTCATCAAGCAGCAGCAGGCAT GGCATTATCCTAAGGTACCACCACGGCCAAATGCAACAGGAA AGAAGCAGGCTGCTGGGTGGGACCCCTGGAAGATCCCCCTCCTCT GTAATTTCCACTGCAAGCTTTTCCCAGGCCTTTT [C/T] AGGCA AAGCGGGGAGTTTTGAAAATAAATCCCCCAGGCTTGGAGAAGCA AAGAATCAATGCTAAGCAGCTCCGGAAATAATAGCTTCCATCTC TCTGATATATAAAGAGGATAAGGAAGGCAGAAAGAAGGGGCATG ATATTATGAGATTGCAACAATACATTGCAACATTACATTAAAGA ATTACAGAAAGCAAGATCTAGCTTCAGATGCCAGTTCATGCACT TACTCCCTGTGTGACCCTGGGAATCACTTAAGCTGTCTGAGACT TAGCTTGTCTAATGACAACTGGGGATACTAATATCACCTCCCA GGATTGTTGGGAAGGTAAATGGAGATTGACAAATGTGAACACAC TTAGTATGTCTTTACATAGTAGGTATTCAATAAACTCTTCTATA TATCTTCTCTTTCTGAAAATCTGAATATGGGGAGCATGGATATG	SEQ ID NO. 210
KCP_1989 33	GTCCCCACCCTCCTTTTTATTGTCAGAGGGAATTGACATTCAGG GAATGGAAATGCCAGCCAGCAATTGGGGATGTGGTCTGGGAAC CCAGGCTCTCCATCCCACTCCCTCGCCCTCTCACCCCTCCCGC TGGTCAGTGTCTTTGTCCTCTGCTGGCATCCCTGGGGACGGGC CAGCCCCCATCCCCCGACACACACACATTGTCCCTTCAAGATG GAGCCAGGCTGACACCACGTAGAATGACCTGGAAGCCCCCACTC AGTCTACCAGTCCCTCCCTCCTCACACAGGAATAGATGGGAGGGA AATGAAATAAGCTGCCATCTGCTGTGCATCCTCTGTGTGCCATG CTCTGGGTACCCATCTAATCCTCGTGAAGACCCTGAGAAGTGAG TGTTCTTCACAGACTAGGCAACACCAGAAGGCAG [G/A] TGAAG AACGTACAGAAGCTACAGAGTGACAGGTGACAGGTATGAGAGC CAAGCCATTCAAACCTCCCTGGGTATAGGACCCAGCTCTTCCCAC GTCTCTGCCTTTACCGAATCAAACACCTGAGCACGGAAGACCCT CCATCAACATGAACCTGCTTTGAATTGACATGAACAAGCTTCAAT CAAACATAAATGCTGAAATTTTTCAATTATAGAAAGTATTTGA AAGATCCCATAAATTCCTGTGTCATATCACGTGAGCTGCATTTA CTGCAGCAGACACTTTTTATCTCGGGCTTGGAGGAAGGATTAGC AAGAAGAAAGTGGAGGGGGTCTGAGGAAGGGCTGGCAGCCTAGA GGAGGACAGCAGCAAGAAGCAGGCTGGAGGCAGTTCTGTGCTGC CGGCCTTCATGGGTGTGGCCTTTGGACAGCACCTTAGCAGGAAT GTGGTGGAGAGCAGCCCCATTCACTCCAGAGGAGAGC	SEQ ID NO. 211
KCP_1993	AAGACCCTGAGAAGTGAGTGTTCTTCACAGACTAGGCAACACCA	SEQ ID

65	GAAGGCAGGTGAAGAACGTACAGAAGCTACAGAGTGACACAGGTG ACAGGTATGAGAGCCAAGCCATTCAAACCTCCCTGGGTATAGGAC CCAGCTCTTCCCACGTCTCTGCCTTTACCGAATCAAACACCTGA GCACGGAAGACCCTCCATCAACATGAACCTGCTTTGAATTGACAT GAACAAGCTTCAATCAAACCTATAAATGCTGAAATTTTTCAATTA TAGAAAGTATTTGAAAGATCCCATAAATTTCCCTGTCTATATCAC GTGAGCTGCATTTACTGCAGCAGACACTTTTTATCTCGGGCTTG GAGGAAGGATTAGCAAGAAGAAAGTGGAGGGGGTCTGAGGAAGG GCTGGCAGCCTAGAGGAGGACAGCAGCAAGAAGCAGGCTGGAGG CAGTTCTGTGCTGCCGGCCTTCATGGGTGTGGCCTTTGGACAGC [A/G] CCTTAGCAGGAATGTGGTGGAGAGCAGCCCCATTCACTC CAGAGGAGAGCCTCAAACCTCTCAGGCAGATCTAGCCTAGGTAG AATCTTGGCCTGGCCCCTCCGGGATGACAGGTGCCATTGCCCAA GAATGGGGAAAAGGCTGAAGTGCTCCAGCCAAAGACCCCAATTT ATCTTCAGGACAATTTTCACTGGAAACCTTGCCTCACCCTGCC CACTTTTTTCAAGTAATTAGAATGCTAATCTATAAGAAAGATG ACTATTAAAAATAAATTAATAATAGATAATACATTTTGGCCTTAC AATTTTGAATAATATAGCCATCCCATCTTAAAGTAAAAATTCAT ATATTTTTAATAAGCCTGAGACATGTTTTCCAATGAACCACAGA TGGTTCATTTTTATTATCTATAAAGAGACATTATGGGCAAGTG TTTTTTAAATGGTAAACAGAACCTTAGAGCAGCTCTCTTTT	NO. 212
KCP_2002 41	GGCAAGTGTTTTTTTAAATGGTAAACAGAACCTTAGAGCAGCT CTCTTTTGAAGATCTCTAAGCACTTTCTAAGCATCAGGACCCCC TTCTGTCATCACAGAGACTGAAATGAGGAGATGGTCTCTGTCTAC CCCCTCACTCACCAGTGAGCCCCAGACCTTCATCCCTGATCAGA TGGAAGCAGTGTGGCATGATTACAGTTTCATATTTCAACTCTGCC ACTCAATGACTAATAGCCAAGCACTAATAATGCAGAAAAATGTAA ATTTAAAAATAATCTTCTGAGATTGGTTATGAAATGCACTCA ACACAGCACCATCCACAGAGAGGTTCTTTTAAATGCTCTTTTC TTTCCTCTCGACACCCAGAATCACAAAGCATGCCTGAAAGCGTC ACACATATATGTCTGTGACCATAACATGGCATTGCACATGCAAA GGAAATAA [A/G] TAGGTGTTACCCATGTGACAAAGGTCCATGA GCTCTGTCCGCAAAAAGCTGTTGAGTTTAAAGAACAAATAATTC TGAAAAATCTTCCAGGAGATGAAATTTGTAGAACTCAAGGGCAG TAAACTAGCTGCTTTCCAAGGACTTGTCTAGCTTTATTGACTT ACAATAGCCAAAGATAAGTCAGTATTAATCAAACCCATTCTCTA GAAAAACCTCATCATCACTGGGGCCAGGGCAGAGAAGTGTGACA CAGCTCTCTCCAGCTTCCCCACTTCACAGCATGGTTCCACCATC CACCCAATTGCTAAAGCCTGGATAGTCTTCTTGTACCTCCCCG ATCCCCCTCTCTAACACCCATCCCCCGGCCACCCAACATCAGCA AGTCTGGTGGTTTCTCTCTGTCTCAGAGATTCAAGATCTTCCC	SEQ ID NO. 213
KCP_2019 85	TCGTAGTGTTTCATAGACTCTCCTTCCTTAACCTTAAAGAGG CTCCTTCTGGTTTTTCTCTTCATACACTTCCCTCACTTTTTCT TCACTGCACTAAAGATGATTTCTAATTGCATAGTCATTGATGCC AGTATTTGTTTATTGTGTCTTCTGCTGAACAGAGGATGGGCC TGACTTATTGTTGGGACCATGTTGCTGATGCCTGGACCTAAGCCTG GCACAGAGTAGGAGCTCAACAAATTTGTTAAATGAGTGGCTGAA TGGCCATACTCTCAAAGGACCCACAGTCTAGGAGAGACAGAAGA ATCTTTGTCTTTTTGTCTTGCAGTGGGATGGAAGCTGCAGGGAG GGGTCTGTCTCATTTGATACTGTCTGGGAAGACAGAAAACTT CAGTTTCAGAGGAGGTAGCCCTTGAAAC [G/A] AGATTGAGAG AGGGCAGCACATTGTACAACCTCATGGGCACCATGCAATTGTA GTCCAGATAAACAGAGCCCCCTTGGAGATATGTGAGGCATGGGAT AGACTCAGAGAAACCCAGGAAATAACCCCTTCAGGCATCTGACA TGCAAAGATGTGGAAGTGTCAACCAGGAAGTCATGTTGGGGGAA CAGCAAGTATTTACAGAAAGTGACTGTGTGTGTCTGTGTAGGAG GGTGACTTTGTATAGGAGAGATAAAACCTGTGAGCTAATCAAGG	SEQ ID NO. 214

	AGAAGATCATAAAAGACCTTCATAAAGAGCATGGCCTTTTTCCT GCAAGCAGTGAGGAGCCATTGAAGGCTTTAGCATAAGGACAGTC AGATGTACTTCCCTAGAATGCACATTTCTTCTGCTCCAGAACT TCTGCACAGGAGGCTCCTAAAAGCTCTCCCCATCCTCCCTGTAC ACGTAGAATCTGCCTCTGTCTCTCTTTCTCTCT	
KCP_2020 67	CACTTCCCTCACTCTTTTCTTCACTGCACTAAAGATGATTTCT AATTGCATAGTCATTGATGCCAGTATTTGTTTTATTGTGTCAATC CTGCTGAACAGAGGATGGGCCTGACTTATTTGGGACCATGTTGC TGATGCCTGGACCTAAGCCTGGCACAGAGTAGGAGCTCAACAAA TTTGTAAATGAGTGGCTGAATGGCCATACTCTCAAAGGACCCA CAGTCTAGGAGAGACAGAAGAATCTTTGTCTTTTGTCTTGCAG TGGGATGGAAGCTGCAGGGAGGGTCTTGTACATTGATACTGT CTGGGGAAGACAGAAAACTTCAGTTTCAGAGGAGGTAGCCCTT GAAACGAGATTTGAGAGAGGGCAGCACATTGTACAACCTCCATGG GCACCATGCACATTGTAGTCCAGATAAACAGAGCCCCCTTGGAG [A/G] TATGTGAGGCATGGGATAGACTCAGAGAAACCCAGGAAAT AACCCCTTCAGGCATCTGACATGCAAAGATGTGGAAGTGTCAAC. CAGGAAGTCATGTTGGGGGAACAGCAAGTATTTACAGAAAGTGA CTGTGTGTGTCTGTGTAGGAGGGTGACTTTGTATAGGAGAGATA AAACCTGTGAGCTAATCAAGGAGAAGATCATAAAAGACCTTCAT AAAGAGCATGGCCTTTTCTGCAAGCAGTGAGGAGCCATTGAA GGCTTTAGCATAAGGACAGTCAGATGTACTTCCCTAGAATGCAC ATTTCTCTTCTGCTCCAGAACTTCTGCACAGGAGGCTCCTAAAAG CTCTCCCCATCCTCCCTGTACACGTAGAATCTGCCTCTGTCTCT CTTTCTCTCTCCTCCTCCTCCTCCATCTCCTCCTCCTCCTCCTC	SEQ ID NO. 215
KCP_202 795	GCTCCAGAACCTTCTGCACAGGAGGCTCCTAAAAGCTCTCCCCAT CCTCCCTGTACACGTAGAATCTGCCTCTGTCTCTCTTTCTCTCT CCTCCTCCTCCTCCATCTCCTCCTCCTCCTCCTCCTCCTCCTC TCGCTGTCTCACACACACATACACACACTCCTTCTTCTCTAT CTAGTCAGATTCCACTCCTTGGGATTTTCAAGGCCACCGTCACTC CTCAGGGAAGCCTGCCCTGAATGCCTGCACTACACAGGGCCCC TTTCCCCCTGCCCCCATCCCAGAGCACCAATAGCTTTCCCTTGC AGCACTTCTCACAGCTGTCAATTTATGTTTGTGTCTGTGATTCT TAGGTTAAGTCCCTCATGCACCAATCATAAGATCTGGGAACAA GGACCACACCTGTCTG [C/T] TCATCACTGTAATCATCACT GCCTGCCAAAGTGCTTGCACATATTAGATACCTTAGTAGTTATG TGTTCCATGAATGACTCTTTAAGAGATCTTCTAGCTGTTCTTGC AAAGAACCCATTGGTAAGGTTGAACCTACAGGCTGATACTTGC ACTAGTCTCAGGAAGAGATGGTGAGTACATGAAATTGAGTCCCC CAGAGGTTAATGCCCAGTGCCCCAGCTAGGAAACGTCCAAGGAG GCAATTTGAACCCCATCTGTCTGGCTGCAGAGCCTAGCCCTCTA ATGCATTCAAGGGTCTTAGCTCCTCGAGGATGCCACTGTGCCGT GAACCTTCTTCTGACCTCATGGCTCCAGCACAGCATCCACAC TCAGAAGTGCAAGATGAATGTTTGCAGATAATGAACATAAGCT CTCAGGAACCTCATCTCCTGAGAATCTGCTTTGGCCCCCACAG CAGGTCTGGGTGTGGACCTTCCCCA	SEQ ID NO. 216
KCP_2042 42	GTGGCAAAGTTGGGATCTTAACCCAGTTCTATGTGGCTATAAAG TTCATGGAATAGAATGCTGCAGTTAAGAACATGGGCTTTGGCAT CAAGCAGACCTGTATTTGAGCCCCACCTCTGCTGTTTATTAAC GTGGCCCTGGGCAGATGACCTTACATCCTTAAGTCTCTAGTTCT TTGTCTTTAAAGGGTGGCAGAATGTACCTCACTGGTTTTAGGA AGGTACATGAGATAGTGACATGAAGCCCTAGGCATGGGAAAA TTCTTCTAAAATGTGAGCTGCCATTCTGATCACTGCAAGACCC CACCCCAATACTCCCAATTGTACCACCCACCCCACTCACCAG TGTCTCAGAAATGCCTCCTCCAGAAGGAAGGCATCCTGTCTAAC CCACTGCTTCTAGCCAAGCTGTCTTTCTTCAAGGTAGAAAAA GATTGTTAGTCATTGTTTAAATCTTTATTGAGTATATACCGCCAC	SEQ ID NO. 217

	<p>ACCAATTGCACTGCCA [C/T] TCATTATCTCATTTAAATCTGAC AAGAGCCTTGTAAGTAGGGATTATTTCCACCATTTCCCAGATG TTGAAACTGAAATTGATAAACACGACATGTTGCCATGGCTACAT GAAGATCTCCAAGCCGGAGGATCTCCACCCTCACCTGCCTAGCT TCCCAGACCTCTCTGCAGAAAAGGGACTGACCCCAAGACAGCC CTGGCCTCTGGGCTCCACCCCTTCCACATCCATCCCAGGGCCGC TGAGGACTGAAGAGTTCTCCACGTTTGCCCTTTAAAGTGACTTA AAAATAATCTTTATGAATTTCTTCATATACAAAATTTGTACTTA CTCATTGCAGCAAATTTAGAAAATACACATAAGCAAAAAAGAAC GTAACAGCCATCCATAACCCTAACTCTCAGAGATCACCACTATT AAAATGTTTATTATCTAAGAGAGAGATGATATAGACAAAGATGA GACAGATTGACACAGAGAAGATGGGTACATGATAGAT</p>	
KCP_2062 67	<p>TGCTCAACTGTAATCAAACATTATTTTTAAAAAATCATTCCAGC CTGGGAAACAGTGAGAAACCCATCTCTACAAAATAAAAAATAAA AATTAGCTTGGCATTGTGGCATCTGCCCCGTGGTCCCTGCTACTC AGGAGGCTGAGATGAAAGGATCACTTGAGCCTGGGAGGTTGGGG CTGTGGTAAGCCGTGATTGCCCCATTGCACCTCATTCTAGGCCAA CAGAGTGAGACCCTGTCTCAAAAAAATATTATTCAATTAATAT CTGTTGCCACCACAGGACTGATCCCTCTGTGAGGGCAGAGATTG TTCATGCATGGAATTGTGATTATAAGCACTGGCTCTGGAGCCA GGTTGCCTGAGCACGGAGCCAGCTGTGCCCTGCGGGACACCTGT GGCACACTTCACTCCTGGGACACCTGGGACACGCACACAATAGA AATGTTTACATTTTACTAGGCAATGCCAGTCACATAGTCCTACC TAATTTCAAAGGGTA [A/G] AAGGTACACCCAACACGCATCAG GAAGGAGGAGGACCAGAAATTGTTGGTGACAAGCACAAATGACC ACCCCAATATAATATTTTGTGTTGGAAGGCATTTTATTCCACAAA AACAACATTACAATAAACACAACAACAAACACTGGTTGCAGTA GAACCAACTTTCCAGACCTATCTGCACAGCACAACCATTATCCC ACTCAAAATGTCATGTTTTTACCCAAAAACATTAAATTTTAAAA GCAATTCAAACCCATAGCTTAAAAAATGTTCCAACCAGTAATAA AAGGAAAAGTGTGCCCTCCTCCTCCCAACTCCCTACCCACAAT CGCAAGATATTATCCTTATAGGCGAAAAGGGTTTTCAGGATTTGA GATGCAGGCTGGGAGGTCTGAGAAGACTTCCTATAGAAGACATG ACTTCAAACCTCTTTCTTGATGTGAGATTTAATTTTCAAAGACT CCTCTGATCCAACCTTAAGCTTTATGGTAAATCACCTT</p>	SEQ ID NO. 218
KCP_2076 61	<p>ATATGCCAGCGCTCTATCTGCAGGGGTTCTTTTGATAGCAGCAG ACTGAGAGATGATGTTACTGTCCCCTTTTCTGTTGTTGGCAA CTGAGACTCAGAGGATGGAAGTGACTTGCTCAGGTCCACCACCT CTTCAGCTGTGGAGCTGCGACAGGAGCCTTTGTTTGACTTCAA GCTCACCATCACTCCTCTCTCACTGATGCTCAAGTGGGCTATCA CCTCGCCTTTCTTGAGCCTTTCCTTCGCTATCCTAAAACAGCGCC TCCCGAAATCACCATAAAGAACTTATTGATGTAACCAAACACC AGCGGTTCCCCTAAAAACCTATGGAAATAAAAAATTAATAATAA AACAGTGCCTCCCATGACCCATGTCTCTCCAGTCCCATAACTCT GCTCTATTTCCATTACAGCTCCATCCCCACCTTTATGTCTTTT GTTCACTGCTTTATCCCCAGTGCCTAGAAGAGTGCTTGGCACCT AGTAGACACTCAGTAA [C/G] TATTTGTGGAATGAGTTAATAAG GTTGTGAAAAGAACGTTAGATTACTGGAAGGATTCATCTGAGTT TAATTTCTGCTATGCTGGGAATCCAGTGTGCGGCCTTGATGAAG CCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCTGTACATTTAG AGGGCAGGAGAAAAGCCACACGCTCTGTGACTTATACAATTTGT TGCCCAGAGTGGAGGCTGCTTTGATGCTCAGAAAAAAGAAACAA ACATGGAAAATGCTAAATGGGTGGCAGAGAGCTTGAGGGAGGAAG GAGATGGGGAGGGTACTCTTGAAACTGTTTGGTGTCTTCCCTCC TGCCCCCTCAGTACCAATTGTCAAGTACAGAAAGTGAAGGAGAC TTGTATTAGTGGAATTTGGTCCCTGACTTGTATAGAGACACAA TTACAAAGACACAAGAGTGGGCCAGCAGAGACCCCTTAGGGTGG</p>	SEQ ID NO. 219

KCP_2079 65	<p>TCCCTTGAGGTTCCAAAGCATCTGCCCATCAAGCAGA</p> <p>CACCAGCGGTTCCCCTAAAAACCTATGGAAATAAAAAATTAAAAA TAAAAACAGTGCCTCCCATGACCCATGTCTCTCCAGTCCCATAA CTCTGCTCTATTTCCATTACAGCTCCATCCCCACCTTTATGTC TTTTGTTCACTGCTTTATCCCCAGTGCCTAGAAGAGTGCTTGGC ACCTAGTAGACACTCAGTAAGTATTTGTGCAATGAGTTAATAAG GTTGTGAAAAGAACGTTAGATTACTGGAAGGATTCTCTGAGTT TAATTCTGCTATGCTGGGAATCCAGTGTGCGGCCCTTGGATGAAG CCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCTGTACATTTAG AGGGCAGGAGAAAAGCCACACGCTCTGTGACTATACAACCTGT TGCCCAGAGTGGAGGCTGCTTTGATGCTCAGAAAAAGAAAACAA ACATGGAAATGCTAAATGGGTGGCAGAGAGCTTGAGGGAGGAAG GAGATGGGGAGGGTAC [C/T] CTTGAAACTGTTTGGTGTCTTCC CTCCTGCCCCCTCAGTACCAATTGTCAAGTACAGAAAGTGAAGG AGACTTGTATTAGTGGAATTTGGTCCCTGACTTGTATAGAGAC ACAATTACAAAGACACAAGAGTGGGCCCAGCAGAGACCCCTTAGG GTGGTCCCTTGAGGTTCCAAAGCATCTGCCCATCAAGCAGATGA TGTGATTAGTCTCTGTGACCCCAAGGATGCCTCCTGAAATTGCT GATTCAATTTCTCTAATAAAATAGGAACAATAATTAGCTAATA AGAAATCAACAATTAAAGCTATGAGAGAATTAAGTGAGATCATG TAAGCAAAGTACATGTCACAGTGCTCTGCAAATAGGCAGTGCTC AGAAGTGTACCTTTTCTCTTTCTCTCTGAGCCTCCGTCTTCT CTTCGGTAAAAATGAGAATAATATTATGCATACCTCACAGGGGTT AAGCAATGTGAAAGTACTCTGTAAAGTATAAGGCTGA</p>	SEQ ID NO. 220
KCP_2115 25	<p>GAGATGATCAACAGTCTTTTCATCCAGAGGGTTGTGTTTGTCTGGT GGCCATTACCTTTAACATAAAACGATCATATTTACTTTATCCTA TTCATGTCCAACCTCAACTGACAATTGAGTTGTGTCTCTGACAA TAAATAGCAGAAAAAGGAAATCTTCCTATACTGAAGAGAAACAC AATTAATTAAGTAGATCCATCAGGAAAGGTACAATCATGATTGA GACAGTGTTTAACAGATGTGACTATTGGATTCTGTTGTTGAGAA TGACCCTTAAAATCACAGTCAAAATATACGACAAGATGGAAATA ACATTTTTGAGCACCTACTATGCATGTAGAGCATCTTACATACC TTATCTCACTTAGATTTACAGCTGCAAGGTGGGTATGATTCTAG CTTGAATTAGTCTAATAACCATATACCTCCTAGGGGCAGTGAGA TGATTAGATCAATTCTAAAACCTATTACCATGCTCTCTGAGTCA CCAAGACAGGCAGTTA [A/G] TACAAGGATACATTAATACCGAA TCCAGCAAAGCTCACATGGCCAGCTTCCATTATGTTTCTATTT GTGATTATTCTGTATCAAGCACAGAAATGTATGTTACACGAAC AACAAAGAAGGGGTTTATTAGTGTGATTACAGGGCCTAAGCCT ACCTCTGAAACTGGTTTTTGGAGTCTTTAGCACGCTTGTGTTGGG ACAGTTAAACATGTGCCAGCTATTCTAAAACAGTAGCAGTAATG TGATAGAGCTGGGTCATACCGTGCTTCCCAAAGTATGATCACTT CATTTCAACAACCTTCACTAACAAGCCTGAACTGGGCTGTGAAG GGAATATTTAGACCAAGGAAACTGGAAAACCTGTATCAATCAGGC TTTTCCACCCTCCCCAAGAGCCAGTTGTCAGATATCTACCAGCC TACCAACGCTAGCTCTCTAATCAGAAACCATCACTTAGCAAGTT CCCAAATTATCTGCAGAGCAATGAACCTCTCTCTTC</p>	SEQ ID NO. 221
KCP_2118 50	<p>CTATGCATGTAGAGCATCTTACATACCTTATCTCACTTAGATTT ACAGCTGCAAGGTGGGTATGATTCTAGCTTGAATTAGTCTAATA ACCATATACCTCCTAGGGGCAGTGAGATGATTAGATCAATTCTA AACTATTACCATGCTCTCTGAGCTACCAAGACAGGCAGTTAA TACAAGGATACATTAATACCGAATCCAGCAAAAGCTCACATGGC CAGCTTCCATTATGTTTCTATTTGTGATTATTCTGTATCAAGCA CAGAAATGTATGTTACACGAACAACAAAGAAGGGGTTTATTAG TGTGATTACAGGGCCTAAGCCTACCTCTGAAACTGGTTTTTGG AGTCTTTAGCACGCTTGTGTTGGGACAGTTAAACATGTGCCAGCT ATTCTAAAACAGTAGCAGTAATGTGATAGAGCTGGGTCATACCG</p>	SEQ ID NO. 222

	<p>TGCTTCCCAAAGTATGATCACTTCATTTCAACAACCTTCACACTA ACAGCCTGAACTGGGC [C/T] GTGAAGGGAATATTTAGACCAAG GAAACTGGAAAACGTATCAATCAGGCTTTTCCACCCTCCCCAA GAGCCAGTTGTGATATCTACCAGCCTACCAACGCTAGCTCTC TAATCAGAAACCATCACTTAGCAAGTTCCCAAATTATCTGCAGA GCAATGAACTCCTCTTCTTCAGAAAGCAGGCTGAAAGATACACT GTTACATCTTAGCCTGACCTGGACCCAGTGAGTTTCCATCAGT GAGAAAATTCTGTGCTAACTTGAGATAATACTATTCTTGTGGCA ATTTTACTTTTCTTTGAGCGATTCTTCAACCTCTCTCTGCCC CTTCATTTTTCGGTCTTAAAACTAAAAGTGCCCTTTCTCCCTGG ACACTCCTCATTGTGAATGAATTGTCACTTTCAGCTCCTCAGTCA AGAGGAGTAATGAAATCCCACCCGTGTTAATCCTCTTATATCCC GCAGAAATATTGTAGACCCACTCACCCCTAGGCAACAT</p>	
KCP_2127 75	<p>AGTAATGAAATCCCACCCGTGTTAATCCTCTTATATCCCCGAGA AATATTGTAGACCCACTCACCCCTAGGCAACATGCCCTCTCTCTT CAACACAGGTCATCAATTGTTCACTTACTGGCTATCTCCATGTA CTGGAACTTCAGGGTGGTGTCCAGCTGGGTTCAAAGGAGAAACA GTGGGAAGTTTCTCCACTGCCACCTGAATTAGATGAGAAAGAGT TGTCTACTGAAATACACTAGCTGGTGGCAGGATTGGGACGTCAT TTGACTAATTGCCTCCTAGAGCTGCAGAGACTGCTGGAACTACC TAAGTAAATCATCAAAAAAAAAAAAAAAAAAATCATCCCAGGG CACTTTTTTCCAGACAAAAAGGTCCACTTAAACATCCTCTAGAG ATCTGTGCCTGAAGCTGAGCTGCTGCAATGAACTGACATTTCT GCCTTGCAGCCTGGCCATGGGCTTAGCTGGACTAAAATGCTGCT GCAGTGGTGAGGGCAC [A/G] TGAGAGTCCCTAATGTACATGGC CTTGCTCCTTGTCTGACACATCTTTTAGGGCTGCTGCTTTCTC TAGTGCTGGAATCTAGATAATTCCTTTCCAGCCGTTTGTCTCT TCAATCTTGGAAAATATCTGGATGAATGTAACACTGTACACAC AAACAGAATTATGACTTACGTCACATTCTATGTCGTGATTTTGT GGACTTTTAATAATTGCATTACATTTGTGACCATTAATTTCCAC CATCGCCCTGCTCCTGAGAATCTGTAAGGGACATTTGACACTCC TCTCCCCACCCACCTCAACATTTGTGCTGACCTGAAGGTACAT TAAAAACATACCCATTTGGAGAGAAAGATCTGTCTACTGAAATA CACTAAATATTGAAGAAATTTCCAAGTCATTTGATCTTGAAACT CCATCTAATGGAAGCAGAAACACTCAAAGGTTTTTTTTTTTGA CTCCCTTTTTTTCAGGACACTTTTCAGGACTGAGGTATAT</p>	SEQ ID NO. 223
KCP_2217 99	<p>TCAGACTTTGAACAAACCTCAGAAGGAAGTGTCAAGGAGGCTCC CCACGGGTTACGCTCTTCTCTCCTCCTGCACACAGGGAACAGG GCCATTCTCCTTCTTACTGGGACTACCTGGGCTTCATCCAGG GAATCCCCAGGTGGCAACAGGAGGGTGGTGAACCCGCTGCCCG TCACCTGTAAAGTTTCTGTGAATGTGTCTACAGCGGCCAGCAC CACAAGGCATACAAAGAAAGGGAAGGGAGAGCTGATGTGAGAGC GGCAGCGTGGGCACTCCTGTGAGGTTGCCACAGCTGTAGACAAG TTAAATCAGTGCAGTTCAATCAAAGTCATGACCCATGAGCGTC ACAACCAGCAGAGTCTACAAAGGAATACATTAATACTAAGACC AGAGCACAGCTCACATTAGTGAGGGATGGGATCATTTTCATGGAG TTTTTGTTCAAAAATATTTCAATTAACATTTCACTTATATACATG TGTGTATACTGGGTTGTGAT [A/T] TAAATTACAATTCTTACTA TAAATACAGCAAAAGAAAGAAAGAAACAAAGAGAGGGCCACTGG TTTACCTAACATCCACAGGCAGGCTACTTCCCAGCATCTTGAGC CCCAAAGAAAGTAAATTTCTTCCACAACCGATGTTACCAAGCC TGACACTTAGCCAATGATGAAAACGAAAAACAAAACAAAAGCTT GGCAGTCAGTATCCAAATATGCAGATACTACAGAATCTGTTTGA TGTAGAAGTTGATCCTGCTACCCAGACAGCAAAACACTCATTTA TTAATAAAGTCCAGTTCTCTTAATGAAGTGGGTTAATAGTT GATATCTCAATAATTACTTAGTGCATTTTTTATGAAGGTGATGG GAAACAAGTGCTGTTTCTTGAGTCGGAAAGAGTCTCTCAAGCTC</p>	SEQ ID NO. 224

	CCACAAAGAAATTTCCCGAGCTTGTGAGGAATTCAGTCACAGGA AGATCAAGGAATT	
KCP_2235 68	GATCTAATGCTAGGAGATTCAAACCAACAATTAATTTCTCTGTT AAAATGGGTTAAAATAGATGTAAAATATTAATATGTATATAAGC ATTCTGAATTAGACTTATGTGAATTTTTCTCCTTTCTTTCTTT CTTTTTGAGAATAAGCCCTTTCATTTACGTAGAAATGCTTCAGC GTTTAGATAATTGCTACTTATCTTGTTAGCTACAAACACAACCA TAATTAAAGGCTCTGTAAGAATTATGAATTCTGGGGAAATTGGC CACTTGTCTCTGTGGCGTAAACAGTATCTAATTTATAACAAATC ATCTGCCTTAGTCCCAGCAGGATAAGGTGATATGTATTGCCAG CACATGAGAAAGATGGCAATTAGGAATTGTTACCAAGTTACGGG AGCCTCACACGAACATCCATCACCTTTGGGGATATGTACAAGAT ACAACTTAATTTGATGGATTCTTTTGTATTGGGATCAAAGTC TCAAAGGGAAAGTGACAATTTCAAGGAAAATCTGGTGCAATGA GACCAACACTGATGAGAGAAAATGCACACAATTTAATACACCTGC TCACCTGATGTGGCAACTCAGCCTGTGCTTGTGCTGTGGGTTGCCA CAGGATGAGACATGGTCTGTGCATATTTCCAGCAGCCACCCATC TCATCACTATTCTTGCCAGCCAGATTACAGTTGTTCAATAGA TGGATTTGGTAATATCTGCATGACAACAACAGGCAGAGAAGGTT AGATGGCAATTGATTCTTGATTGGTGTAAAGTTTATAGAACACAT TCTGGCAGGGCCCCAAAGGAAATCACTCACCTACCCCTCTGTGAT GGTAAAACGTTGAAAATTCCACGACTTGGACCTTGTGATCCTT CAGTGAAGATGGGCAGATTCTTGTCTTTAATTGACAGACACTT TCTAAATAACTAATGCAATCTTATATTACATTATAGTCCATAAG GGAGACATACTTAACTACTACTTACAACAAC [G/T] GTTTTTA GAGCCTTTCAAATGGTTTGTACAAAGTAGCTCCCATTTAAGATA TTTTCTCTAGTATTTAAGGCTATCTAGTAGACATTACAAAACAAT ACGCTGTAAATACATTAGATTTTTTATCAGTAATACCTTAACATG CCGTAATTTGAACTTTCTGCTAAATCATGCTATCCATTCTTAGT TGGCCCCAATGGTGAGAGTTTACTGTTTCTTTAAATAATTTTGT TTCCCTTTGCTGTCTAGAGGTGTTATCATCTGCTTACTTGCC TGTGTCTCTGGAATATTGAGAAGGTTCCATGGGAAACAATTTGA ATATGCAAAGAAGTTATTTTTAAAGCAAGGAAAATGTTTTCATA TGGATTTATTTTGAGCACTTCTGCCTTTGCCTCCACTGGGAACA TGTTTCTCTCCAACGCCGAAGCCCCCTCCCTGTGTGGTGTGTA CGCAGAGGCTGACAGGGCAGGGAAGTGGGGTTCAAGATAGGAAG GCCATTGGCAGTGTGACCCAGCCACAGTCCTAGATCCCAGGT CGTGACACCACTCTTTTGACAGCCAGATTGTTACCTAACAAGA ATGACTCCCAAGCTCAACCATTCCAATGCCATCTCCTCTGGTTC CAGATAAGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCAT CGCCCCGAGGGACTGGAGCAGCTCGAGGCCAGACCAACTTCAC CAAGAGGGAGCTGCAGGTCCTTATCGAGGCTTCAAAAATGTAA GACCCGTGCACGCTCTGAAGGCCTGGGGGGGGTTCCACGTGAG GCTACACTCTCCCCAATGCAAGGGAGCTCATAAGGCGTTTCCC ATATGTGAGGCTGTACAAGGAAGGCCAGCTCTATAAAGGGGGCA TGAGAGGGAGATCACCTGGCTAGAAAGGAAGGCTCCAGGCGAGG ATGGAGCAACCTCAGGAGACAGTAAACGGCCAATGCCAGAAA TTTCACAGGGTGGCACATCCTCAAG	SEQ ID NO. 225
KCP_1152	GATTTTTATCAGTAATACTTAACATGCCGTAATTTGAACTTTCT GCTAAATCATGCTATCCATTCTAGTTGGCCCCAATGGTGAGAG TTTACTGTTTCTTTAAATAATTTGTTTCCCTTTGCTGTCTAGA GGTGTTTATCATTCTGCTTACTTGCTGTCTCTGGAATATTC AGAAGGTTCCATGGGAAACAATTTGAATATGCAAAGAAGTTATT TTTAAAGCAAGGAAAATGTTTTCATATGGATTTATTTTGAGCAC TTCTGCCTTTGCCTCCACTGGGAACATGTTTCTCTCCAACGCCG AAGCCCCCTCCCTGTGTGGTGTGTTGACGCAGAGGCTGACAGGGC AGGGAAGTGGGGTTCAAGATAGGAAGGCCATTGGCAGTGTGACC	SEQ ID NO. 226

	<p>CCAGCCCACAGTCCTAGATCCCAGGTCGTGACACCACTCTTTTG ACAGCCCAGATTGTTACCTAACAAGAATGACTCCCAAGCTCAAC CATTCGAATGCCATCT [C/T] CTCTGGTTCCAGATAAGATTGAA GATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCCGAGGGACT GGAGCAGCTCGAGGCCCAGACCAACTTCACCAAGAGGGAGCTGC AGGTCCCTTTATCGAGGCTTCAAAAATGTAAGACCCGTGCACGCT CTGAAGGCCCTGGGGGGGGTTCCACGTGAGGCTACACTCTCCCC AATGCCAAGGGAGCTCATAAGGCGTTTCCCATATGTGAGGCTGT ACAAGGAAGGCCAGCTCTATAAAGGGGGCATGAGAGGGAGATCA CCTGGCTAGAAAGGAAGGCTCCAGGCGAGGATGGAGCAACCTCA GGAGACAGTAAACGGCCAACTGCCCAGAAATTTACAGGGTGGC ACATCCTCAAGGAATTCACCTGGCCCAGGGTCAAGCCTTAGCC CTTAACATAATCATACCTTCCAACCTGGTGGTGCCCCACAATA ATGGGATTTGGCCCTGCTGACTTATGCTAACCAGGCT</p>	
KCP_1333	<p>GGCAGGGCCCAAAGGAAATCACTCACCTACCCCTCTGTGATGGT AAAACGTTGAAAATTCACGGACTTGGACCTTGTGATCCTTCAG TGGAAAGATGGGCAGATTTCCTTGTCTTAATTGACAGACACTTCT AAATAACTAATGCAATCTTATATTACATTATAGTCCATAAGGGA GACATACTTAAACTACTACTTACAACAAGTGTCTTTAGAGCCTT TCAAATGGTTTGTACAAAGTAGCTCCCATTTAAGATATTTTCT AGTATTTAAGGCTATCTAGTAGACATTACAAAACAATACGCTGT AAATACATTGAGATTTTATCAGTAATACTTAACATGCCGTAAT TTGAACTTTCTGCTAAATCATGCTATCCATTCTAGTTGGCCCC AATGGTGAGAGTTTACTGTTTCTTTAAATAATTTTGTTCCTT TGCTGTCTAGAGGTGTTTATCATTCTGCTTACTTGCTGTGTCT CTGGAATATTGAGAAGGTTCCATGGGAAACAATTTGAATATGCA AAGAAGTTATTTTTAAAGCAAGGAAAATGTTTTCATATGGATTT ATTTTGAGCACTTCTGCCTTTGCCTCCACTGGGAACATGTTTCT CTCCAACGCCGAAGCCCCCTCCCTGTGTGGTGTGTGACGCAGAG GCTGACAGGGCAGGGAAGTGGGGTTCAAGATAGGAAGGCCATTG GCAGTGTGACCCCAGCCCAGTCCTAGATCCCAGGTCTGTGACA CCACTCTTTTGACAGCCCAGATTGTTACCTAACAAGAATGACTC CCAAGCTCAACCATTCGAATGCCATCTCCTCTGGTTCCAGATAA GATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCC AGGGACTGGAGCAGCTCGAGGCCAGACCAACTTCACCAAGAGG GAGCTGCAGGTCTTTATCGAGGCTTCAAAAATGTAAGACCCGT GCACGCTCTGAAGGCTTGGGGGGGGTTCCAC [A/G] TGAGGCT ACACTCTCCCCAATGCCAAGGGAGCTCATAAGGCGTTTCCATA TGTGAGGCTGTACAAGGAAGGCCAGCTCTATAAAGGGGGCATGA GAGGGAGATCACCTGGCTAGAAAGGAAGGCTCCAGGCGAGGATG GAGCAACCTCAGGAGACAGTAAACGGCCAACTGCCAGAAATTT CACAGGGTGGCACATCCTCAAGGAATTCACCTGGCCCAGGGTC AAGCCTTAGCCCTTAACATAATCATACCTTCCAACCTGGTGGTG CCCCACAATAATGGGATTTGGCCCTGCTGACTTATGCTAACCA GGCTCACCGAGACTGATGTGTAAGCCGAATGTCGGTGTATTAAT TTACCTTGGGAAATGGAAGTACAGTGGAAACAGACACTCCTCT CCCTTCGCTGGGACCCGCTCTCCTTGGAGCCACATGGAAGCCA GGTTACAATCAAAAGTGGAGTCAGAGGACGGGAGTTCTTGT AGTTGTACTTTAAATACATTAATGTGTTCTGCACTCTCAGGC CAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTATTT TTTAAGTTTAACTCTCAGAGTGCAATCTTATCCCAAATCCTGG AGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGGTCA CCCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGGTCA GTTCCAACTGACCACAGCCTCAATGTTCTCCAACTGCTGACC CACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTGCTG GGATGCCTCTTCTTCCACACTAGCCTTGACTGCACATGCCAAG TGCCCAGTTTCTACCATTAGGGCTTCTTTCCTTCGATGGCAGC</p>	SEQ ID NO. 227

	ATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGTGGGAAAG TTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCATCCAGAAA AGAGAAGAAATCTACACTGCTTGGC	
KCP_2252 20	AATTTACCTTGGGAAATGGAAGTGCAGTGGAAACAGACACTCC TCTCCCTTCGCTGGGACCCGCTCTCCTTGGGAAGCCACATGGAAG CCAGGTTACAATCAAAAGTGGAGTCAGAGGACGGGAGTTCCTTG TTTAGTTGTTACTTTAAATACATTAATGTGTTCTGCACTCTCA GGCCAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTA TTTTTTAAGTTTAACTCTCAGAGTGCAATCTTATTTCCAAATCC TGGAGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGG TCACCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGG TCAGTTCCAACTGACCACAGCCTCAATGTTCTCCAAACTGCTG ACCCACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTG CTGGGATGCCTCTTCCTTCCACACTAGCCTTGACTGCACATGCC AAGTGCCCAAGTTTCCT [A/G] CCATTAGGGCTTCTTTCTTCGA TGGCAGCATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGT GGGAAAGTTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCAT CCAGAAAAGAGAAGAAATCTACACTGCTTGGCATCTACCATGGA CTCAATACCACCTAACATAGGTTCATAAGATACCCTTGGGGAAG TTATTGTTACCCCCATTTTACAGGTAAGGATATTGAGGATCAGA GACTGGCTTGGCCAAAGTCACAAAGCTTAGTATTGGCTGAGCCA GGATTTAAACCCAGGTTTTTCTGATCTTAAAGCCCCAAATCTCT CCACCTCACAGTGGCCATTCTCTGACAATGTCTCATATTTTGC AAAGCAGCTCCAGTCTGAGATGGCACTACTTGGGAGAAGTGGA AATGCACAGGTCCCTGTCCCTGGGGATCATGAGGAACCCAGAC ACCAAGGCTGGGCCAGTCTTCTCCTAGTGCTGGCCC	SEQ ID NO. 228
KCP_2649	GGCTCACCGAGACTGATGTGTAAGCCGAATGTGGTGTATTAAT TTACCTTGGGAAATGGAAGTGCAGTGGAAACAGACACTCCTCT CCCTTCGCTGGGACCCGCTCTCCTTGGGAAGCCACATGGAAGCCA GGTTACAATCAAAAGTGGAGTCAGAGGACGGGAGTTTCCTTGTTT AGTTGTTACTTTAAATACATTAATGTGTTCTGCACTCTCAGGC CAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTATTT TTTAAGTTTAACTCTCAGAGTGCAATCTTATTTCCAAATCCTGG AGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGGTCA CCCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGGTCA GTTCCAAACTGACCACAGCCTCAATGTTCTCCAAACTGCTGACC CACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTGCTG GGATGCCTCTTCTTCCACACTAGCCTTGACTGCACATGCCAAG TGCCCAAGTTTCTTACCATTAGGGCTTCTTCTTCTCGATGGCAGC ATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGTGGGAAAG TTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCATCCAGAAA AGAGAAGAAATCTACACTGCTTGGCATCTACCATGGACTCAATA CCACCTAACATAGGTTTCATAAGATACCCTTGGGGAAGTTATTGT TACCCCCATTTTACAGGTAAGGATATTGAGGATCAGAGACTGGC TTGGCCAAAGTCACAAAGCTTAGTATTGGCTGAGCCAGGATTTA AACCAGGTTTTTCTGATCTTAAAGCCCCAAATCTCTCCACCTC ACAGTGCCCATTTCTCTGACAATGTCTCATCATTTTGCAAAGCAG CTCCAGTCTTGAGATGGCACTACTTGGGAGAAGTGGAAATGCAC AGGTCCCTGTCCCTGGGGATCATGAGGAACCC [C/T] AGACACC AAGGCTGGGCCCCAGTCTTCTCCTAGTGCTGGCCCTCAAATGCCT CCCGCTGACTCTCTCCCTTCCCACAGGAGTGCCCCAGTGGTGT GGTCAACGAAGACACATTCAAGCAGATCTATGCTCAGTTTTTCC CTCATGGAGGTGAGTCTGACCTTGAAATCTATCTTGCCAGCTC CCTCTCTGGTAAGCAGCCTTCCCTTCTCCAAGTCTCTCTTCC TTGCCATTTGCTTCTTCTCGAGGAAGAGACAAACTCAGGGCAG GACACCTCCCTCATCGTGAGAGGTGGGAGTCTCCAAAGCTTTAG CAGGAAAGAACTCTGAAAATGAACCCACCTGGAAGGGGAAGAA	SEQ ID NO. 229

	<p>GGGCTGATAATGCAACATCACAACGTCTCAGAACAGCTCTAGAA AGCAGGTATTATAATCCCAGATGGAGTAACTGAGTTTCGGGGAA GATAAGCAGTGTACTCAAGATTGCACAGCTGGTGAGTAGCAAAC CAGGATTAGATTCCATAAGGGTCTGAAACAGGTTTTGCCATGCT GGCACCACCATTGTGCAGGGCACTTTTGAATCTTTTCCTTAAAA TAGCTGAGACAAGCTGGAAATTTGTAAAAGAACTTCAGTAAATA CCGAAGACTATAAAAAATAAATAAATGAAAAAGAGGCAGGAAAC ATAAAGTTGTGCTTATTAAGCCAGTTTACAAGTGTGCCAGGCCC ACAACAGCTGCTCTGTGTGCCCTGCCCGACTCCTGTGGGAACCAG CTGTGTCCCCATGGGCCTGGGACCACATCGGTGACTCCTCCTGT GGCCTCCATGTGTACATGCCACTTTGCATCCTGTACCAAGAG CTGTCTCCTGCAAGACATCTTCCCTGGATCCTGACAAAATGCAA ATCCAAGTATTCCAAACACTTCTTGGGCCCTGTTTCTCATGGGC CTTTTTGGCAGCAGACAGATGCCCTTCTTGGTGTGTGGGGCCCC TACCCAGATCAGGTGGGGGAGGCAG</p>	
KCP_2278 71	<p>CCTCTGGTTCTGCATCACCTCCCCCTCTAAATCTCAAGGCATTG GGGGAAGGTCTGGACCATCAAAGCTCTCAGTCAGACCAAAGAC ATGTTTATCCATTGTGTAAGCATTTCTTAAAGATGGGGAAAAGCA GCAGCAACTTTCCCTGGCCTGCAGGAACTCAGGGACTCAGGGGA CTAATAACAACAGTGTATGAGCTTCCGGGCACACTGCTTCCCAG TGGCAGCCCCCTGTACTTAGGGCTTTGTATGTATTAATTCAATTA CTCCAATTCCCACAATAACCTATAGGGTAGGGTTTTATTATTG ATTACCTTTTTACAGAAGAGGAGAGTAAGGCAAAGAGAGATAGA GTAGTTTTCCCAAGGTCAAAGAGCACATAAATGATAAAGGATGG ATTTGAATGTAGGCAGAATGACCCTCAATACAGACTGTTCTCTAC AGTCCACGTCTCAGCCACTAGACCATACGGCCACTGGGATGAT AGACAGACCACTGCAG [C/G] CATGGATAAGGCAAACAGGGC TGGCTGTGTGATCTGTGTCTCTCAGAGCTCCATTCTTCTCAA GGGGGCACCTTGCAAAAAAACAACAAAAATGGGGCAGGGTAGG GAACTGAAGGCAGGAGCTCTTACAGAGCATAGCCACATCCTCC AGGCAGACAAGAGGACGCAGGAGGCACCATTTCTGTGAGAGTATC ACAGTCTGACCCAAAGACACAGCTTCAACTGTCTGATGGCTTG ATGGTTAATGTCACTCTGCCTTTTCCCCCTTCTCAGGACTTTGTA ACCGCTCTGTGATTTTATTGAGAGGAAGTGTCCACAGAAACT AAGGTGGACATTTAATTTGTATGACATCAACAAGGACGGATACA TAAACAAAGAGGTAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGC TCCAGTGAAGGTAACCAACCAACAGAAAACAGCCCCAGGCATG AGGATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTG</p>	SEQ ID NO. 230
KCP_2279 87	<p>TGTGCCATTTCATACACCAACGACTCCATGCATAGACAGGCAGGA GAATGGTTTTCTCATGATGGCTAGAGGGAGGGGCAAGGGCTCAT CTCACTTTTTTGCTAGATCTAACTTCAACCCAAACCCAAAGAGT TGAGTCAATGGGCCCCACTCCATAATTTCTCCTTTCCATCACC CTAGCATCACTCTCCTCTCTTTCTTGTGCAAGCCCTGCCTTGT TGGAAGGTTCTCCCTGTGTGGAATTCCTGCCCCCATCACCTGCC CTCCTTTTCTGCCTTGTAGATGCCAGCACGTATGCCATTACCT CTTCAATGCCTTCGACACCACTCAGACAGGCTCCGTGAAGTTCTG AGGTACGCTCATCTGGGGTCCACTCTAGGGGTCTCTGTTCTG CATCACCTCCCCCTCTAAATCTCAAGGCATTGGGGGAAGGTCTG GACCATCAAAGCTCTCAGTCAGACCAAAGACATGTTTATCCAT TTGTAAGCATTTCTTAAAGATGGGGAAAAGCAGCAGCAACTTC CCTGGCCTGCAGGAACTCAGGGACTCAGGGGACTAATAACACA GTGTATGAGCTTCCGGGCACACTGCTTCCCAGTGGCAGCCCCCTG TACTTAGGGCTTTGTATGTATTAATTCATTTACTCCAATTCCCA CAATAACCTATAGGGTAGGGTTTTATTATTGATTACCTTTTTTA CAGAAGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTCCCA AGGTCAAAGAGCACATAAATGATAAAGGATGGATTTGAATGTAG GCAGAATGACCCTCAATACAGACTGTTCTACAGTCCACGTCCT</p>	SEQ ID NO. 231

	<p>CAGCCACTAGACCATACGGCCACTGGGATGATAGACAGACCACT GCAGCCATGGATAAGGCCAAAAACAGGGCTGGCTGTGTTGATCTG TGTCTCTCAGAGCTCCATTCTTCCTCAAGGGGGCACCTTGCAAA AAAAAACAAAAAATGGGGCAGGGTAGGGAAAC [C/T] GAAGGCA GGAGCTCTTCACAGAGCATAGCCACATCCTCCAGGCAGACAAGA GGACGCAGGAGGCACCATTCTGTGAGAGTATCACAGTCTGACCC AAAGACACAGCTTCACACTGTCTGATGGCTTGATGGTTAATGTC ACTCTGCCTTTTCCCCCTTCTCAGGACTTTGTAACCGCTCTGTCTG ATTTTATTGAGAGGAACGTGTCCACGAGAACTAAGGTGGACATT TAATTTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGG TAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGT AACTAACCCAAACAGAAAACAGCCCCAGGCATGAGGATAGCACTG TCTGAATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCC CTGGCAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCT GTTCCCAAGCGCCAGAAAGGATTAAACAGATTCACTCTCACTG GGTCACCTAGATTTCAGTAGATATTACACAGTGGATAAAAAATGAC TTGTTTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATT TGGAATTGTAGGCAGCACCTAGAATAGAAAAGAAAGATTTTAA GGAAGAGGAACCTACAATTGGGTCAATTTGGCCTTAACTATTT TGCCTATTAATACAACCGCCAAGGGGGTAATGGAAGGTACAGCT GTCTTTACAGAAATTATCACAATAATTTCTGAATCTTCACTGC TTTGCACTTTTAGAACCTCAGAGGACATGTCTCTAGCCAGTGAA ATACCCTCAGGTCTATCTCAAACTCACTTTGGTATCCACTGTA TCCTGGTATCTCAGTGGAAGCTGGAATTTGGCATCCTGTAAACAC TCCACTTGCTGAGCTCCTGTGTGCCAGGCACGGTGCCTGGAGGT ATAGATATCAGACCAATCTTCACC</p>	
KCP_2281 07	<p>TAGGGCTTTGTATGTATTAAATTCATTTACTCCAATTCCACAAT AACCCTATAGGGTAGGGTTTATTATTGATTACCTTTTTACAGA AGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTCCCAAGGT CAAAGAGCACATAAATGATAAAGGATGGATTTGAATGTAGGCAG AATGACCCTCAATACAGACTGTTCTTACAGTCCACGTCTCAGC CACTAGACCATACGGCCACTGGGATGATAGACAGACCACTGCAG CCATGGATAAGGCAAAAACAGGGCTGGCTGTGTTGATCTGTGTC TCTCAGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAA AACAAAAAATGGGGCAGGGTAGGGAACTGAAGGCAGGAGCTCT TCACAGAGCATAGCCACATCCTCCAGGCAGACAAGAGGACGCAG GAGGCACCATTCTGTGAGAGTATCACAGTCTGACCCAAAGACAC AGCTTCACACTGTCTG [A/T] TGGCTTGATGGTTAATGTCACTC TGCCTTTTCCCCTTCTCAGGACTTTGTAACCGCTCTGTCTGATTT TATTGAGAGGAACGTGCCACGAGAACTAAGGTGGACATTTAAT TTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGGTAAG TGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGTAAC AACCACACAGAAAACAGCCCCAGGCATGAGGATAGCACTGTCTG AATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCCCTGG CAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCTGTTT CCAAGCGCCAGAAAGGATTAAACAGATTCACTCTCACTGGGTC ACCTAGATTTCAGTAGATATTACACAGTGGATAAAAATGACTTGT TTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATTTGGG AAGGTTAGGAGCCACAAGTCAAAGCTAAAAGTTGAAA</p>	SEQ ID NO. 232
KCP_2325 21	<p>ATTTCTTAAAGTAGATAAATTTGACTTTATCAAAGTTAAAAATT TTGTGCTTTTAGAAGACACCTTTAAGAAAATGGAAATGCAAGCCA TGGACTTGGAATAAATGTTTGCATAATTATATACCAGATATATAA AGATACCAGGATACCAAACCAATATAAAGACTGGCATCCAAAAT ATATAAGGGACATTTATAATTTAATACAAAGATAAACAACCTTCA TATAAATAGGCAAAAGATTGATGAGATATTTAAGAAAAGAAG ATATATGAATGGCCAGTAAACCCATGAAAGGTTGCTCTATATCA</p>	SEQ ID NO. 233

	<p>CTGGTCTTCAAAGAAATGCAAATTATAACTATAATGAAATACAA TTGCACAGAATGGCCACAATTAAAAAGACTGATAATACCAAGCA TTGGCAAAGATGTGGAGCAATAGAACTCTCATAGATTAGCTGGC AGAAATGTAAATGGTACAAACACGTTGGGAAACATTTTGGCATC TTTGATAAAGCTCAGCACACACTTAACATACAACCCAGAAATCC CATTCAGTCAGGCATGGTGGCTTACGCCTATAATCCCAGTACT TTGGGAGGCTGAGGCAGGCGGATCACTTGAGCTCAGGTGTTCAA GACCAGACTGGGCAACATGGCGAGACACTGTCTCTACTAAAAAT ACAAAAAAGCCAGACATGGTGGTAAACACCT GTGGTCCCAGCTACTAGGGAGGCTGAGGTGGGAGAATTGCTTAA CCCTGGGGAGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGC ACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAAAGA AAAAAGAAGAAGAAAAAGTCCCACTCCTGGATATTTACCCC CAAAAGAAAAATATGTAATTCATAAAGACTTGTACAAAGATGT TCATAGCAGCTTTATTCATAGTAATCTCAAACTTAAATGACCC AAATGTCTGTCAACAGGACAAATGGGTAAATAC [A/T] TCATAGT CTGTTTCATCCAATGGAATATTACTCAGCAGTAAAAAGGAATGTT ATAGTTGCATGCAGCAATGTGTATGAAGCTCATAAACCTCATGC TGAGTAAATGAAGCCAGACGCAAATGAGTTTACACTGTTTTACT CCATTTACATGAGATTTTAGAAAAATACAACTAATCTATAGTAA CAGAAATTAGATCTGTGGTTGCCTGGTGTCAAAGCTTGAGAGGC ACTCACTGCGAAGAAGTGTGAAGGGATGTCTTTTGGTTGTGAAA ATGTTCTATATCTTGAGTGTGGTGGAGGTTACATGGGTGGATAC ATTTGTCAACATTCATCAAACAGTACACTTAAATGGGTGAATT TGTTATAAGTAAATTATGCTCCAATAAATTTGATTTATTTGTTG AAAACTTGGTGTAAGGGGGGAAGTGCCTAACCAATAGAAGACAC TCAAAAAATGTGTTGAAGGAAAAAATCCTGTGAAATAAAGCAG GTAAGAGAAAAATAAGAACTCAATATCATCCAAATATAGATTAC AAATCCTAAATGAGATAATAGGAAATTAATCCCAGTGCTCTGTT TAAAGGCTCATACCTGTAATCCCAACACTTTGGGAGACTGAGGC AGGAGGATGGGTTGAGCCCAGGAGTTCAAGACCAGCCTGGTCAA CATAGGGAGAGCCTGTCTCTTCAAAACAAAAATTTAAAAATTAC CTGGGTGTAGTGGCACGTGCCTGTGCTCCCAGCTACTCCAGAGG CTGAGGCAGGAGGATAGCTTGAGCCCAGGAGTTCAAGCCTGCCC TGAGCCATAATCACTGCACCACACTCCAGCCTGGGCAACAGAAC AAGACCCTTCCTCAAAAAAGCAATAAAATAAAATAAAGAAATGC ACATGACTAACATAGGGTTTATTCCAGGAATGCAGGAATAGCCC AGTAGCAGAGAAAGCCTATTAAATAATTTATCACATTAATATAT CAAAAGATCAAACCATTTGATGCTA</p>	
KCP_2336 55	<p>TTTACTCCATTTACATGAGATTTTAGAAAAATACAACTAATCTA TAGTAACAGAAATTAGATCTGTGGTTGCCTGGTGTCAAAGCTTG AGAGGCACTCACTGCGAAGAAGTGTGAAGGGATGTCTTTTGGTT GTGAAAATGTTCTATATCTTGAGTGTGGTGGAGGTTACATGGGT GGATACATTTGTCAACATTCATCAAACAGTACACTTAAATGGG TGAATTTGTTATAAGTAAATTATGCTCCAATAAATTTGATTTAT TTGTTGAAAACTTGGTGTAAGGGGGGAAGTGCCTAACCAATAGA AGACACTCAAAAAATGTGTTGAAGGAAAAAATCCTGTGAAATA AAGCAGGTAAGAGAAAATAAGAACTCAATATCATCCAAATATA GATTACAAATCCTAAATGAGATAATAGGAAATTAATCCCAGTGC TCTGTTTAAAGGCTCATACCTGTAATCCCAACACTTTGGGAGAC TGAGGCAGGAGGATGGGTTGAGCCCAGGAGTTCAAGACCAGCCT GGTCAACATAGGGAGAGCCTGTCTCTTCAAAACAAAAATTTAAA AATTACCTGGGTGTAGTGGCACGTGCCTGTGCTCCAGCTACTC CAGAGGCTGAGGCAGGAGGATAGCTTGAGCCCAGGAGTTCAAGC CTGCCCTGAGCCATAATCACTGCACCACACTCCAGCCTGGGCAA CAGAACAAGACCCTTCCTCAAAAAAGCAATAAAATAAAATAAAG AAATGCACATGACTAACATAGGGTTTATTCCAGGAATGCAGGAA</p>	SEQ ID NO. 234

	<p> TAGCCCAGTAGCAGAGAAAGCCTATTAAATAATTTATCACATTA ATATATCAAAAGATCAAACCATTTGATGCTAAAATCACATTTGA TATAATTTACCATTTATTCATAATAATTTTCAGGATTCAATTA TTAGGAATAAAATACTTCTTCAGCATAATAGAAAATACCCCAGC CTGGTACACAGCTTCATACTTTATGGTAACAC [A/G] CGGAGAT TCTCACTGAAGAAAAGATGAGGCAAGAAAAGATGATGAAGAAAA GATGAGGCAAGAAAAGATGATGTCTGCACACTGTCAGACATCAC CACTGTTTAAATTTCTCTGAAAGCTCTTCAAACACAGTGAAACA GAAAAGGAAATGCGATCTAAATAGGAAAAATTACAACATTCCTT GTTAATGACATGATTTTCTATCTGAGAAAAAGACAGCAAGAAA ATCAACTTAAACAACACTAGAACTTTTAAAAAGCTGGCAAAGTGA CTGGTAATAAAATACATATGCAAAAAGAAATGTGTAGCCCAATA TATCAGTTGTGACTAGCTAGAAAATTGTAATACAAATATTCTCA TTGTGATCACAATAAAATTTAAAGCACATGGGCATTTTAAATA TCCATAATTTAGATGAAGAGAAAGAAAATTTTGATAAGTAGAGA AACATACCATCTTCTGAAAGGATGTATATTATAAGATAGCAAT ATTATAATGACAGCAATTCTTCTCTAATTAAATTTATTTTATTT TGAATCAAAATGGAAGTGTTATTTGGGAAGGAAATTTGGCACAA TTGTTATAAAGTTACATTGGAAGATTAATCAGATGAAAATAGCA AAGATAATTTTCAAAAAGAAGAAAAATGGTGGGATTTGTTCTAC CAGATACTGAAATATATTATAAAGCTGAAACTATTAAAAATTA TAATATCAGAGAAGGAACAGGTAGATCAATGGAACAAAATAGAA ATCCCAGGTACAAATACCATCTTGGTTCATAATAAGGGAGCAT ATTGAATAGAGAGGTAATGAATCATTAAATGATTCTTGGAACAC TGGTTAACTATTTTGGCAATAAGTAAGTAAATATTCTTACTCGG TACCATAAACACAAAATCACTATAGATATGTACAGTTGCTTTTT AACTAAAAAGAAGCTAAAAATCATATGTGAATATCTGATCAAAG AATGGAAAAAGCATAAAAATCAAAGT </p>	
KCP_2375 05	<p> GCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCGGGAGGATCAC TTGAACCCGGGAGGTCGAGGCTGCAGTGACGGGGATTGTGCCAC TGCCTCCAGCCTGGGTGACAGAGCAAGAACCTGTCTCAAAAAA AAAAAAAGAAAAAGAAAAAAGAATGAGAACTCATAACAGA TTAGAAGAGACTAAGGAGACACAACAAATAAATGCAATGTAGAA TCATTGAAGGGAAAAAATATTAGTTGAAAAGCTGAGATCCCCG CACTGCCTCCAGCCTGGGCCACAGAGCGAGACTCCGTCTCAAA AAAAAAAGAAAAAAGAAAAAAGAAAAAGCTGATAAAATTT TGAATAAGCCCTGTAGTTTGTAGTTAATAATAGTGAAGCCATGTTA ATTTCTTGGGTTTGGTCTATGTGCTCTGGTTATGCAAGTTGTGTA ACATTAGAGGAGACTGAGTGAAAGGTATGCATGAACTCTCTGTA CTAATTTTGTAAATTT [C/T] CTGTAAGTCTAAAATTATTCATA ATATGCAAAAATTAACAAAAAATAAAATAAAATAAGCACATGG AATGAGACTGTCCCCTGGGTCTCTGTAGAAACCAGGTCAAACAT CCCAAATGCTCTTTTACCCCCATTCTGAGTTGGGCCAGAATGGT CAGAATAATGGTTCCCAATGTACCTTGATAAACACGGAACTCT CAGGACCGAGTCCTAAGGTTCTCTGATTCAATAGGTTTGGAGTG GACTTGAGAACTGATCTTTTTAATAAGGGCCTCAGTCTGTGGAA CTATTGGCCTCATGTGCCCTGTGGATAATCTTGGCTGTTGGTTC ATTTTCTTAACTGAAAACAGTGGCAGAACTATGGGGATTTTT AAATCTCTAGGCTAGAACATTAACTTTTTAAAAATTCAGAATAG TATTTTATTTGCCCTCAAGCCTGTGAATGGGGATCCCACAAATCA CCCCCACTGAAGACAATGCCCATACAAGGTAACCT </p>	SEQ ID NO. 235
KCP_1540 0	<p> TTATGCAAGTTGTTAACATTAGAGGAGACTGAGTGAAAGGTATG CATGAACTCTCTGTACTAATTTTGTAAATTTTCTGTAAAGTCTAA AATTATTCATAATATGCAAAAATTAACAAAAAATAAAATAAA TAAGCACATGGAATGAGACTGTCCCCTGGGTCTCTGTAGAAACC AGGTCAAACATCCCAAATGCTCTTTTACCCCCATTCTGAGTTGG GCCAGAATGGTCAGAATAATGGTTCCCAATGTACCTTGATAAAC </p>	SEQ ID NO. 236

	ACGGAAACTCTCAGGACCGAGTCCTAAGGTTCTCTGATTCAATA GGTTTGGAGTGGACTTGAGAACTGATCTTTTAAATAAGGCGCTC AGTCTGTGGAACATTGCGCTCATGTGCCCTGTGGATAATCTTG GCTGTTGGTTCATTTTTCTTAAGTGAACAGTGGCAGAACTA TGGGGATTTTTAAATCTCTAGGCTAGAACATTAACTTTTTAAAA ATTCAGAATAGTATTTTATTTGCCTCAAGCCTGTGAATGGGGAT CCCACAAATCACCCCCCACTGAAGACAATGCCATAACAAGGTA ACCTACCCATGAGCTTCTGAGGGATTTAGGAATTGTCTACCATC TCCTCTCTAAGAAGGGCTCCCACAATATATCCCCTTCTGCTTGC TTCTAACTCCCTATCACCTGCTAAAGAAGGACCTCACCTTTTAA TCACTTTTCATTGCCAAGGGGCACAAGGAGCCCCAACTCTGTCA CCTAGGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTT ATGTCCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTA TGACATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACA CTCCAAGGCAGCATGTGGACGTCTTCTCCAGGTAAGTGCACAC ACCTTGACATGAGCTGTAAGCCAGCCTAGATCAAGTCAACCC ACGAGCATCTGAGCAAATGATTGTGTCCAAC [C/T] CTGTACT AAGCATGGTTGGTAACAGAAAAGAATTATAAGATACATTGTCCCT CAAGAAACAGATGATCTCCTTAAGCTGCAAGTGTACATGACAGA AGAGAACAAGAAAGTATATTATTAAACGCTAGTGGTATAGTATG AACTCTAAATCCATAAAAAATTTGGGGATCAGGGTAAACACGAAA GACTTCATTAATTACAACCTGTGGAGGTGTTAAGCATTGTGTCT GGGAAGTAAGGGGAAATAAGATTGGAAACTAGGATAGGGCCAGA TTATGAGACCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACA GGATGGGCAGCTAGTGTGATCCTTGACTAAGGGAGTGGTATAA TCATTGGGGCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTAT CAGAGAATATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTGC AGATGGGAAAAGAGAGTCTCTCTGGCCTTGTCAGGTTTGTAC AGCAAGTAACAGGCCAGAAATCAGAACCTCTTTTGCCAGTGTTC TGCCAGATGGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAA TAAGCCAGCAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGA TTTAAGGAAGCTCATGGGGCTCAAAGTGTGTGAATCAGGACCTA ATTGGAGTTGTCTGGCCAGTGAAGACAACTCTCATTCTCAGGG CAAAGTTGGTTAATGAATGAATGAATGAGCTCCAGCTCGTTA CTCTGAGCTCCAGCAAGAAAGCAGGGGAGTAAGCTTTGGAATGG AGATCACCAGATTCTGTAAAGTGCTTTCTGTTATGTCTTTCAGA AAATGGACAAAAATAAGATGGCATCGTAACTTTAGATGAATTT CTTGAATCATGTGAGGAGGTAAGGAGAGATCTCAGGGCACAATA ACTCTACATCTGGGAAAGGAAACCTGGGGCCTGGGGACCTGCAG AAGGAAGGTGATGAGAAACCTGCAC	
KCP_2385 91	TCTAACTCCCTATCACCTGCTAAAGAAGGACCTCACCTTTTAAAT CACTTTCATTGCCAAGGGGCACAAGGAGCCCCAACTCTGTAC CTAGGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTTA TGTCCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTAT GACATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACAC TCCAAGGCAGCATGTGGACGTCTTCTCCAGGTAAGTGCACACA CCCTGCACATGAGCTGTAAGCCAGCCTAGATCAAGTCAACCCA CGAGCATCTGAGCAAATGATTTGTGTCCAACCCTGTACTAAGCA TGGTTGGTAACAGAAAAGAATTATAAGATACATTGTCTCAAGA AACAGATGATCTCCTTAAGCTGCAAGTGTACATGACAGAAGAGA ACAAGAAAGTATATTATTAAACGCTAGTGGTATAGTATGAACCTC TAAATCCATAAAAAAT [C/T] GGGGATCAGGGTAAACACGAAAG ACTTCATTAATTACAACCTGTGGAGGTGTTAAGCATTGTGTCTG GGAAGTAAGGGGAAATAAGATTGGAAACTAGGATAGGGCCAGAT TATGAGACCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACAG GATGGGCAGCTAGTGTGATCCTTGACTAAGGGAGTGGTATAAT CATTGGGGCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTATC	SEQ ID NO. 237

	AGAGAATATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTTGCA GATGGGAAAAGAGAGTCCTCTCTGGCCTTGTCAGTTTGTACA GCAAGTAACAGGCCAGAATCAGAACCTCTTTTGCCAGTGTTCT GCCAGATGGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAAT AAGCCAGCAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGAT TTAAGGAAGCTCATGGGGCTCAAAGTGTTGTAATCAG	
KCP_1615 2	GGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTTATGT CCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTATGAC ATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACACTCC AAGGCAGCATGTGGACGCTCTTCTCCAGGTAAGTGCACACACCC TGCACATGAGCTGTAAGCCCAGCCTAGATCAAGTCAACCCACGA GCATCTGAGCAAATGATTTGTGTCCAACCCTGTACTAAGCATGG TTGGTAACAGAAAAGATTATAAGATACATTGTCTCAAGAAAC AGATGATCTCCTTAAGCTGCAAGTGTACATGACAGAAGAGAACA AGAAAGTATATTATTAAACGCTAGTGGTATAGTATGAACTCTAA ATCCATAAAAATTTGGGGATCAGGGTAAACACGAAAGACTTCAT TAATTACAACCTGTGGAGGTGTTAAGCATTTGTGTCTGGGAAGTA AGGGGAAATAAGATTGGAACTAGGATAGGGCCAGATTATGAGA CCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACAGGATGGGC AGCTAGTGCTGATCCTTGACTAAGGGAGTGGTATAATCATTGGG GCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTATCAGAGAAT ATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTTGCAGATGGGA AAAGAGAGTCCTCTCTGGCCTTGTCAGATTGTACAGCAAGTA ACAGGCCAGAATCAGAACCTCTTTTGCCAGTGTTCTGCCAGAT GGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAATAAGCCAG CAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGATTAAAGGA AGCTCATGGGGCTCAAAGTGTTGTAATCAGGACCTAATTGGAGT TGTCTGGCCAGTGAAAGACAACCTCTCATTCTCAGGGCAAAGTTG GTTAATGAAATGAATGAAATGAGCTCCAGCTC [A/G] TTACTCT GAGCTCCAGCAAGAAAGCAGGGGAGTAAGCTTTGGAATGGAGAT CACCAGATTCTGTAAAGTGCTTTCTGTTATGTCTTTCAGAAAAT GGACAAAAATAAAGATGGCATCGTAACTTTAGATGAATTTCTTG AATCATGTGAGGAGGTAAGGAGAGATCTCAGGGCACAATAACTC TACATCTGGGAAAGGAAACCTGGGGCCTGGGGACCTGCAGAAGG AAGGTGATGAGAAACCTGCACATACCTGCAACCCCTCCCACTCAG AGCCAACAACACCAGCAACAACCTGTGAAGTCCACAGTTCCACTC CTCAACCTGACCTGCAGTTGGTCTTGGCTAAGCACAAGACTGAA CAGAGAGCCTAAGTAGGGGTCTGGGGGCATGTGAAAACCTCAGAG GGGGTCTCTGTGAAAATAGACTTCCCGAGAGGGCAACACCATTA TTTTTTAGCCTGCCTCTGGCTTGATGACCCATTTCCAGACTAC AAGGAAGCAGCTGGGGGGAAAAAACCTACAATTGTGTGATTCT CAAACCACAGTGTGCATAAAAATTGCCTGGAATGATTCTGAAAA TGCATATTTCCAGGCCTCAATCCCAGAGACTCTAGATCTGGGTC ACTTTAACACAAAATGTCCTGGACCAATGCTTCTAACACTTTAAT GTGTGAAACAATATCCTTGATGATTTTGTAAATGCAGATTCT AATTCCATAGGTCTGGGGTAGGGCCTGAGATGTTACTTTTCTCA CATTCTCCCCAGTCACACTGGTGATGCTGATCCTGGGAACACAA CTTTCATTAAGTCTAACCAATAGACCAGCCCCAGAGTCCACCAG AGACTGAACTGGAAATAATTGCTTCATCTACTTTTGAGAAATCC ATTTGTACCCCCACATTATTTTAGAAATGTTAGAGTTACTCTG AGCTCCAGCCAAGAAGAAATAGCAAATGTAAGAAAGCCGGGGAGA AGTTCCTAGCAGATACTGAGCCCC	SEQ ID NO. 238
KCP_1806 9	TTGAAAGAGAGCGCTTTGGGGGGTTTTCTTACTGTATGTCTCTA TTGCATGTTCTGTATTTTACATTTTCTATTATTTCTTCTCTGA GGTATAGTATTGAATGTAGAAAAATCCTCAAATGTTCCGTATTA AGCAATACACTTCTAATTCATGGTTCAGAGAAGAAAATATCTCG AATAAAAATAAAAATAAAAATATGACTTATCAAATTTGTAGGAT	SEQ ID NO. 239

	<p>CTAAAGCAGTATTCCAGGAATGCAAGGTTGGTTTAAACATTCAAT AATTGGTCAGTGTAATTAATCACATTAATAGAAATAAAAGAGAA AAAATATAATCATTTCAGTGGATGTAATTGTTTCAGAGCTTCTTA AAAGAAGCAACTCACTATTTTACTAGATGATTGTTTCTTCTGA ATTCTCTTTAAGGCTACAGGTGGTGCTTCTTACTTTGAACTGA TCACTTTCTAGGTCCCCACCCTTACTTCTTGTTTTCATACCCT TGTAGAGTTTCTCCA [C/T] ATAGGAAACCCATGCTTGACATT TGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGACTCAGAGTT CTAACCCCTCTTGCCCTCCTTTTTTCCCAGGACGACAACATCATG AGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGTGGTGACACT CAGCCATTTCAGCTCTCAGAGACATTGTACTAAACAACCACCTTA ACACCCTGATCTGCCCTTGTTCTGATTTTACACACCAACTCTTG GGACAGAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAG ACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGC CAACTCTTCTCTTTCTTCTTCTTGAGAGAGACAAGATGAAATT TGAGTTTGTGTTTGAAGCATGCTCATCTCCTCACACTGCTGCCC TATGGAAGGTCCCTCTGCTTAAGCTTAAACAGTAGTGACAAAA TATGCTGCTTACGTGCCCCAGCCCACTGCCTCCAAG</p>	
KCP_2415 27	<p>ACTTTGAAGTATCACTTTCTAGGTCCCCACCCTTACTTCTTGT TTTTTCATACCCTTGATAGATTTTTCTCCATATAGGAAACCCATGC TTGACATTTGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGAC TCAGAGTTCTAACCCCTTGCCCTCCTTTTTTCCCAGGACGACA ACATCATGAGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGT GTGACACTCAGCCATTTCAGCTCTCAGAGACATTGTACTAAACAA CCACCTTAACACCCTGATCTGCCCTTGTTCTGATTTTACACACC AACTCTTGGGACAGAAACACCTTTTACACTTTGGAAGAATTCTC TGCTGAAGACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCT CTGATTGCCAACTCTTCTCTTCTTCTTCTTGAGAGAGACAAG ATGAAATTTGAGTTTGTGTTTGAAGCATGCTCATCTCCTCACAC TGCTGCCCTATGGAAG [G/T] TCCCTCTGCTTAAGCTTAAACAG TAGTGACAAAAATATGCTGCTTACGTGCCCCAGCCCACTGCCT CCAAGTCAGGCAGACCTTGGTGAATCTGGAAGCAAGAGGACCTG AGCCAGATGCACACCATCTCTGATGGCCTCCCAAACCAATGTGC CTGTTTCTCTTCTTCTTGGTGGGAAGATGAGAGTTATCCAGAAC AATTAGGATCTGTCATGACCAGATTGGGAGAGCCAGCACCTAAC ATATGTGGGATAGGACTGAATTATTAAGCATGATATTGTCTGAT GACCCAACTGCCCATGTCAATTTGTTTCCAGAAACGAGGACCAA TAATTCCTCTCACACTGGCATTGTTGCTGGTAGTACAAGTCCTTT AATATGTCCAGGAAGGGAGCCATTGCCCAGTGGTCCATATCTCC ACCACATCCCCTGCTTGAGCCAGCGCTGCATGTCCCTCCCAAG AAGTCCAGAATGCCTGCAAATGCTGTAATTTTATAC</p>	SEQ ID NO. 240
KCP_2418 04	<p>CTGATCTGCCCTTGTTCTGATTTTACACACCAACTCTTGGGACA GAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAGACTTT CTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGCCAACT CTTCTCTTTCTTCTTCTTGAGAGAGACAAGATGAAATTTGAGT TTGTTTTGGAAGCATGCTCATCTCCTCACACTGCTGCCCTATGG AAGTCCCTCTGCTTAAGCTTAAACAGTAGTGACAAAAATATGC TGCTTACGTGCCCCAGCCCACTGCCTCCAAGTCAGGCAGACCT TGGTGAATCTGGAAGCAAGAGGACCTGAGCCAGATGCACACCAT CTCTGATGGCCTCCCAAACCAATGTGCCTGTTTCTTCTCTTTG GTGGGAAGATGAGAGTTATCCAGAACAAATTAGGATCTGTCATG ACCAGATTGGGAGAGCCAGCACCTAACATATGTGGGATAGGACT GAATTATTAAGCATGA [C/T] ATTGTCTGATGACCCAACTGCC CATGTCAATTTGTTTCCAGAAACGAGGACCAATAATCTCTCACA CTGGCATTGTTGCTGGTAGTACAAGTCCTTTAATATGTCCAGGA AGGGAGCCATTGCCCAGTGGTCCATATCTCCACCACATCCCCTG CTTGAGCCCAGCGCTGCATGTCCCTCCCAAGAGTCCAGAATGC</p>	SEQ ID NO. 241

	CTGCAAATTGCTGTAATTTTATACCATGTTCTAACCAATAAACA GAACTATTTCTTACACTCTCAATCACTTCTTCATGACTCCGTTA GGTAAGAGAGGTAAGCTGTGAAAAGGGAAGGCTAGTCCATTCA TTGACACCCAATTATTAGTGCAGTTGTCCCTCCATATGTGTGAA GGATCAGTCCCAGGACTCTCCATACCAAATCTGCAGATACTCA AGTCCCACAGCTAGCCCTGAGGGACTCGTGTTCAGAAAATTT GGCCTCCATATATGCAGGTTTCACATCCTATAAATAC	
KCP_1324	CCCAAGCTCAACCATTCCAATGCCATCTCCTCTGGTTCCAGATA AGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCC GAGGGACTGGAGCAGCTCGAGGCCAGACCAACTTCACCAAGAG GGAGCTGCAGGTCCTTTATCGAGGCTTCAAAAATGTAAGACCCG TGCACGCTCTGAAGGCCTGGGGG	SEQ ID NO. 242
KCP_1520 4	TTGTCTACCATCTCCTCTCTAAGAAGGGCTCCCAATATATCC CCTTCTGCTTGCTTCTAACTCCCTATCACCTGCTAAAGAAGGAC CTCACCTTTTAATCACTTTTCATTGCCAAGGGGCACAAGGAGCCC CAAACCTGTCTACCTAGGAAGAGCTTGACCTCATGGTTTCCACA CTGTGTGCTTTTATGTCCCTGCTC	SEQ ID NO. 243
KCP_4957	ACCCTCAATACAGACTGTTCTACAGTCCACGTCCTCAGCCACT AGACCATACGGCCACTGGGATGATAGACAGACCACTGCAGCCAT GGATAAGGCAAAAACAGGGCTGGCTGTGTGATCTGTGTCTCTC AGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAACA AAAAATGGGGCAGGGTAGGGAAC	SEQ ID NO. 244
KCP_5011	GCCACTGGGATGATAGACAGACCACTGCAGCCATGGATAAGGCA AAAACAGGGCTGGCTGTGTGATCTGTGTCTCTCAGAGCTCCAT TCTTCTCAAGGGGGCACCTTGCAAAAAAACAATAATGGG GCAGGGTAGGGAACGAAGGCAGGAGCTCTTCACAGAGCATAGC CACATCCTCCAGGCAGACAAGAGG	SEQ ID NO. 245
KCP_5051	GGCAAAAACAGGGCTGGCTGTGTGATCTGTGTCTCTCAGAGCT CCATTCTTCTCAAGGGGGCACCTTGCAAAAAAACAATAATGGG TGGGGCAGGGTAGGGAACGAAGGCAGGAGCTCTTCACAGAGCA TAGCCACATCCTCCAGGCAGACAAGAGGACGCAGGAGGCACCAT TCTGTGAGAGTATCACAGTCTGAC [C/T] CAAAGACACAGCTTC ACACTGTCTGATGGCTTGATGGTTAATGTCACTCTGCCTTTTCC CCTTCTCAGGACTTTGTAACCGCTCTGTCTGATTTTATTGAGAGG AACTGTCCACGAGAACTAAGGTGGACATTTAATTTGTATGACA TCAACAAGGACGGATACATAAACAAGAGGTAAGTGAGCTGGGG CCAGGGGTGT	SEQ ID NO. 246
KCP_5202	GACAAGAGGACGCAGGAGGCACCATCTGTGAGAGTATCACAGT CTGACCCAAAGACACAGCTTCACTGTCTGATGGCTTGATGGT TAATGTCACTCTGCCTTTTCCCTTCTCAGGACTTTGTAACCGC TCTGTCTGATTTTATTGAGAGGAAGTGTCCACGAGAACTAAGGT GGACATTTAATTTGTATGACATCA [A/C] CAAGGACGGATACAT AAACAAAGAGGTAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCT CCAGTGAAGGTAACCAACCAAGAAAACAGCCCCAGGCATGA GGATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTGGGGCTAAC AGAGCTGGTCCCTGGCAAAATAAGAAGGCCTCCCTCATTGCCC TACCCTGCCC	SEQ ID NO. 247
KCP_e1a_ 249924	CCACCAGGGTCCCTTCCAACCTCAGGAGCCTATGGTACTGAATG GCAGCCAGGTTTTTTATGGAGCAATAGCTGGACTTCACATTTGC ATAATGCCTTGCACTTTCACCTGTTAAGAGTACTGCATTGTATTC TAATTATATGAATCTCGGTCATTCCTTTATGACATTTCTGAGGA ATACTATCTCAATCAAGAAAAGCCCTAATTGCACTCCTCTCCTA TCCCGGTGAGAGAGCACAGACTCGTGCCTGCTCCGCAGGGGTGG AGGCTGGAATTCAGTAGTCTGAGTCGGGGATGCCTGGAGCAGGA GGTGGTCAGGGGCATTGTCTCTTTCCAAGTCAGGAAGGCAGACAG CACCTGCTGTTGGTGCCAAGGTTACTGGACAGGCTGCAGGGCT CTGTCTGTCTGTCCGATGTTACAGGCCAGCTCCCCGGAGGCTC	SEQ ID NO. 248

	AGCACTCAGCCCAGCTTCTCCGAGATGCAAACCAGGCCACTCTG AGGCTGCCTACAACTTTCTGCTGAGTGCCGACAGCTGCTTCCCT GCTCTGCGGGGAGTTCTTCCAGATCCTGATCAAGGCACAGAGAA TTGATCTATCAGATTAACCAGGAAGGAAAGAGTGGGAGAGCGAG TGTGGGAGGCTGTGGGGCTGAGTGTTTTCTGCGTAGCAGTCCCC TCCCTTCTGACTTGAGTATTAATTGCTACATTACCGCTGCCATG TAAGAAAGACAGTCAGCAAAGCCTGGGAGAGCTCCAGCTCCTCC CTCCCTGCTCTGCTCAACTTCACTCTCCTCCTCGGTTCCCTTGG AGTACCTTGTGCCCCGGCAGTGCTGTCCCGGCCCTGGCATCCTG AGGTCTTCCCGTGGTGAGGACTTAAGTGGACA [C/G] CAGGAGT GGGTGGAGAGAGGGAGGGAGAGTTTGGCCTGCAGGCTCTCTGGA TGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTGCTGTTCCCGG AGCCTGGCTTCAGGGGTGCATCCGTCACTCAGGGTTTATTACAC CAGGCAGGCTCCAAGTTCTTGGGGTGACAAGGTGGGCACTGTC CCTTCTGGGTGCTGACAGCAGAGCCTGGCTCCCCCTCCGCCACCA TGAGCGGCTGCTCCAAAAGATGCAAGCTTGGGTTCGTGAAATTT GCCCAGACCATCTTTAAGCTCATCACTGGGACCCCTCAGCAAAGG TATGGAACTGGCCTTGACCTTGCTTTCTGTCTTGATATGGCC TGCTGTGTCGCATTGCCTCGGTGTGGTGAGCGTGACCATTTCTGG TGCACCCAGGTCTTGGAAAAAGCTGGGGAAATTGGTGGCTGGGA TTTCGAGGTGTGCTGACAACCTGCGTCTGGCTTTGAGTAGGCGGG CACCCAGCCAGGGAACCTCAGCTGGCTGTAATTGCCTGGAACCTT GGAAATGGAGTTGGTGGTGTGTGGCTGATACGTTATGGGCGGGC AGAGGGATAGAACCCTTTCCAGAGCATTGGAAGTGGCTTAGCGT GACTGGAGTTTCAAGAAGTTATCCATGGAAGGTGTATTTTGT GATAAAAGAGAGATTGATGCAGTGGGTTGTGAGTAATTCTGCA GAACAGAGACGCTTGAGGGGGCCAGTGGGAGGTGGTGTATGGGCC GGCATCTGCTTTGCCCTGGTGGCTTCAGAAACCGGATCAGCTCT GCACCTCAAGTGCCAAGAGCCTCCTCTCATAGGGTTCCAGCGTC TCGTGCTTCTGGGGCTTCATTATCGTTCTGCTTTCTTGGATCC CTGTCCCTCCACATTTTCATGCCTA	
KCP_ela_250027	CAAGGCACAGAGAATTGATCTATCAGATTAACCAGGAAGGAAAG AGTGGGAGAGCGAGTGTGGGAGGCTGTGGGGCTGAGTGTTTTCT GCGTAGCAGTCCCCCTCCCTTCTGACTTGAGTATTAATTGCTACA TTACCGCTGCCATGTAAGAAAGACAGTCAGCAAAGCCTGGGAGA GCTCCAGCTCCTCCCTCCCTGCTCTGCTCAACTTCACTCTCCTC CTCGGTTCCCTTGGAGTACCTTGTGCCCGGCAGTGCTGTCCCG GCCCTGGCATCCTGAGGTCTCCTCCCGTGGTGAGGACTTAAGTGA CAGCAGGAGTGGGTGGAGAGAGGGAGGGAGAGTTTGGCCTGCAG GCTCTCTGGATGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTG CTGTTCCCGGAGCCTGG [C/T] TTCAGGGGTGCATCCGTCACTC AGGGTTTATTACCCAGGCAGGCTCCAAGTTCTTGGGGTGACA AGGTGGGCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTGGCT CCCCTCCGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTTG GGTTTCGTGAAATTTGCCCCAGACCATCTTTAAGCTCATCACTGGG ACCCTCAGCAAAGGTATGGAAGTGGCCTTGACCTTGCTTTCT GTCTTGATATGGCCTGGCTGGTGCATTGCCTCGGTGTGGTGAG CGTGACCATTCTGGTGCACCCAGGTCTTGGAAAAAGCTGGGGAA ATTGGTGGCTGGGATTGAGGTTGCTGACAACCTGCGTCTCTGGC TTTGTAGTAGGCGGGCACCCAGCCAGGGAACCTCAGCTGGCTGTAA	SEQ ID NO. 249
KCP_ela_250049	ACAGAGAATTGATCTATCAGATTAACCAGGAAGGAAAGAGTGGG AGAGCGAGTGTGGGAGGCTGTGGGGCTGAGTGTTTTCTGCGTAG CAGTCCCCCTCCCTTCTGACTTGAGTATTAATTGCTACATTACCG CTGCCATGTAAGAAAGACAGTCAGCAAAGCCTGGGAGAGCTCCA GCTCCTCCCTCCCTGCTCTGCTCAACTTCACTCTCCTCCTCGGT TCCCTTGGAGTACCTTGTGCCCGGCAGTGCTGTCCCGGCCCTG GCATCCTGAGGTCTCCTCCCGTGGTGAGGACTTAAGTGGACAGCAG	SEQ ID NO. 250

	GAGTGGGTGGAGAGAGGGAGGGAGAGTTTGCCCTGCAGGCTCTC TGGATGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTGCTGTTT CCGGAGCCTGGCTTCAGGGGTGCATCCGTCACT [A/C] AGGGTT CATTCACCCAGGCAGGCTCCAAGTTCCTGGGGTGACAAGGTGG GCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTGGCTCCCCTC CGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTGGGTTCG TGAAATTTGCCAGACCATCTTTAAGCTCATCACTGGGACCCTC AGCAAAGGTATGGAACTGGCCTTGACCCTTGCTTTCTGTCTTG ATATGGCCTGGCTGGTCGCATTGCCTCGGTGTGGTGAGCGTGAC CATTCTGGTGCACCCAGGTCTTGGA AAAAGCTGGGGAAATTGGT GGCTGGGATTGAGGTTGCTGACAACCTGCGTCCTGGCTTTGAG TAGGCGGGCAGCCAGCCAGGGAATCAGCTGGCTGTAATTGCCT GGAACTTTGAAATGGAGTTGGTG	
KCP_UTR1 _382206	TGGCCACCTTCAGGGTCATGAGGATTCATAAACCTATTCTGC GAAGTGCCTCCAGGAATCATCAAGGGAGCTAGGGCAGCTCTGAG TCTCCACCCAGGCCACCTCCGCTCTCAGGGCTGAGCTTCACT TCCCTTCCCAAAGGGGCCAGGGAGAGGGGCTGCTGATGACATGA TCTCAGAGGAAGGCCAAGGCCTCCAGGCTGCCTCTGGGCCTGGC ACAGGAAGGAGGAGGAGAAAATAGGGAGCCCAAGGAAAGATCAA CCCAGCCCAGCCCAAGGACCCCCAGCCCCAGCCCCAGCCCCAGC TGGGCTCAAATAATTGAAAACAGACTGGAAAAGGCTGCTTTTG CCCTTCTCTAGACTCAGCATCATCAAGACTGGAGGGACAGAGC ATTTGAATCATCAGACGCTGGGCCAGA [C/T] GTCACCCACGC GTTTTCTCATTTTATCGTCCTAAGAAAGCCAGAAAGGTGCGTAAA ATGGCCTGTCCCAAACAGATGAGGACATTACCTTTCTCCTCTTC CTCCTCCTCCTTCTTCTTCTTCTTTTGCTTCATTTTCTT TCATTTTTTCCCCAGATGTTGCATTTAGAGAGGCTGAGCGTG TTGACTAAGGTACACAGCTACAAACATCAGGGACCTGCGAAAA AGCTCTGTTCCCTGGTGACAGGTGTTCTGTGATCCTAACACAGC CGGAGGTGGGGACAACGTCCTTGAGTAACAAAGGCCCTGTTGC TCAACTCAGTGGACATCAGGCCCTGTTTTCATTATTAGCAGGT CAGGGATTCCAGTGTACCTGTGCCATGTATTCCAGCTGATCTA CCTGCAAGCCTCTACTCCCCATTTTCCAGCAGCAGCCGCAGAC ACCACCAACTGG	SEQ ID NO. 251
KCP_UTR1 _382272	GGGTGATGAGGATTCATAAACCTATTCTGCGAAGTGCCTCCAG GAATCATCAAGGGAGCTAGGGCAGCTCTGAGTCTCCACCAGGCC CACCTCCGCTCTCAGGGCTGAGCTTCACTTCCCTTCCCAAAG GGCCAGGGAGAGGGGCTGCTGATGACATGATCTCAGAGGAAGG CCAAGGCCTCCAGGCTGCCTCTGGGCTGGCACAGGAAGGAGGA GGAGAAAATAGGGAGCCCAAGGAAAGATCAACCCAGCCAGCCC AAGGACCCCCAGCCCCAGCCCCAGCCCCAGCTGGGCTCAAATA ATTGAAAACAGACTGGAAAAGGCTGCTTTTGCCCTTCTCTAGA CTCAGCATCATCAAGACTGGAGGGACAGAGCATTGTAATCATCA GACGCTGGGCCAGACGTACCCCCACGCGTTTTCTCATTTTATCG TCCTAAGAAGCCCAGAAGGTGCGTAAAATGGCCTGT [A/C] CCA AACAGATGAGGACATTACCTTTCTCCTCTTCTCCTCCTCCTTC TTCTTCTTCTTCTTTTGCTTCATTTTCTTTTATTCTTTCCCC CAGATGTTGCATTTAGAGAGGCTGAGCGTGTGACTAAGGTCA CACAGCTACAAACATCAGGGACCTGCGAAAAAGCTCTGTTCCCT GGTGACAGGTGTTCTGTGATCCTAACACAGCCGAGGTGGGGAC AACGTCCTTGAGTAACAAAGGCCCTGTTGCTCAACTCAGTGA CATCAGGCCCTGTTTTCATTATTAGCAGGTGAGGATTCCAGT GTCACCTGTGCCATGTATTCCAGCTGATCTACCTGCAAGCCTCT ACTCCCCATTTTCCAGCAGCAGCCGCAGACACCACCAACTGG CAGAAATTTCAAACAAGGGGTTCTGCCTTGCACTCCGGTGCAAG GGTTGGGCACGTGACTCACAT	SEQ ID NO. 252
KCP_3UTR	CACAAAACAAATCCGGGACTTTAAGCCTGATCTGCTTGACCTGA	SEQ ID

2_395068	<p>AACTCATATCTACTTCCCTGCCCTCTGAAGATCTATATGTCCTA TGTCATCACTTCACTGTTTACACAAGGTGATACCTGGCTTCTCC AAGCACCTGCTACCCTGAACCTTACTGCACCACTCTTTCCTTCCCT AGCCTGAATGCAATTTTGCAATGAGGAGATGATTGATTTTCTTC AGCCCTAGACCTCCAGCTTCTTGAGAGCAGGTACTCTTGCCCTCT TCTTGCTCATTATTGATCCATATATTTAGAATAGCGCTGGCAG GTAGATGGTGCTTAATAAATATTATTGAATAAATGAATGAATG AATGATCCAATGAGCCCCAAAGCAAATAACAATAAAGGACATTT GCAGAGTGCTCTACAGAGAGACAAGTGCTTTCCCTTT [A/G] CT TTATCTTACCCCATTTCTCACACAATCCCTGACATGATTGGGT TCATGTTTACAGATGAGGAGGCTAACGGCCAGGTGTACATACC AGGGGACATGGGACTGGGTTTATATGAGCTCAGGGGTAAATGAT GACACCCCTTTCCCTGCCCTGAAGGATCTCAGTTTGAGTATTTG TAGCACACTTAGGATGTTCTGGGCCAGGCTGAGTGGCGGTGGAT GGGGGCGGTGGAGGTGGGGTATGCAAAGCAGGAACTCGGCCCTT TGCTTTCTAAAAGCTCCCACTCTATTTGAGGCCAGACTTATGCA TGCAGAACATTTGGGAAATGGTACAAGACAGCAGCAAGCATAGT GCTGAATTGCACATAATCAGGTGCCAACTGCATTCCCTTCCCTTA ACTAATCT</p>	NO. 253
KCP_3UTR 3_398480	<p>AACTTTCTCCTCAGCAAAGAGCTCTCCTCTGTTCCCTGAATCCT GGATATCCCACTGGGTCTCTAGTGACCCCAAGCTTCAGCCTCG CATGCCCTCTTCTCGAACAGAGAAGGCAGGAGGGAAGCAGGGAC CAGCCCCCTGCTCCATCTTCCAGGATTCCAGGCCTCCCTGGCCTG GACAAGCCCTGAGCTGGCAGTTAGGAGAGCAGAGGTTGTGAATC TGGTGGGACCCCCAGCAGGTCTTCTGGCTCAGTGCCCTCATCT GTGAGCAGGGGTTCCCCCAGGAGACCACGACAGAGGCCTGGAACC CAAGTTCTAATCCCATCTCTGGCTGGGCAACTTCAGGCAAATT TCTAACACAAGGTAAGCCTCAATTTCTCTCTGGGGTAATGATCA GGCACCTGCTTAATTCACAGGGGTTTGGTGGGCATCA [C/T] GT GGACAATGTGGTTGCACAGCAGTGCGCAATGCAAAGGAAAGGAA GTATGTTAGTAAGTGCCCCCTCCCCTGTTGCACAAAACAGGACAC ATGCTGGGATTGCAGAAAAGCAATAAATGCTGCACAGGTGAAGA AACTATTCAAGGACCCTGGCCAAGTCACAGGCTACCTGTGGCC CTGAGGGGACAGCTCATGGGTTGGCATTAGGGGAAGCAGCTCTC AAGGGGCCCTGTATCCTGGGGATTCAACTCTGTGCCTATGTGGCA TTGAGCCTGTGTGAATGTGGTGAATGTGCTGCTGCTGCTGCTG TGTGCGTCTGCATGCCCTGTGTGTTTGTGTGCTCTCCACCTTCG TGGGGGGCAACTGTAGGTGTATTATGAGCCTTGGGTCTGTCTGT GTGTACAATAGCAATGTCTGTGCGGACTTAAGGACCTGCGCCCA TATGTTTGTGGGACTTTC</p>	SEQ ID NO. 254
KCP_3UTR 3_398605	<p>CAGAGAAGGCAGGAGGGAAGCAGGGACCAGCCCCTGCTCCATCT TCCAGGATTCCAGGCCTCCCTGGCCTGGACAAGCCCTGAGCTGG CAGTTAGGAGAGCAGAGGTTGTGAATCTGGTGGGACCCCCAGCA GGTCTTCTGGCTCAGTGCCCTCATCTGTGAGCAGGGGTTCCCC AGGAGACCACGACAGAGGCCTGGAACCCAAGTTCTAATCCCACA TCCTGGCTGGGCAACTTCAGGCAAATTTCTAACACAAGGTAAGC CTCAATTTCTCTCTGGGGTAATGATCAGGCACCTGCTTAATTCA CAGGGGTTTGGTGGGCATCACGTGGACAATGTGGTTGCACAGCA GTGGGCAATGCAAAGGAAAGGAAGTATGTTAGTAAGTGCCCCCTC CCCTGTTGCACAAAACAGGACACATGCTGGGATTGCAGAAAAGC AATAAATGCTGCA [C/T] AGGTGAAGAAAATATTCAAGGACCC TGGCCAAGTCACAGGCTACCTGTGGCCCTGAGGGGACAGCTCAT GGGTTGGCATTAGGGGAAGCAGCTCTCAAGGGGCTGTATCCTG GGGATTCAACTCTGTGCCTATGTGGCATTGAGCCTGTGTGAATG TGGTGAATGTGCTGCTGTTTTGCTGTGTGTGCGTCTGCATGCGT GTGTGTTTGTGTGCTCTCCACCTTCGTGGGGGGCAACTGTAGG TGTATTATGAGCCTTGGGTCTGTCTGTGTGTACAATAGCAATGT</p>	SEQ ID NO. 255

	CTGTGCGGACTTAAGGACCTGCGCCCATATGTTTGTGGGACTTT CTGGGCATGCATGCTTGTATTATGAGGCCATACATCCGGGTATTC TGTGAACTGCTAGCATGGTGTGTATCTGTGTGGCAGACAGAAAA TGGCTGGGTGGGA	
KCP_e1b_ 399912	ATCTCAGCACTTTGGGAGGCCAAGGCGGGTGGATCACCTGAGGT CAGGAGTTCAAGCCCAGCCAGCCCAACATGGCGAAACCCCGTCT CTATTAAAAAATACAAAAAATTTAGCTGGGCCTAGTGGTGGGC GCCTGTAATCCCAGCTACTCCGGAGGCTGAGGCAGGAGAATCGC TTGAATCTGGGAGGCAGAGGTTGCAGTGAGCAGAGATCGCACCA CTGCACTCCAGCCTGGGCAACAGAGCGGAGACTCCGTCTCAAAAA AAAAAAAAAAGAAAAAGAAAAATGAGAGTGTAAGGGCCAGAG GGGCTGAGGGCTCCTTTCTCCTCCCAACTCCTGTCTCAGTAGAA GGTGGGCCCCGCCATAGGAGGATTCTGCAGAACCCCTCAAGGACC CGCGGAGCAGGACGGCACCTTCTTCCCATGACCACCCATTGGA TGTGTTTTTACCCCTTTCTGGGTGGGGCAGACTTTCCCCCTCC CCATGAGTTCAGGCAG [G/T] GGGTTAAATAAGATTTCCCTTGA AGTCGAATGAAATCACAATGCACCACACACAGGGACACACACAC ACACACACGCACGCACGCACATCACACACACACACACACACACA CACACACACACACACATACACACACACAGTCTCCCTGGGGCC AATCTACTGCCCCCTGAACCTCACCCATCAGCCAGGTGCCTGGC CCCCGGTCTGTCTTTAGGGTTACATGCTCCCCGGGCTCCCGCA CATACCCCGGCAGATGAGGGTGCAGGGGTGAGGGCGCAGGGC TGGGCGTCCCCCGCCCCCACCCTGCAGCCCTCGCCCCGCCCCG CCCCCTCCGTAGTTGCCCGCCCGCCGCCCTCCGCCGCCCTC CGCCGCTCCGACTCTCGCCCCGAGCGCTGGCAGCAGGCAGCAGG CAGCAGGCGGGCGCGCTGTGGCTCCGCGCCGCGCGGTCCGGGCT CTGTTCAATCATGATTGGTACTCGGCCCTCCGAGACC	SEQ ID NO. 256
rs102685	AGCACTCCTGGGGCTCATTGTAAAGTTTATAAACTCAGAGCTG ATGAGTTGTGTGCACTGTGTGGGTCTGAGTGGGCTTATGACTCC CCTCCAAGCCTGGCTGTAAGAATCTAAGACTTAAAGCTGAAGGA CCAAATGGGACTTTCTGTCCCATCCCCTCTCTGCTCCATGCAAG CACCAA [C/T] GTGGATTTTTGCCCCCTAATTATATTAGGGAACG CTGTCAATCAAAAAGATGATGTTAAACTCATCCAGAACAAACCA AACCATGTTTAAGGGGAAGAAAAGATTACATCTTCAAATGCCAG CATGCCATCATTAATACAATGTCTAATGTAGTCAATATAGTTCA GGCAACATTGAAAATGAACCACTGCAATACTAGGAATACAATT TCAAGAGGAAGCACAAACATTCTGTGTTTCTATGCACACAGTCCT GTAAATTATTTGCAGCTCAAGTATGTATGTTCTTTTAAATTTT CCCCCTGGGTACAGCTTGAACAACCTTCTACAAGTGTTGATATGT CATATTCTCATTATCATTTAGTTCAAAATTACCATGATTTAATT ACCATGAGGTTGCTTTTGTGATACATGAGTTACTTAGAAATTGA ATTAggctaggcatgggtggcttccacctataatcctagcacttt ggaaggccaaggcaggaggattgcttgagtttgaggccagtcta ggcaatatagtgagacctcatctccccaaaagtacaaaaaaact agccaggcatggggacacatgcctatagttccagctactcaaag gctgaggtggggaggattgctttgagcctggg	SEQ ID NO. 257
rs905808	GCCAGCTATCCCAGAGACATCACAGGAGAAGGAGCAGAAGCTG GAACATCATCCGGGAGCTGGACTAGAACGTCCCGGGAACCTTCA GCCTGGCTTCTGCTTTGTCCCGAAAACCCAGGGGCTCCAGCTCC AGGGCTGTGTCTTAGAATGAGGCAGTTTATCTGTTTCAGGGCTTC TCTTAGTTTTTAATCCCAATAGGACACA [C/T] GTTGTATTAAA AAGCCATGCGAGATGGAAGAAGGAAATTGAATGAAATTTGAGGG CAGGTAGGAGCAGAGACAATAATAATTGAGCAGTGAAGGAAGC AGAAAAAAGATTGCACTCATTTGCGCCTTCAACAATTATACTAA ACACCTGCTCTGGGCCACAGAAGGGCCAGATCCCATTCCTGTGC TCAGGAAGCCACAGGCCGGCAGGGAGAGGCTGGTTGGAATGTG TGCTTTGCACTGTAACGGAGGCATCGAGCATGGTAAGGGACTGG	SEQ ID NO. 258

	CGGTGACTGCTGCCTGCGGACGTCGAGACAGGGGCCTTTGAAGA GGCAGGACCTGTCTGGAGTCTTACCTGGGCCTTGGCCTGGCAAT GGGG	
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Table 1. The Build 33 location of SNPs and microsatellites employed for the first-pass association analysis across KChIP1.

5

Start (B33)	Marker	Public Alias	deCODE alias	Variation
169788696	DG5S47			
169794522	DG5S1592			
169843903	DG5S119			
169869845	rs933656	rs933656	DG00AAFCS	A/G
169869955	rs2339091	rs2339091	DG00AAFCI	G/T
169961410	DG5S13			
169964087	rs905808	rs905808	DG00AAFCEG	C/T
170006645	rs883849	rs883849	DG00AAFCK, DG00AAIOG	A/G
170015858	DG5S123			
170037283	rs2135046	rs2135046	DG00AAFCJ, DG00AAIOH	C/T
170041996	DG5S124			
170056955	rs2339139	rs2339139	DG00AAFCR	A/G
170064881	rs329468	rs329468	DG00AAFCH	A/G
170070041	rs50057	rs50057	DG00AAFCE, DG00AAIOI	A/G
170070735	rs102685	rs102685	DG00AAFCE, DG00AAIOJ	C/T
170073252	rs50364	rs50364	DG00AAFCD	A/G
170081291	KCP_1152		SG05S176	C/T
170081473	KCP_1333		SG05S921	A/G
170082788	KCP_2649		SG05S923	C/T
170085115	KCP_4976		DG00AAGHK, DG00AAHUT, DG00AAINX	C/T
170085217	KCP_5077		DG00AAINZ	A/T
170095540	KCP_15400		SG05S946	C/T
170096291	KCP_16152	rs486818	SG05S948	A/G
170098209	KCP_18069	rs1363712	SG05S189	C/T
170105556	D5S625			

5 Table 12. The Build 33 location of SNPs found through sequencing across KChIP1(from exon 1b to exon 8).

Build 33 Pos	Project Pos	DECODE ALIAS	SEQ PROJECT ALIAS	PUBLIC ALIAS	SNP
169866787	9677	DG00AAHAP	KCP_9677		C/G
169867465	10355	SG05S229	KCP_10355		A/T
169867556	10446	DG00AAHA R	KCP_10446		C/G
169871957	14847	SG05S485	KCP_14847	rs486768	A/T
169872129	15019	SG05S1298	KCP_15019	rs4867973	A/G
169872417	15307	SG05S437	KCP_15307		A/C
169872421	15311	SG05S438	KCP_15311		A/T
169872435	15325	SG05S439	KCP_15325		C/G
169872949	15839	SG05S440	KCP_15839		A/G
169873539	16429	SG05S486	KCP_16429		C/T
169873680	16570	SG05S487	KCP_16570		A/G
169875123	18013	SG05S488	KCP_18013		A/T
169875568	18458	SG05S1002	KCP_18458		A/G
169876302	19192	SG05S489	KCP_19192		A/G
169878365	21255	SG05S490	KCP_21255		G/T
169878734	21624	SG05S491	KCP_21624	rs486769	A/G
169879678	22568	SG05S492	KCP_22568		A/C
169879717	22607	SG05S493	KCP_22607		C/T
169881496	24386	SG05S494	KCP_24386		A/G
169882681	25571	SG05S495	KCP_25571		A/C
169883265	26155	SG05S496	KCP_26155		A/G
169883333	26223	SG05S497	KCP_26223		C/G
169883413	26303	SG05S498	KCP_26303		A/G
169883465	26355	SG05S1171	KCP_26355		C/G
169883518	26408	SG05S499	KCP_26408		A/T
169883738	26628	SG05S500	KCP_26628		A/G
169883811	26701	SG05S501	KCP_26701		A/G
169884084	26974	SG05S1172	KCP_26974		C/T
169884145	27035	SG05S502	KCP_27035		G/T
169884439	27329	SG05S503	KCP_27329		C/T
169884682	27572	SG05S504	KCP_27572		A/G

169884707	27597	DG00AAJHT	KCP_27597		A/G
169884973	27863	SG05S505	KCP_27863		A/G
169885005	27895	SG05S506	KCP_27895		A/G
169888453	31343	SG05S507	KCP_31343	rs4867975	C/T
169889433	32323	SG05S60	KCP_32323		C/T
169889680	32570	SG05S508	KCP_32570		A/G
169890025	32915	SG05S509	KCP_32915		A/G
169890055	32945	SG05S1173	KCP_32945		A/G
169890089	32979	SG05S1174	KCP_32979		A/C
169890291	33181	SG05S510	KCP_33181		A/G
169892122	35012	SG05S1175	KCP_35012		A/C
169892332	35222	SG05S511	KCP_35222		A/G
169892524	35414	SG05S61	KCP_35414		G/T
169892619	35509	SG05S512	KCP_35509		C/T
169892687	35577	SG05S513	KCP_35577		G/T
169893157	36047	SG05S514	KCP_36047		C/T
169893169	36059	SG05S515	KCP_36059		C/T
169893871	36761	SG05S516	KCP_36761		A/C
169894061	36951	SG05S517	KCP_36951		A/G
169894358	37248	SG05S518	KCP_37248		C/G
169895507	38397	SG05S1176	KCP_38397		C/T
169895699	38589	SG05S953	KCP_38589		A/C
169896322	39212	SG05S519	KCP_39212		G/T
169896357	39247	SG05S520	KCP_39247		A/G
169896369	39259	SG05S521	KCP_39259		A/G
169896451	39341	SG05S1177	KCP_39341		A/G
169896647	39537	SG05S522	KCP_39537		C/T
169896750	39640	SG05S523	KCP_39640		A/T
169896914	39804	SG05S524	KCP_39804		A/G
169897484	40374	SG05S525	KCP_40374		C/T
169897594	40484	SG05S526	KCP_40484		A/G
169897621	40511	SG05S527	KCP_40511		C/T
169897856	40746	SG05S528	KCP_40746		C/T
169898205	41095	SG05S529	KCP_41095		C/T
169898252	41142	SG05S530	KCP_41142		C/T
169898371	41261	SG05S531	KCP_41261		A/G
169899446	42336	SG05S532	KCP_42336		A/G
169899693	42583	SG05S533	KCP_42583		A/G
169900156	43046	SG05S534	KCP_43046		A/G

169900425	43315	SG05S1178	KCP_43315		C/G
169900629	43519	SG05S535	KCP_43519		C/T
169902212	45102	SG05S536	KCP_45102	rs211261	A/G
169902400	45290	SG05S537	KCP_45290		G/T
169903206	46096	SG05S538	KCP_46096		C/T
169903615	46505	SG05S539	KCP_46505		C/T
169903676	46566	SG05S540	KCP_46566		A/C
169903766	46656	SG05S541	KCP_46656		A/C
169904530	47420	SG05S542	KCP_47420		C/T
169904757	47647	SG05S543	KCP_47647		A/G
169906262	49152	SG05S1179	KCP_49152		A/G
169906576	49466	SG05S544	KCP_49466		A/G
169906846	49736	SG05S545	KCP_49736		A/T
169907866	50756	SG05S1180	KCP_50756		A/G
169908937	51827	SG05S1181	KCP_51827		C/T
169909190	52080	SG05S1182	KCP_52080		C/T
169910099	52989	SG05S546	KCP_52989		A/G
169910133	53023	SG05S547	KCP_53023		C/T
169911784	54674	SG05S548	KCP_54674		A/C
169911823	54713	SG05S549	KCP_54713		A/C
169913086	55976	SG05S1183	KCP_55976		A/G
169913415	56305	SG05S62	KCP_56305		A/G
169913670	56560	SG05S954	KCP_56560		C/T
169913988	56878	SG05S550	KCP_56878		C/G
169914731	57621	SG05S551	KCP_57621		A/G
169914887	57777	SG05S552	KCP_57777		A/G
169915597	58487	SG05S553	KCP_58487		A/G
169917130	60020	SG05S554	KCP_60020		C/T
169917579	60469	SG05S555	KCP_60469		A/G
169917813	60703	SG05S556	KCP_60703		A/G
169919206	62096	SG05S557	KCP_62096		A/G
169919909	62799	SG05S233	KCP_62799		C/T
169921008	63898	SG05S558	KCP_63898		A/G
169921407	64297	SG05S559	KCP_64297		A/G
169921917	64807	SG05S560	KCP_64807		G/T
169922010	64900	SG05S1184	KCP_64900		A/G
169922309	65199	SG05S955	KCP_65199		A/G
169922397	65287	SG05S561	KCP_65287		G/T
169923449	66339	SG05S562	KCP_66339		A/G

169923611	66501	SG05S563	KCP_66501		A/G
169924005	66895	SG05S564	KCP_66895		A/G
169925422	68312	SG05S565	KCP_68312		A/C
169926039	68929	SG05S566	KCP_68929		C/T
169926454	69344	SG05S567	KCP_69344		A/G
169926756	69646	SG05S568	KCP_69646		C/T
169927013	69903	SG05S569	KCP_69903		A/G
169927893	70783	SG05S570	KCP_70783		C/T
169928063	70953	SG05S571	KCP_70953		A/T
169928076	70966	SG05S572	KCP_70966		A/C
169928444	71334	SG05S573	KCP_71334		C/T
169928522	71412	SG05S574	KCP_71412		A/T
169928555	71445	SG05S575	KCP_71445		C/T
169928665	71555	SG05S576	KCP_71555		C/T
169928700	71590	SG05S577	KCP_71590		C/T
169929635	72525	SG05S578	KCP_72525	rs4269297	A/G
169929849	72739	SG05S579	KCP_72739		C/G
169930171	73061	SG05S580	KCP_73061	rs4867613	C/T
169930506	73396	SG05S581	KCP_73396		A/T
169930538	73428	SG05S582	KCP_73428	rs4867978	A/G
169930644	73534	SG05S583	KCP_73534	rs4867979	C/T
169931073	73963	SG05S584	KCP_73963		C/G
169931425	74315	SG05S585	KCP_74315		A/G
169931663	74553	SG05S586	KCP_74553		G/T
169931670	74560	SG05S587	KCP_74560		C/T
169932137	75027	SG05S588	KCP_75027		C/T
169932696	75586	SG05S589	KCP_75586		A/C
169932998	75888	SG05S590	KCP_75888		C/T
169933181	76071	SG05S591	KCP_76071	rs386758	A/G
169933212	76102	SG05S592	KCP_76102	rs386759	C/T
169933256	76146	SG05S593	KCP_76146		A/G
169933389	76279	SG05S594	KCP_76279	rs4368746	C/T
169933420	76310	SG05S595	KCP_76310		C/T
169933699	76589	SG05S596	KCP_76589		C/T
169933756	76646	SG05S597	KCP_76646		C/T
169934348	77238	SG05S598	KCP_77238		G/T
169934429	77319	SG05S599	KCP_77319		C/G
169934556	77446	SG05S600	KCP_77446		C/T
169934663	77553	SG05S601	KCP_77553		C/T

169934751	77641	SG05S597	KCP_77641	rs4242157	A/G
169934936	77826	SG05S598	KCP_77826		C/G
169934949	77839	SG05S599	KCP_77839		A/G
169935134	78024	SG05S600	KCP_78024	rs4867981	A/G
169935240	78130	SG05S601	KCP_78130	rs4867614	C/T
169935254	78144	SG05S602	KCP_78144		A/C
169935713	78603	SG05S603	KCP_78603		C/T
169935892	78782	SG05S604	KCP_78782		A/G
169935939	78829	SG05S605	KCP_78829		A/G
169935989	78879	SG05S606	KCP_78879		C/T
169936272	79162	SG05S607	KCP_79162		C/T
169936275	79165	SG05S608	KCP_79165		C/T
169936329	79219	SG05S609	KCP_79219		G/T
169936495	79385	SG05S610	KCP_79385		C/T
169936910	79800	SG05S611	KCP_79800		C/G
169937029	79919	SG05S1189	KCP_79919		A/G
169937270	80160	SG05S612	KCP_80160		A/G
169937896	80786	SG05S613	KCP_80786		A/G
169938126	81016	SG05S614	KCP_81016		C/T
169938400	81290	SG05S615	KCP_81290		A/G
169938894	81784	SG05S1190	KCP_81784		A/G
169939578	82468	SG05S957	KCP_82468	rs4242158	A/G
169940311	83201	SG05S616	KCP_83201		C/T
169940995	83885	SG05S617	KCP_83885		A/G
169941106	83996	SG05S618	KCP_83996	rs4867615	A/G
169941897	84787	SG05S1191	KCP_84787		A/T
169942667	85557	SG05S619	KCP_85557		A/G
169942775	85665	SG05S620	KCP_85665		C/T
169942903	85793	SG05S958	KCP_85793		C/T
169943046	85936	SG05S621	KCP_85936		A/G
169943817	86707	SG05S622	KCP_86707		A/T
169944237	87127	SG05S623	KCP_87127		C/G
169945487	88377	SG05S624	KCP_88377		C/T
169945857	88747	SG05S625	KCP_88747		A/T
169945886	88776	SG05S626	KCP_88776		C/T
169945923	88813	SG05S627	KCP_88813		A/G
169946380	89270	SG05S628	KCP_89270		A/G
169946491	89381	SG05S629	KCP_89381	rs4867983	A/G
169947228	90118	SG05S630	KCP_90118		A/G

169947236	90126	SG05S631	KCP_90126		G/T
169947285	90175	SG05S632	KCP_90175		C/T
169947471	90361	SG05S633	KCP_90361		C/G
169947529	90419	SG05S634	KCP_90419		C/T
169947661	90551	SG05S635	KCP_90551		A/G
169947834	90724	SG05S636	KCP_90724		A/G
169948187	91077	SG05S637	KCP_91077		A/G
169948683	91573	SG05S1192	KCP_91573		A/G
169948703	91593	SG05S1193	KCP_91593		G/T
169948722	91612	SG05S1194	KCP_91612		A/G
169948755	91645	SG05S1195	KCP_91645		C/T
169948788	91678	SG05S1196	KCP_91678		A/G
169948798	91688	SG05S1197	KCP_91688		C/T
169948977	91867	SG05S638	KCP_91867		C/T
169949063	91953	SG05S639	KCP_91953		C/T
169949229	92119	SG05S640	KCP_92119		C/T
169949277	92167	SG05S641	KCP_92167		A/T
169949352	92242	SG05S642	KCP_92242		A/G
169949354	92244	SG05S643	KCP_92244	rs4867984	A/G
169949449	92339	SG05S644	KCP_92339		C/T
169950146	93036	SG05S63	KCP_93036		A/G
169950148	93038	SG05S645	KCP_93038		A/G
169950333	93223	SG05S646	KCP_93223	rs4867985	C/T
169950655	93545	SG05S64	KCP_93545		G/T
169950703	93593	SG05S1198	KCP_93593		C/G
169950754	93644	SG05S654	KCP_93644		G/T
169950844	93734	SG05S655	KCP_93734		C/T
169950855	93745	SG05S656	KCP_93745		G/T
169950892	93782	SG05S1199	KCP_93782		C/G
169950990	93880	SG05S657	KCP_93880		C/T
169951245	94135	SG05S1200	KCP_94135		A/C
169951290	94180	SG05S1201	KCP_94180		A/G
169951422	94312	SG05S658	KCP_94312		A/T
169951577	94467	SG05S659	KCP_94467		A/G
169951689	94579	SG05S660	KCP_94579		A/G
169951702	94592	SG05S661	KCP_94592		A/G
169951831	94721	SG05S662	KCP_94721		C/G
169951838	94728	SG05S663	KCP_94728		A/G
169951848	94738	SG05S664	KCP_94738		C/T

169951855	94745	SG05S665	KCP_94745		A/G
169952144	95034	SG05S1202	KCP_95034		A/G
169952209	95099	SG05S666	KCP_95099		A/C
169952705	95595	SG05S667	KCP_95595		A/G
169952838	95728	SG05S670	KCP_95728		A/G
169952962	95852	SG05S671	KCP_95852		A/G
169953175	96065	SG05S672	KCP_96065		C/G
169953185	96075	SG05S673	KCP_96075	rs43546	A/G
169953207	96097	SG05S674	KCP_96097	rs4374772	C/G
169953297	96187	SG05S675	KCP_96187		A/G
169953327	96217	SG05S676	KCP_96217		A/G
169953334	96224	SG05S677	KCP_96224		A/G
169953426	96316	SG05S678	KCP_96316		A/G
169953728	96618	SG05S1203	KCP_96618		C/G
169953902	96792	SG05S679	KCP_96792	rs4867987	C/T
169954134	97024	SG05S680	KCP_97024	rs4867988	C/T
169954165	97055	SG05S1204	KCP_97055	rs486798	C/T
169954260	97150	SG05S1205	KCP_97150		A/G
169954800	97690	SG05S681	KCP_97690		A/T
169954954	97844	DG00AAJIA	KCP_97844	rs222438	A/T
169955450	98340	SG05S682	KCP_98340		C/T
169956638	99528	SG05S683	KCP_99528		A/C
169956932	99822	SG05S684	KCP_99822		C/T
169957089	99979	SG05S685	KCP_99979		A/G
169957538	100428	SG05S1206	KCP_100428		G/T
169958211	101101	SG05S1207	KCP_101101	rs449521	A/G
169958651	101541	SG05S1208	KCP_101541		A/G
169958784	101674	SG05S686	KCP_101674		A/C
169959085	101975	SG05S687	KCP_101975		A/G
169959172	102062	SG05S1209	KCP_102062		A/T
169959537	102427	SG05S688	KCP_102427		A/G
169959561	102451	SG05S1210	KCP_102451		C/T
169959860	102750	SG05S1211	KCP_102750		C/T
169959992	102882	DG00AAJIB	KCP_102882		C/T
169961135	104025	SG05S689	KCP_104025	rs486799	A/G
169961268	104158	SG05S690	KCP_104158		G/T
169961404	104294	SG05S691	KCP_104294	rs4867991	A/G
169961971	104861	SG05S692	KCP_104861		A/G
169962144	105034	SG05S693	KCP_105034		A/G

169962410	105300	SG05S694	KCP_105300	rs4242159	A/T
169962429	105319	SG05S695	KCP_105319	rs4428429	C/G
169962889	105779	SG05S696	KCP_105779		A/G
169962929	105819	SG05S697	KCP_105819		C/T
169963467	106357	SG05S698	KCP_106357	rs236561	A/G
169963592	106482	SG05S699	KCP_106482		C/T
169963741	106631	SG05S700	KCP_106631		A/G
169963761	106651	SG05S701	KCP_106651		A/G
169963827	106717	SG05S702	KCP_106717		A/T
169964021	106911	SG05S703	KCP_106911	rs9587	C/G
169964087	106977	SG05S1212	KCP_106977	rs9588	C/T
169964112	107002	SG05S1213	KCP_107002	rs9589	C/T
169964368	107258	SG05S988	KCP_107258	rs95811	A/G
169964490	107380	DG00AAJIC	KCP_107380		A/G
169964862	107752	SG05S705	KCP_107752	rs95812	A/T
169964998	107888	SG05S706	KCP_107888		A/T
169965204	108094	SG05S707	KCP_108094		C/T
169965210	108100	SG05S708	KCP_108100		C/T
169965293	108183	SG05S709	KCP_108183		C/T
169965384	108274	SG05S710	KCP_108274		C/T
169965778	108668	SG05S1214	KCP_108668		C/T
169965813	108703	SG05S230	KCP_108703		G/T
169965814	108704	SG05S711	KCP_108704		A/G
169965989	108879	SG05S712	KCP_108879		A/T
169966345	109235	SG05S713	KCP_109235		C/G
169966790	109680	SG05S714	KCP_109680		A/C
169966813	109703	SG05S715	KCP_109703		A/G
169966833	109723	SG05S716	KCP_109723		A/G
169966856	109746	SG05S718	KCP_109746	rs95813	A/G
169967196	110086	SG05S719	KCP_110086		C/T
169967509	110399	SG05S720	KCP_110399		C/G
169968134	111024	SG05S721	KCP_111024		A/C
169968258	111148	SG05S722	KCP_111148		C/T
169968588	111478	SG05S723	KCP_111478	rs289191	C/G
169968602	111492	SG05S724	KCP_111492		A/G
169968614	111504	SG05S725	KCP_111504		C/G
169969010	111900	SG05S726	KCP_111900		A/G
169969185	112075	SG05S727	KCP_112075		A/G
169969769	112659	SG05S728	KCP_112659	rs4867994	C/T

169970341	113231	SG05S729	KCP_113231		A/G
169970367	113257	SG05S730	KCP_113257	rs4867616	A/G
169970440	113330	SG05S733	KCP_113330		A/G
169971048	113938	SG05S734	KCP_113938		A/G
169971464	114354	SG05S736	KCP_114354		A/G
169971531	114421	SG05S1215	KCP_114421		C/T
169971568	114458	SG05S737	KCP_114458	rs2879337	C/T
169971621	114511	SG05S738	KCP_114511		C/T
169972209	115099	SG05S740	KCP_115099	rs1553537	A/G
169972598	115488	SG05S741	KCP_115488		C/G
169973254	116144	SG05S742	KCP_116144	rs113922	C/T
169973325	116215	SG05S743	KCP_116215		A/G
169973369	116259	SG05S744	KCP_116259		A/G
169973465	116355	SG05S745	KCP_116355	rs289192	A/G
169974479	117369	SG05S746	KCP_117369	rs8719	A/T
169974926	117816	SG05S747	KCP_117816	rs1553538	C/T
169976065	118955	SG05S1216	KCP_118955		C/T
169977940	120830	SG05S748	KCP_120830	rs95819	C/T
169978197	121087	SG05S749	KCP_121087		C/T
169978247	121137	SG05S192	KCP_121137		A/G
169978339	121229	SG05S193	KCP_121229		C/T
169978427	121317	SG05S1217	KCP_121317		C/T
169980304	123194	SG05S751	KCP_123194		A/G
169980403	123293	SG05S752	KCP_123293		A/G
169980481	123371	SG05S1218	KCP_123371		A/G
169980664	123554	SG05S753	KCP_123554		C/T
169981035	123925	SG05S1219	KCP_123925		A/G
169981067	123957	SG05S754	KCP_123957		A/G
169981628	124518	SG05S755	KCP_124518		C/T
169981632	124522	SG05S756	KCP_124522		G/T
169981987	124877	SG05S194	KCP_124877	rs4146511	C/T
169982473	125363	SG05S757	KCP_125363	rs222436	A/T
169982868	125758	SG05S758	KCP_125758		C/T
169983196	126086	SG05S195	KCP_126086		A/G
169983318	126208	DG00AAJHA	KCP_126208		T/C
169983565	126455	SG05S1220	KCP_126455		C/G
169983591	126481	SG05S759	KCP_126481	rs2221441	C/G
169983692	126582	SG05S760	KCP_126582		A/G
169985824	128714	SG05S1221	KCP_128714		A/G

169985916	128806	SG05S151	KCP_128806		A/G
169985985	128875	SG05S761	KCP_128875		C/T
169986162	129052	SG05S763	KCP_129052	rs4867617	C/G
169986174	129064	SG05S762	KCP_129064		C/G
169986189	129079	SG05S764	KCP_129079	rs4867618	C/T
169986203	129093	SG05S152	KCP_129093	rs4867995	C/G
169986237	129127	SG05S480	KCP_129127	rs4867619	A/G
169986334	129224	SG05S765	KCP_129224	rs486762	G/T
169986478	129368	SG05S766	KCP_129368		C/G
169986579	129469	SG05S181	KCP_129469		A/G
169986800	129690	SG05S182	KCP_129690	rs4867996	G/T
169986957	129847	SG05S767	KCP_129847		A/G
169986984	129874	SG05S985	KCP_129874	rs4867997	A/C
169986999	129889	SG05S986	KCP_129889	rs4867999	A/G
169987419	130309	DG00AAJHB	KCP_130309		A/G
169987667	130557	SG05S196	KCP_130557	rs95822	C/G
169988155	131045	SG05S768	KCP_131045		A/G
169988354	131244	SG05S197	KCP_131244	rs95824	A/G
169988368	131258	SG05S769	KCP_131258	rs95825	C/T
169988581	131471	SG05S770	KCP_131471	rs95826	A/G
169988714	131604	SG05S1222	KCP_131604		A/G
169988812	131702	SG05S771	KCP_131702	rs95827	C/T
169988905	131795	SG05S65	KCP_131795	rs48681	C/T
169988964	131854	SG05S153	KCP_131854		G/T
169989037	131927	SG05S772	KCP_131927		A/G
169989257	132147	SG05S773	KCP_132147		C/T
169989533	132423	SG05S774	KCP_132423		A/G
169989704	132594	SG05S775	KCP_132594	rs48682	G/T
169989739	132629	SG05S776	KCP_132629		A/G
169989787	132677	SG05S154	KCP_132677		A/G
169990284	133174	SG05S777	KCP_133174		C/T
169990366	133256	SG05S1223	KCP_133256		A/G
169990548	133438	SG05S778	KCP_133438	rs4867621	A/G
169990840	133730	SG05S779	KCP_133730		C/T
169990962	133852	SG05S780	KCP_133852		A/G
169991155	134045	SG05S198	KCP_134045		C/T
169991415	134305	SG05S199	KCP_134305		C/T
169991521	134411	SG05S781	KCP_134411		C/T
169991729	134619	SG05S1224	KCP_134619		A/C

169991939	134829	SG05S782	KCP_134829		C/T
169992076	134966	SG05S783	KCP_134966		A/G
169992155	135045	SG05S784	KCP_135045		A/G
169992628	135518	SG05S200	KCP_135518	rs48683	G/T
169992821	135711	SG05S785	KCP_135711		G/T
169993032	135922	SG05S786	KCP_135922		A/G
169993096	135986	SG05S183	KCP_135986		A/G
169993146	136036	SG05S481	KCP_136036		A/C
169993585	136475	SG05S787	KCP_136475		C/T
169994082	136972	SG05S201	KCP_136972	rs48684	A/G
169994770	137660	SG05S202	KCP_137660		A/G
169995924	138814	SG05S788	KCP_138814		C/T
169997343	140233	SG05S789	KCP_140233		C/T
169997640	140530	SG05S1225	KCP_140530		A/G
169998201	141091	SG05S1226	KCP_141091		A/G
170000256	143146	SG05S1227	KCP_143146	rs95361	C/T
170000611	143501	SG05S1228	KCP_143501		C/T
170000722	143612	SG05S66	KCP_143612	rs4867622	A/G
170000869	143759	SG05S790	KCP_143759		C/T
170000983	143873	SG05S1229	KCP_143873		C/T
170001571	144461	SG05S1230	KCP_144461		C/T
170001578	144468	SG05S1299	KCP_144468	rs93185	C/T
170002070	144960	SG05S203	KCP_144960	rs2279873	C/T
170002435	145325	SG05S791	KCP_145325		C/T
170002801	145691	SG05S1231	KCP_145691		A/G
170003438	146328	SG05S792	KCP_146328		A/G
170003572	146462	SG05S793	KCP_146462		G/T
170003856	146746	SG05S482	KCP_146746		C/T
170003940	146830	SG05S1232	KCP_146830		C/T
170004075	146965	SG05S794	KCP_146965		C/T
170004199	147089	SG05S1233	KCP_147089		C/G
170004733	147623	SG05S204	KCP_147623	rs2292146	C/T
170005151	148041	SG05S795	KCP_148041		C/T
170006326	149216	SG05S205	KCP_149216		A/G
170006485	149375	SG05S796	KCP_149375	rs883848	G/T
170006645	149535	SG05S206	KCP_149535	rs883849	A/G
170006910	149800	SG05S1234	KCP_149800		A/G
170007023	149913	SG05S797	KCP_149913	rs4867623	C/T
170007516	150406	SG05S798	KCP_150406	rs48685	G/T

170007640	150530	SG05S987	KCP_150530		C/T
170007808	150698	SG05S799	KCP_150698		G/T
170007921	150811	SG05S155	KCP_150811		A/G
170008215	151105	SG05S800	KCP_151105		G/T
170008937	151827	SG05S801	KCP_151827	rs449672	A/G
170009218	152108	SG05S1235	KCP_152108		A/G
170009587	152477	SG05S802	KCP_152477		C/T
170009592	152482	SG05S803	KCP_152482		A/C
170010385	153275	SG05S1236	KCP_153275		C/T
170010518	153408	SG05S1237	KCP_153408		C/T
170010943	153833	SG05S804	KCP_153833		C/T
170011041	153931	DG00AAJHC	KCP_153931	rs2879338	A/G
170011269	154159	SG05S805	KCP_154159		A/G
170011475	154365	SG05S1238	KCP_154365		A/G
170011963	154853	SG05S806	KCP_154853		C/T
170012367	155257	SG05S807	KCP_155257		C/G
170013726	156616	SG05S808	KCP_156616		C/T
170013842	156732	SG05S207	KCP_156732	rs924876	A/T
170015154	158044	SG05S809	KCP_158044		A/G
170015582	158472	SG05S810	KCP_158472		C/T
170015603	158493	SG05S811	KCP_158493		A/G
170015680	158570	SG05S812	KCP_158570		C/T
170015727	158617	SG05S67	KCP_158617	rs236559	C/T
170016200	159090	SG05S813	KCP_159090		A/G
170016255	159145	SG05S814	KCP_159145		A/G
170016259	159149	SG05S815	KCP_159149		C/T
170016791	159681	SG05S1239	KCP_159681		A/G
170016798	159688	SG05S1240	KCP_159688		A/G
170017255	160145	SG05S208	KCP_160145		A/G
170017524	160414	SG05S816	KCP_160414		G/T
170018297	161187	SG05S817	KCP_161187		A/G
170018356	161246	SG05S818	KCP_161246		C/G
170018549	161439	SG05S819	KCP_161439		A/G
170018573	161463	SG05S820	KCP_161463		C/T
170019258	162148	SG05S821	KCP_162148		C/T
170019314	162204	SG05S1241	KCP_162204		A/C
170019379	162269	SG05S822	KCP_162269		A/T
170019414	162304	SG05S823	KCP_162304		C/G
170019958	162848	SG05S824	KCP_162848		C/G

170020197	163087	SG05S825	KCP_163087		C/G
170020606	163496	SG05S826	KCP_163496		A/G
170020870	163760	SG05S827	KCP_163760		A/G
170021444	164334	SG05S1242	KCP_164334		A/G
170022007	164897	SG05S209	KCP_164897		A/G
170022125	165015	SG05S828	KCP_165015		G/T
170022343	165233	SG05S1243	KCP_165233		C/T
170022545	165435	SG05S1244	KCP_165435		C/T
170023275	166165	SG05S829	KCP_166165		A/G
170024034	166924	SG05S1245	KCP_166924	rs4867624	C/T
170024668	167558	SG05S830	KCP_167558		A/G
170025753	168643	SG05S1246	KCP_168643		A/G
170025970	168860	SG05S1247	KCP_168860	rs222439	C/G
170026021	168911	SG05S1248	KCP_168911		A/G
170026162	169052	SG05S1249	KCP_169052		A/G
170026344	169234	SG05S156	KCP_169234		A/G
170028032	170922	SG05S1297	KCP_170922	rs48688	A/C
170028055	170945	SG05S831	KCP_170945		C/G
170028163	171053	SG05S1250	KCP_171053	rs48689	A/G
170028303	171193	SG05S1300	KCP_171193	rs48681	G/T
170028752	171642	SG05S1251	KCP_171642		G/T
170028987	171877	SG05S832	KCP_171877		A/G
170030482	173372	SG05S833	KCP_173372		A/G
170030815	173705	SG05S834	KCP_173705		C/T
170030958	173848	SG05S210	KCP_173848		A/G
170030986	173876	SG05S1252	KCP_173876		C/T
170031092	173982	SG05S157	KCP_173982		A/C
170031149	174039	SG05S835	KCP_174039		C/T
170031150	174040	SG05S836	KCP_174040		A/G
170031353	174243	DG00AAJHF	KCP_174243		A/G
170031709	174599	SG05S837	KCP_174599		C/T
170031812	174702	SG05S838	KCP_174702		C/T
170031962	174852	SG05S839	KCP_174852		A/G
170031972	174862	SG05S840	KCP_174862	rs46285	G/T
170032216	175106	SG05S158	KCP_175106	rs233995	C/G
170032280	175170	SG05S211	KCP_175170		A/G
170032361	175251	SG05S841	KCP_175251		C/T
170032362	175252	DG00AAJHG	KCP_175252		A/G
170032610	175500	SG05S842	KCP_175500		A/G

170032814	175704	SG05S843	KCP_175704		A/G
170033021	175911	SG05S844	KCP_175911		A/G
170033923	176813	SG05S845	KCP_176813		A/G
170033946	176836	DG00AAJHH	KCP_176836		A/G
170034620	177510	SG05S184	KCP_177510	rs486811	A/C
170034720	177610	SG05S1253	KCP_177610		G/T
170034980	177870	SG05S846	KCP_177870		G/T
170035009	177899	SG05S847	KCP_177899	rs486812	C/T
170036929	179819	SG05S848	KCP_179819		C/T
170037010	179900	SG05S1254	KCP_179900		G/T
170037283	180173	SG05S159	KCP_180173	rs213546	C/T
170037347	180237	SG05S212	KCP_180237	rs213547	C/G
170038967	181857	SG05S1255	KCP_181857		C/T
170039237	182127	SG05S1256	KCP_182127		C/T
170039419	182309	SG05S849	KCP_182309		A/T
170041190	184080	SG05S160	KCP_184080	rs2292147	C/G
170041385	184275	SG05S964	KCP_184275		A/G
170042689	185579	DG00AAJDX	KCP_185579		C/A
170043158	186048	SG05S213	KCP_186048		A/G
170043789	186679	SG05S161	KCP_186679		C/G
170043953	186843	SG05S850	KCP_186843		A/C
170043997	186887	SG05S965	KCP_186887		C/T
170044226	187116	DG00AAJDY	KCP_187116		A/G
170044277	187167	SG05S851	KCP_187167		C/G
170044368	187258	SG05S852	KCP_187258		G/T
170044661	187551	SG05S853	KCP_187551		A/G
170044798	187688	DG00AAJDZ	KCP_187688		T/A
170044904	187794	SG05S966	KCP_187794		C/T
170045075	187965	SG05S967	KCP_187965		C/T
170046043	188933	SG05S968	KCP_188933		C/T
170046441	189331	SG05S214	KCP_189331		A/G
170047120	190010	SG05S854	KCP_190010	rs2221442	A/G
170047129	190019	SG05S855	KCP_190019		C/G
170048070	190960	SG05S856	KCP_190960		C/G
170048074	190964	SG05S857	KCP_190964		C/T
170048090	190980	SG05S858	KCP_190980		C/G
170048315	191205	SG05S859	KCP_191205	rs486815	C/T
170048733	191623	SG05S860	KCP_191623		A/G
170049238	192128	SG05S990	KCP_192128		C/T

170049852	192742	DG00AAJEB	KCP_192742	rs1973529	T/C
170050303	193193	DG00AAJEC	KCP_193193		G/A
170051066	193956	SG05S163	KCP_193956	rs22244	C/T
170051438	194328	SG05S861	KCP_194328		A/T
170051462	194352	SG05S862	KCP_194352		A/G
170051726	194616	DG00AAJEE	KCP_194616	rs23656	T/C
170051899	194789	SG05S970	KCP_194789		C/T
170052012	194902	SG05S863	KCP_194902		A/G
170052171	195061	SG05S971	KCP_195061		G/T
170052988	195878	SG05S864	KCP_195878		C/T
170053658	196548	DG00AAJEF	KCP_196548		A/G
170053669	196559	SG05S865	KCP_196559		A/G
170053840	196730	SG05S866	KCP_196730		G/T
170053939	196829	SG05S867	KCP_196829		C/G
170054581	197471	SG05S972	KCP_197471		A/G
170054620	197510	SG05S973	KCP_197510		C/T
170054788	197678	DG00AAJEG	KCP_197678	rs96284	T/C
170054803	197693	SG05S884	KCP_197693		A/G
170054885	197775	DG00AAJEH	KCP_197775		C/T
170055781	198671	DG00AAJEI	KCP_198671		A/G
170055957	198847	SG05S974	KCP_198847		A/G
170056043	198933	DG00AAJEJ	KCP_198933		G/A
170056137	199027	SG05S975	KCP_199027		A/G
170056475	199365	DG00AAJEK	KCP_199365		A/G
170056516	199406	SG05S164	KCP_199406		A/T
170056578	199468	SG05S1257	KCP_199468		C/T
170057283	200173	SG05S165	KCP_200173		C/G
170057351	200241	DG00AAJEL	KCP_200241		A/G
170057605	200495	SG05S976	KCP_200495		A/G
170057933	200823	SG05S991	KCP_200823		A/C
170058193	201083	SG05S992	KCP_201083	rs4464713	C/T
170058699	201589	SG05S885	KCP_201589		C/T
170059095	201985	DG00AAJEM	KCP_201985		G/A
170059177	202067	DG00AAJEN	KCP_202067	rs222144	A/G
170059203	202093	SG05S977	KCP_202093		A/C
170059905	202795	DG00AAJEO	KCP_202795	rs875184	C/T
170060219	203109	SG05S1258	KCP_203109		A/G
170060292	203182	SG05S978	KCP_203182		A/G
170060393	203283	SG05S979	KCP_203283	rs95818	A/G

170061018	203908	SG05S980	KCP_203908	rs95817	C/T
170061292	204182	SG05S981	KCP_204182	rs872435	G/T
170061352	204242	SG05S166	KCP_204242		C/T
170061419	204309	SG05S982	KCP_204309		A/G
170061618	204508	SG05S983	KCP_204508	rs872436	A/G
170061670	204560	SG05S1259	KCP_204560		A/G
170061727	204617	SG05S984	KCP_204617		C/T
170061799	204689	SG05S1260	KCP_204689	rs95816	G/T
170061809	204699	SG05S1261	KCP_204699		A/T
170061845	204735	SG05S1262	KCP_204735	rs95815	C/T
170062696	205586	SG05S886	KCP_205586	rs329466	C/T
170062747	205637	SG05S887	KCP_205637		A/C
170062756	205646	SG05S888	KCP_205646	rs329467	C/T
170062777	205667	SG05S889	KCP_205667		A/G
170062940	205830	SG05S167	KCP_205830		C/T
170062950	205840	SG05S890	KCP_205840		A/G
170063305	206195	SG05S891	KCP_206195		C/G
170063313	206203	SG05S892	KCP_206203		C/T
170063377	206267	SG05S168	KCP_206267		A/G
170063732	206622	SG05S893	KCP_206622		A/G
170063817	206707	SG05S894	KCP_206707		C/T
170063983	206873	SG05S1263	KCP_206873		A/T
170064013	206903	SG05S1264	KCP_206903		C/G
170064648	207538	SG05S895	KCP_207538		C/T
170064760	207650	SG05S969	KCP_207650		A/G
170064771	207661	SG05S169	KCP_207661		C/G
170064881	207771	SG05S896	KCP_207771	rs329468	A/G
170065075	207965	SG05S170	KCP_207965		C/T
170065694	208584	SG05S171	KCP_208584		A/G
170065711	208601	SG05S232	KCP_208601	rs329469	A/C
170065715	208605	SG05S897	KCP_208605		A/G
170065740	208630	SG05S172	KCP_208630		C/T
170065834	208724	SG05S1265	KCP_208724		C/T
170066123	209013	SG05S1266	KCP_209013		C/T
170066260	209150	SG05S1267	KCP_209150		A/G
170067967	210857	SG05S898	KCP_210857	rs2194162	A/G
170068018	210908	SG05S899	KCP_210908		C/G
170068420	211310	SG05S900	KCP_211310		A/G
170068510	211400	SG05S901	KCP_211400	rs41348	A/G

170068614	211504	SG05S902	KCP_211504		A/G
170068635	211525	SG05S173	KCP_211525		A/G
170068731	211621	SG05S903	KCP_211621		A/G
170068759	211649	SG05S1268	KCP_211649		G/T
170068960	211850	SG05S185	KCP_211850	rs32947	C/T
170069885	212775	SG05S186	KCP_212775	rs434973	A/G
170070003	212893	SG05S1269	KCP_212893		G/T
170070041	212931	SG05S1270	KCP_212931	rs557	A/G
170070593	213483	SG05S904	KCP_213483		A/G
170070700	213590	SG05S1271	KCP_213590	rs12684	C/T
170070735	213625	SG05S905	KCP_213625	rs12685	C/T
170070768	213658	SG05S1272	KCP_213658	rs12686	A/G
170071584	214474	SG05S1273	KCP_214474	rs329471	C/G
170071665	214555	SG05S1274	KCP_214555	rs433936	C/T
170071715	214605	SG05S1275	KCP_214605	rs432615	C/G
170072023	214913	SG05S1276	KCP_214913		A/G
170072363	215253	SG05S906	KCP_215253	rs441562	C/T
170072373	215263	SG05S907	KCP_215263	rs172944	C/T
170072484	215374	SG05S908	KCP_215374		A/G
170072485	215375	SG05S909	KCP_215375		A/G
170072562	215452	SG05S910	KCP_215452	rs191297	A/G
170072712	215602	SG05S1277	KCP_215602	rs186646	A/C
170072813	215703	SG05S174	KCP_215703		A/C
170073179	216069	SG05S1278	KCP_216069		C/T
170073555	216445	SG05S1279	KCP_216445	rs136379	A/G
170073565	216455	SG05S1280	KCP_216455	rs329474	C/G
170074202	217092	SG05S993	KCP_217092	rs984559	A/G
170074303	217193	SG05S994	KCP_217193		C/T
170074359	217249	SG05S995	KCP_217249	rs329475	A/G
170075932	218822	SG05S996	KCP_218822		A/G
170076291	219181	SG05S997	KCP_219181		A/G
170076439	219329	SG05S998	KCP_219329	rs81987	C/G
170077257	220147	SG05S911	KCP_220147		A/T
170078779	221669	SG05S912	KCP_221669		C/G
170078881	221771	SG05S1281	KCP_221771		C/T
170078909	221799	DG00AAJHJ	KCP_221799		A/T
170078966	221856	SG05S913	KCP_221856		C/T
170079102	221992	SG05S1282	KCP_221992		C/T
170079170	222060	SG05S175	KCP_222060		C/T

170079176	222066	SG05S1283	KCP_222066		A/T
170079986	222876	SG05S1284	KCP_222876		A/G
170080026	222916	SG05S914	KCP_222916		C/T
170080378	223268	SG05S915	KCP_223268	rs486817	C/T
170080480	223370	SG05S916	KCP_223370		C/T
170080678	223568	SG05S917	KCP_223568		G/T
170080917	223807	SG05S918	KCP_223807		C/G
170081127	224017	SG05S919	KCP_224017		A/G
170081263	224153	SG05S1285	KCP_224153		G/T
170081464	224354	SG05S920	KCP_224354		C/G
170081779	224669	SG05S231	KCP_224669		A/C
170082330	225220	SG05S177	KCP_225220		A/G
170082361	225251	SG05S1286	KCP_225251		A/T
170082496	225386	SG05S922	KCP_225386		C/T
170083131	226021	SG05S1287	KCP_226021		A/C
170083226	226116	SG05S1288	KCP_226116		C/G
170083558	226448	SG05S924	KCP_226448		A/G
170083941	226831	SG05S925	KCP_226831		A/G
170084576	227466	SG05S926	KCP_227466		C/T
170084823	227713	SG05S927	KCP_227713		A/G
170084981	227871	SG05S178	KCP_227871		C/G
170085097	227987	SG05S483	KCP_227987		C/T
170085116	228006	SG05S187	KCP_228006		C/T
170085151	228041	SG05S928	KCP_228041		A/T
170085191	228081	SG05S929	KCP_228081		C/T
170085217	228107	SG05S179	KCP_228107		A/T
170085834	228724	SG05S1289	KCP_228724		A/G
170086059	228949	SG05S999	KCP_228949		C/T
170086143	229033	SG05S1000	KCP_229033		C/T
170086250	229140	SG05S1001	KCP_229140		C/T
170086709	229599	SG05S930	KCP_229599		A/C
170086826	229716	SG05S931	KCP_229716		C/T
170087721	230611	SG05S932	KCP_230611		C/G
170087734	230624	SG05S933	KCP_230624		A/G
170087780	230670	SG05S934	KCP_230670		G/T
170087950	230840	SG05S1290	KCP_230840		A/G
170088932	231822	SG05S1291	KCP_231822	rs1422978	C/T
170089182	232072	SG05S1292	KCP_232072	rs219416	C/T
170089631	232521	SG05S1293	KCP_232521	rs1592987	A/T

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170090569	233459	SG05S935	KCP_233459		A/G
170090765	233655	SG05S989	KCP_233655	rs232863	A/G
170091557	234447	SG05S936	KCP_234447		A/G
170091681	234571	SG05S937	KCP_234571		C/T
170091700	234590	SG05S938	KCP_234590		A/T
170092075	234965	SG05S939	KCP_234965		C/T
170092275	235165	SG05S940	KCP_235165	rs136371	G/T
170092318	235208	SG05S941	KCP_235208	rs1363711	A/G
170092468	235358	SG05S942	KCP_235358		A/G
170093047	235937	SG05S1294	KCP_235937		A/C
170093362	236252	SG05S943	KCP_236252		A/T
170094119	237009	SG05S1295	KCP_237009		A/G
170094581	237471	SG05S944	KCP_237471	rs1422979	A/G
170094615	237505	SG05S188	KCP_237505	rs4867628	C/T
170094780	237670	SG05S1296	KCP_237670		G/T
170095344	238234	SG05S945	KCP_238234		C/T
170095662	238552	SG05S947	KCP_238552		C/T
170095701	238591	SG05S180	KCP_238591		C/T
170096774	239664	SG05S949	KCP_239664		C/G
170097477	240367	SG05S950	KCP_240367		C/G
170098637	241527	SG05S190	KCP_241527	rs1363713	G/T
170098914	241804	SG05S191	KCP_241804		C/T
170099451	242341	SG05S951	KCP_242341	rs1363714	A/G
170099467	242357	SG05S952	KCP_242357		G/T

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Table 13. The Build 33 location of SNPs and microsatellites employed for the subsequent association analysis across KChIP1.

Start (B33)	Marker	Public alias	deCODE alias	Variation
169477886	rs1895301	rs1895301	DG00AAGUZ	C/T
169500972	rs1422752	rs1422752	DG00AAESV	C/T
169518355	rs1422754	rs1422754	DG00AAESU	A/G
169653708	DG5S1173			
169661202	DG5S44			
169673518	SG05S872		SG05S872	A/G
169678484	SG05S873		SG05S873	A/G
169693772	DG5S45			
169696877	KCP_rs315773	rs315773	SG05S76, SG05S874	A/G
169702377	DG5S46			
169705505	SG05S876		SG05S876	A/G
169709735	KCP_rs952767	rs952767	SG05S79	G/T
169740666	KNB_24222		DG00AAIGE	A/G
169740703	KNB_24259		DG00AAIGF	A/G
169741172	KNB_24728		DG00AAIGG	G/T
169745438	DG5S1178			
169746339	KNB_29895		DG00AAIGH	C/T
169747941	KNB_31497		DG00AAIGI	A/G
169751683	KNB_35298		DG00AAIGZ	A/T
169751753	KNB_35370		DG00AAIHA	C/G
169751753	KNB_35399		DG00AAIHB	A/G
169753659	KCP_rs314129	rs314129	SG05S83	C/T
169782203	KCP_rs183398	rs183398	SG05S87, SG05S879	C/T
169788696	DG5S47			
169794522	DG5S1592			
169815996	rs1032856	rs1032856	SG05S96	C/G
169833941	rs2055606	rs2055606	DG00AAESP	C/T
169843903	DG5S119			
169859274	KCP_rs888934	rs888934	SG05S93	A/G
169867464	KCP_10355		SG05S229	A/T
169867555	KCP_10446		DG00AAHAR	C/G
169869845	rs933656	rs933656	DG00AAFCS	A/G
169869955	rs2339091	rs2339091	DG00AAFCI	G/T
169890856	rs1862331	rs1862331	DG00AAFCL	C/T

169895698	KCP_38589		SG05S953	A/C
169922308	KCP_65199		SG05S955	A/G
169939577	KCP_82468	rs4242158	SG05S957	A/G
169942902	KCP_85793		SG05S958	C/T
169950654	KCP_93545		SG05S64	G/T
169951970	DG5S955			
169954953	KCP_97844	rs222438	DG00AAJIA	A/T
169959991	KCP_102882		DG00AAJIB	C/T
169961410	DG5S13			
169964489	KCP_107380		DG00AAJIC	A/G
169965813	KCP_108703		SG05S230	G/T
169981986	KCP_124877	rs4146511	SG05S194	C/T
169983195	KCP_126086		SG05S195	A/G
169983317	KCP_126208		DG00AAJHA	T/C
169986202	KCP_129093	rs4867995	SG05S152	C/G
169986236	KCP_129127	rs4867619	SG05S480	A/G
169986799	KCP_129690	rs4867996	SG05S182	G/T
169987418	KCP_130309		DG00AAJHB	A/G
169987666	KCP_130557	rs95822	SG05S196	C/G
169987873	rs905823	rs905823	DG00AAFCK, DG00AAIIMM	A/C
169988353	KCP_131244	rs95824	SG05S197	A/G
169988963	KCP_131854		SG05S153	G/T
169989786	KCP_132677		SG05S154	A/G
169991154	KCP_134045		SG05S198	C/T
169992627	KCP_135518	rs48683	SG05S200	G/T
169993145	KCP_136036		SG05S481	A/C
169994769	KCP_137660		SG05S202	A/G
170000721	KCP_143612	rs4867622	SG05S66	A/G
170002069	KCP_144960	rs2279873	SG05S203	C/T
170003855	KCP_146746		SG05S482	C/T
170006325	KCP_149216		SG05S205	A/G
170006644	KCP_149535	rs883849	SG05S206	A/G
170006645	rs883849	rs883849	DG00AAFCK, DG00AAIOG	A/G
170013841	KCP_156732	rs924876	SG05S207	A/T
170015726	KCP_158617	rs236559	SG05S67	C/T
170015858	DG5S123			
170017254	KCP_160145		SG05S208	A/G
170022006	KCP_164897		SG05S209	A/G
170026343	KCP_169234		SG05S156	A/G

170030957	KCP_173848		SG05S210	A/G
170031091	KCP_173982		SG05S157	A/C
170031352	KCP_174243		DG00AAJHF	A/G
170032215	KCP_175106	rs233995	SG05S158	C/G
170032279	KCP_175170		SG05S211	A/G
170032361	KCP_175252		DG00AAJHG	A/G
170033945	KCP_176836		DG00AAJHH	A/G
170037282	KCP_180173	rs213546	SG05S159	C/T
170037283	rs2135046	rs2135046	DG00AAFCJ, DG00AAIOH	C/T
170037346	KCP_180237	rs213547	SG05S212	C/G
170041189	KCP_184080	rs2292147	SG05S160	C/G
170041996	DG5S124			
170042688	KCP_185579		DG00AAJDX	C/A
170043157	KCP_186048		SG05S213	A/G
170043788	KCP_186679		SG05S161	C/G
170044225	KCP_187116		DG00AAJDY	A/G
170044367	KCP_187258		SG05S852	G/T
170044797	KCP_187688		DG00AAJDZ	T/A
170046440	KCP_189331		SG05S214	A/G
170049851	KCP_192742	rs1973529	DG00AAJEB	T/C
170050302	KCP_193193		DG00AAJEC	G/A
170051065	KCP_193956	rs22244	SG05S163	C/T
170051725	KCP_194616	rs23656	DG00AAJEE	T/C
170053657	KCP_196548		DG00AAJEF	A/G
170054787	KCP_197678	rs96284	DG00AAJEG	T/C
170054884	KCP_197775		DG00AAJEH	C/T
170056042	KCP_198933		DG00AAJEJ	G/A
170056474	KCP_199365		DG00AAJEK	A/G
170056955	rs2339139	rs2339139	DG00AAFCR	A/G
170057350	KCP_200241		DG00AAJEL	A/G
170059094	KCP_201985		DG00AAJEM	G/A
170059176	KCP_202067	rs222144	DG00AAJEN	A/G
170059904	KCP_202795	rs875184	DG00AAJEO	C/T
170061292	rs872435	rs872435	DG00AAFCP	G/T
170061351	KCP_204242		SG05S166	C/T
170063376	KCP_206267		SG05S168	A/G
170064770	KCP_207661		SG05S169	C/G
170064881	rs329468	rs329468	DG00AAFCH	A/G
170065074	KCP_207965		SG05S170	C/T

170068634	KCP 211525		SG05S173	A/G
170068959	KCP 211850	rs32947	SG05S185	C/T
170069884	KCP 212775	rs434973	SG05S186	A/G
170070041	rs50057	rs50057	DG00AAFCF, DG00AAIOI	A/G
170073252	rs50364	rs50364	DG00AAFCF	A/G
170078908	KCP 221799		DG00AAJHJ	A/T
170080677	KCP 223568		SG05S917	G/T
170081291	KCP 1152		SG05S176	C/T
170081473	KCP 1333		SG05S921	A/G
170082329	KCP 225220		SG05S177	A/G
170082788	KCP 2649		SG05S923	C/T
170084980	KCP 227871		SG05S178	C/G
170085096	KCP 227987		SG05S483	C/T
170085115	KCP 4976		DG00AAGHK, DG00AAHUT, DG00AAINX	C/T
170085216	KCP 228107		SG05S179	A/T
170085217	KCP 5077		DG00AAINZ	A/T
170089630	KCP 232521	rs1592987	SG05S1293	A/T
170090764	KCP 233655	rs232863	SG05S989	A/G
170094614	KCP 237505	rs4867628	SG05S188	C/T
170095540	KCP 15400		SG05S946	C/T
170095700	KCP 238591		SG05S180	C/T
170096291	KCP 16152	rs486818	SG05S948	A/G
170098208	KCP 241099		SG05S189	C/T
170098209	KCP 18069	rs1363712	SG05S189	C/T
170098636	KCP 241527	rs1363713	SG05S190	G/T
170098913	KCP 241804		SG05S191	C/T
170105556	D5S625			
170167429	DG5S959			
170361737	rs1551583	rs1551583	DG00AADMS	C/G
170389497	rs1457692	rs1457692	DG00AADMR	A/G

The teachings of all publications cited herein are incorporated herein by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein
5 without departing from the scope of the invention encompassed by the appended claims.

CLAIMS

What is claimed is:

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1. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of a susceptibility to Type II diabetes.

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2. A method of diagnosing a susceptibility to Type II diabetes comprising detecting an alteration in the expression or composition of a polypeptide encoded by KChIP1 nucleic acid in a test sample, in comparison with the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a control sample, wherein the presence of an alteration in expression or composition of the polypeptide in the test sample is indicative of a susceptibility to Type II diabetes.

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3. The method of Claim 1, wherein the polymorphism in the KChIP1 nucleic acid is indicated by detecting the presence of a least one of the polymorphisms indicated in Table 13.

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4. An isolated nucleic acid molecule comprising a KChIP1 nucleic acid, wherein the KChIP1 nucleic acid has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table 10, or the complements of the group of nucleic acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism.

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5. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table 10, or the complements of the group of nucleic

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acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism.

6. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: nucleic acid sequences as shown in Table 10 and the complement of the nucleic acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism and hybridizes to the first nucleic acid under high stringency conditions.
7. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
 - a) nucleic acid sequences as shown in Table 10; and
 - b) complement of one of the nucleic acid sequences are shown in Table 10; andwherein the nucleic acid molecule contains a polymorphism and is operably linked to a regulatory sequence.
8. A recombinant host cell comprising the vector of Claim 7.
9. A method for producing a polypeptide encoded by an isolated nucleic acid molecule having a polymorphism, comprising culturing the recombinant host cell of Claim 10 under conditions suitable for expression of the nucleic acid molecule.
10. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 4 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

11. A method of identifying an agent that alters expression of a KCHIP1 nucleic acid, comprising:

- 5
- a) contacting a solution containing a nucleic acid comprising the promoter region of the KCHIP1 nucleic acid operably linked to a reporter gene with an agent to be tested;
 - b) assessing the level of expression of the reporter gene; and
 - c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent; wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the KCHIP1 nucleic acid.
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12. An agent that alters expression of the KCHIP1 nucleic acid, identifiable according to the method of Claim 11.

13. A method of identifying an agent that alters expression of a KCHIP1 nucleic acid, comprising:

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- a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
 - b) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent;
- 25
- wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the KCHIP1 nucleic acid.
- 30

14. The method of Claim 13, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.
- 5 15. An agent that alters expression of a KChIP1 nucleic acid; identifiable according to the method of Claim 14.
- 10 16. An agent that alters expression of a KChIP1 nucleic acid, selected from the group consisting of: antisense nucleic acid to a KChIP1 nucleic acid; a KChIP1 polypeptide; a KChIP1 nucleic acid receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody, and a ribozyme.
- 15 17. A method of altering expression of a KChIP1 nucleic acid, comprising contacting a cell containing a KChIP1 nucleic acid with an agent of Claim 16.
- 20 18. A method of identifying a polypeptide which interacts with a KChIP1 polypeptide comprising a polymorphism indicated in Table 13, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a KChIP1 polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a KChIP1 polypeptide.
- 25 19. A Type II diabetes therapeutic agent selected from the group consisting of: a KChIP1 nucleic acid or fragment or derivative thereof; a polypeptide encoded by a KChIP1 nucleic acid; a KChIP1 receptor; a KChIP1 nucleic acid binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent
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- that alters KChIP1 nucleic acid expression; an agent that alters activity of a polypeptide encoded by a KChIP1 nucleic acid; an agent that alters posttranscriptional processing of a polypeptide encoded by a KChIP1 nucleic acid; an agent that alters interaction of a KChIP1 nucleic acid with a KChIP1 binding agent; an agent that alters transcription of splicing variants encoded by a KChIP1 nucleic acid; and a ribozyme.
20. A pharmaceutical composition comprising a Type II diabetes therapeutic agent of Claim 19.
21. The pharmaceutical composition of Claim 20, wherein the Type II diabetes therapeutic agent is an isolated nucleic acid molecule comprising a KChIP1 nucleic acid or fragment or derivative thereof.
22. The pharmaceutical composition of Claim 20, wherein the Type II diabetes therapeutic agent is a polypeptide encoded by the KChIP1 nucleic acid.
23. A method of treating a disease or condition associated with KChIP1 in an individual, comprising administering a Type II diabetes therapeutic agent to the individual, in a therapeutically effective amount.
24. The method of Claim 23, wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid agonist.
25. The method of Claim 23 wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid antagonist.
26. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous KChIP1 nucleic acid and a nucleic acid encoding a KChIP1 polypeptide.

27. A method for assaying a sample for the presence of a KChIP1 nucleic acid, comprising:

- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 gene under conditions appropriate for hybridization, and
- b) assessing whether hybridization has occurred between a KChIP1 gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid;

wherein if hybridization has occurred, a KChIP1 nucleic acid is present in the nucleic acid.

28. The method of Claim 27, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said KChIP1 nucleic acid.

29. The method of Claim 27, further comprising amplification of at least part of said KChIP1 nucleic acid.

30. The method of Claim 27, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; or c) capable of selectively hybridizing to said KChIP1 nucleic acid.

31. A reagent for assaying a sample for the presence of a KChIP1 nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide

sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.

32. The reagent of Claim 31, wherein the nucleic acid comprises a contiguous
5 nucleotide sequence, which is completely complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.
33. A reagent kit for assaying a sample for the presence of a KChIP1 nucleic acid, comprising in separate containers:
- 10 a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid, and
- b) reagents for detection of said label.
- 15 34. The reagent kit of Claim 33, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.
- 20 35. A reagent kit for assaying a sample for the presence of a KChIP1 nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleic acid sequence which is at least partially complementary to a part of the nucleic acid sequence of said KChIP1 nucleic acid, and which is capable of acting as a primer for said KChIP1 nucleic acid when maintained under conditions for
25 primer extension.
36. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; b) at
30 least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; or c) capable of

selectively hybridizing to said KChIP1 nucleic acid, for assaying a sample for the presence of a KChIP1 nucleic acid.

37. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 6;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- or
- c) capable of selectively hybridizing to said KChIP1 nucleic acid; for assaying a sample for the presence of a KChIP1 nucleic acid that has at least one nucleotide difference from the first nucleic acid.

38. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- or
- c) capable of selectively hybridizing to said KChIP1 nucleic acid; for diagnosing a susceptibility to a disease or condition associated with a KChIP1.

39. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising a halotype shown in Table 2 or Table 5 at the 5q35 loci,

wherein the presence of the haplotype is diagnostic of susceptibility to Type II diabetes.

5 40. The method of Claim 39, wherein determining the presence or absence of the haplotype comprises enzymatic amplification of nucleic acid from the individual.

10 41. The method of claim 40, wherein determining the presence or absence of the haplotype further comprises electrophoretic analysis.

42. The method of claim 39, wherein determining the presence or absence of the haplotype further comprises restriction fragment length polymorphism analysis.

15 43. The method of claim 39, wherein determining the presence or absence of the haplotype further comprises sequence analysis.

20 44. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising:
a) obtaining a nucleic acid sample from said individual; and
b) analyzing the nucleic acid sample for the presence or absence of a haplotype, comprising a haplotype shown in Table 2 or Table 5 at the 5q35 loci comprising a KChIP1 gene, wherein the presence of the haplotype is diagnostic for a susceptibility to Type II diabetes.

25 45. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 13 in the locus on chromosome 5q35,
30 wherein the presence of the haplotype is diagnostic of a susceptibility to Type II diabetes.

46. A method for the diagnosis and identification of a susceptibility to Type II diabetes in an individual, comprising: screening for an at-risk haplotype in the KChIP1 nucleic acid that is more frequently present in an individual susceptible to Type II diabetes compared to an individual who is not susceptible to Type II diabetes wherein the at-risk haplotype increases the risk significantly.
47. The method of Claim 46 wherein the significant increase is at least about 20%.
48. The method of Claim 46 wherein the significant increase is identified as an odds ratio of at least about 1.2.
49. Use of a Type II diabetes therapeutic agent for the manufacture of a medicament for the treatment of a disease or condition associated with KChIP1 in an individual.
50. The use of Claim 49, wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid agonist.
51. The use of Claim 49, wherein the Type II diabetes therapeutic agent is a KChIP1 antagonist.

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KchIP1 genomic DNA (Build 33 Chr5: 169716198 – 170098453)

caggagtg	gggagagag	gagggagag	ttgccctgca	ggctctctgg	169716247
atgcagaagc	cagactcgct	gcagaggcag	ctgtgctgtt	cccggagcct	169716297
GGCTTCAGGG	GTGCATCCGT	CACTCAGGGT	TCATTACCCC	AGGCAGGCTC	169716347
CAAGTTCCTG	GGGTGCACAA	GGTGGGCACT	GTCCCTTCTG	GGTGCTGACA	169716397
GCAGAGCCTG	GCTCCCCCTC	GCCACCATGA	GCGGCTGCTC	CAAAAGATGC	169716447
AAGCTTGGGT	TCGTGAAATT	TGCCCAGACC	ATCTTTAAGC	TCATCACTGG	169716497
GACCCTCAGC	AAAGgtatgg	aaactggcct	tgacccttgc	tttctgtctt	169716547
gatatggcct	ggctgggtcgc	attgcctcgg	tgtgggtgagc	gtgaccattc	169716597
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gctgaaaaaa	cgtctttaa	tattcatgct	gtctttcagg	aagagtcttt	169717447
gggggctggg	gagagaggca	ctggaagcag	caggcagaat	attcagggaa	169717497
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gaaaggctat	atgcagccag	atctcatgac	atggctcagg	tgcccgccac	169717597
ccagcgggtc	tggcccagtg	tacgttgtgt	ggcatgtgtg	ggtgggtggga	169717647
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aacatgggag	cagggccagg	ctgggagcag	ggtagctgag	aaaggcctgc	169718647
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FIG. 1.1

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ttagattcaa	ccctacatgg	atacattatg	attgcttaat	gattttctgat	169718747
tttaatttga	tttcacttat	tcattattca	ttgcactgag	ttctagattt	169718797
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tgaggaatgt	aaagaatgtg	ttggaccagg	tacctgcttg	ttctatggca	169718897
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FIG. 1.2

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ctggaggtag	ggattgcaat	caccatttca	gcaggtaagg	aaactggggg	169721347
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tcactctccc	cagtcttctt	aggggttacag	aatctccctt	gggccatctc	169722747
tctcagcaga	cccagggtccc	aaatccctga	aagcctttgc	ttcccaaggg	169722797
tggaaagtggc	gatgtgaagt	cactgtggaa	ggaagcagga	tgcagggcgg	169722847
gaaaactctg	gacccagagg	gacctgggct	ccaacctgc	catgcaccaa	169722897
caggacagcc	ttgggcaagc	cattccccat	cttgagtctg	tgtccttccg	169722947
taaatggggc	agtaatttcc	atctcatgtg	gctactggag	atggaatgag	169722997
atgggacatg	tgacaggcac	aggacctggc	tcatacaagc	tgtcagtaa	169723047
aagtcaagtt	ccccaccctt	cttttctatg	atacgaacct	ggatttgtag	169723097
ccaagagaaa	caaggctgag	cctctgtggg	tcaagtcctc	ttccagctc	169723147
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tcttgatgac	aagttctata	attaaaaatg	tgccaacaat	ggaaatgato	169723247
ctttttattt	agttgttcat	gggagaattg	gtcatccatt	ctcatgagaa	169723297
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acgactaaat	gctttccctg	ccgagcaaca	tcaggccatg	tggctggagt	169723447
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gggtgcaggc	ccacactgcc	tatgcatacc	agctggccag	gtgctcaggt	169723697
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ggaggaggga	ccccactgaa	aggcaggcag	caggggagag	gagctttggg	169723797
ggagaggatg	tggaaatgag	gaaattgcac	aggcctcccg	ggccagctgg	169723847
aggaaagaaa	ggccaggact	cctgaaaaag	actcatggga	agtcatttac	169723897

FIG. 1.3

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tatcaccact	gaccacgctc	tctgtcacag	gtcttcagtc	taggggcaga	169723947
agaaagcctt	ccttctctgt	taggatgagg	ggaggaggac	catgaacaca	169723997
aagctaacct	tggtcccctc	tggtctgaagc	cactgagatt	ccattttgtg	169724047
ttcttagaag	aacacccgct	ttggagccag	acctgggttt	gagtccaaat	169724097
cctcacaact	gcttgctgtc	ttaggccatc	aggctgctta	tcaacctgat	169724147
ggcctaagct	accatacaaa	gacacggttg	cttatcaaca	acagaaatgt	169724197
atttctcaca	gttctggaag	ctggaagtct	gagatcagga	tgctagcact	169724247
gtggacttct	cgtggggact	cttcctggct	tacagacagc	atctcctgct	169724297
gtattctgac	gtggaggaaa	gagagtaagc	tagctctctg	gcctcttctt	169724347
atagacacac	ccatttcaag	aggctccgcc	ttcatgacct	catcacctcc	169724397
caaaggcccc	accttcaaat	accatcacct	caggagtggg	atttcaacat	169724447
gtgaatttgg	gggacgggag	gcacaaatat	tcagccatt	gcactaagta	169724497
aatggctttt	ttttctgggc	ttcagtctct	tcatctctaa	aatgaaggag	169724547
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actccatgcc	caatatattt	tttagtgac	atgagaaacc	taggaggtgg	169724697
agtgtcttaa	ttaacccac	ttacagatat	aaagagcgag	cttcagacgg	169724747
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atccccataa	ccgttaccca	taggtcacct	ttcacagtca	aacaacaaaa	169725097
catatgggga	gcaggcccga	cagccaagac	tacagggagg	ggagaaaaaa	169725147
ggaacacacca	cccagcaaga	tttccctgtt	tatttctagt	ctggccaatt	169725197
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gcaggaatca	ggtagggagg	tgtgattctg	gggcttgat	ctgagaagct	169725297
gggggttagcc	taattttctt	tctgtaatct	tttgattaac	tgtgggccag	169725347
tttggatgac	atttttcaaa	ccatctgtgc	ttggcaggct	gggcccagcc	169725397
caggcttact	gctcgggtgc	tgcaaaactc	agcttggagc	cggctatcac	169725447
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actaccaggt	ctgcgacatt	cgattatggc	agcccaagca	gactaatata	169726197
gccccataga	ccattctttg	catagcatcc	tttccctatat	ttttaactgt	169726247
gacaaacata	tataacatta	aatttactat	tttaaccatt	tttaagtga	169726297
cagttgtggc	tttaagtaca	ttcacatgtt	gtgcaaccat	caccaccaac	169726347
catctccaga	acatttttct	tctcgcaaaa	ctgaaactct	gcactgcacc	169726397
cactaaaccc	ttccccattt	ctgtctaccc	tcaggctctg	gcagccacca	169726447
ctgtactttc	tgtctctatt	aacttgactg	ttctaggttc	ctcatataag	169726497

FIG. 1.4

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tgagtcacga	acagtatttg	tgtctggcct	atttcactta	gtgtaatatc	169726547
tttttttttt	ttttttttga	gatagggtct	cactctgtca	tccaagctgg	169726597
agtgcagtgc	tgtcatcaca	gcgcactgca	gcttctacct	cctgggctca	169726647
agcaatcctc	ccacctcagc	ctccagagta	gctgagacta	caggcgtgcg	169726697
ccaccaccac	acccaactaa	ttttttaaaa	ttttttatag	agatgagggt	169726747
tctccatggt	gccccacctg	gtctcaaact	cctagggtca	agtgattggc	169726797
ccaccttggc	ctcccaaagt	gctgggattc	caggctgcca	tacctggccc	169726847
tcacttagtg	ttatgtcttt	aagggttcatt	cctgtaacag	cctgtgtcag	169726897
aattcccttc	ctttttaagt	ttgaacaata	ttccattgtc	tggatactac	169726947
attttgcttt	ttatccattg	atggaccatt	cccataat	taaaataaaa	169726997
aatgaatcat	atacgattat	aatccccctta	ctggaaactg	tctccagtgg	169727047
tttcttgaca	catttagaat	taaatgcaga	ctcctctcag	tggcctgtga	169727097
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cctcctcagt	tctggagctg	gcggggccatt	tggttcatct	ttgatttggt	169728047
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gtgaccttgg	gaagtccaag	ggagtcactc	cttcgagcct	agcctccttt	169728347
tctgtaaaaa	gtgtgcaata	atgccaatac	cacagggtta	ttaaagtaac	169728397
gcacttaaaa	gtgttttagtg	tagggcttgt	gtcaaattaa	ggattcaaca	169728447
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FIG. 1.5

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tctggccaag	ggagcttctg	agagcctgaa	ggtggccagt	atgtgactgg	169729147
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ggatggaggg	tagcctggcc	cctcctggaa	gtggtggcca	cccagcagat	169729347
ggctcttcat	tgccacacag	ccgatgactc	atagactaag	ccaagcaag	169729397
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agctccaggc	ctgcaggtga	ctccttggtc	ggactgtgaa	cttggttgaa	169729547
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gctacttggg	aggctgaggc	aggagaatcg	cttgaaccag	aatgtggagg	169729797
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caaaactccg	tctcaaaaaa	aaagaagaaa	gaaggaaaaga	aggaaaagaaa	169729897
aagaaagaaa	gaaagaaaaga	aagaaagaaa	gaaagaaaaga	aagaaagaaa	169729947
gaaagaaaaga	aagaaagaaa	ggaaagaaaag	aaagaaagga	aagaaaggaa	169729997
agaagaaaag	aaagaaagaa	tgtgcagcac	ccagcacaaag	acctggcata	169730047
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gtaaaaccaa	aggagacctc	tctctcctga	ttttactctt	tctctttaca	169730197
tgtcccagtc	tgcagccttg	ttctttccat	ctgtcactcc	ctttccactc	169730247
tcagaaccgt	tcttgaaatc	tgaacctttc	taacctctca	cccgcctttgc	169730297
tgcagcagcc	tgcagactgc	gtttcttccc	atcttctccc	tttctgactc	169730347
ctccacacca	ttccaaagag	atggcccatc	taacctcttg	accagaagc	169730397
cctacttcta	gaaatctatt	ctaagcaaat	catcacagct	gtgcatacgg	169730447
actttttatt	agagggtatt	attatggtat	tattgcatta	tttataacag	169730497
tgaaaaactg	gaggcaatct	aagtgtcaat	ggaaaaaatt	gtgtattaaa	169730547
taaatttttg	ttcatctgtc	tgatggaaca	atattaaact	gttgaaaaat	169730597
tatttttagga	actaattaat	aacctagaga	aatgctattg	atatcgtatc	169730647
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tgtgggaata	gatgtgtatg	gaaaagtaaa	atagagaaga	aatacactga	169730747
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tgtcaccagg	ctggagtgca	gtggcgcaat	ctcagctcac	tgcaacctct	169730897
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ttgcattgta	gttggatatt	ttcaaaaata	aaagctgggg	aaataaagga	169731647
gcagtgtagt	atagtattta	agggcataaa	ttctgcatga	aattacotta	169731697

FIG. 1.6

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tttcaagttc	cagtcceact	gcctattagt	tgggaagtag	taacattagg	169731747
caaggtactt	actttctaa	actcagattc	ttcatcagta	aaatggggat	169731797
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gtaaagtgt	acagcttttg	aaacttttct	tgcacgggtc	tttttctgoc	169732047
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gcactgaacc	ccaaatgaga	atctcaaagg	gttcaagctg	tactttaaag	169732197
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ctattcccat	gggcttcctt	gagataaggc	atcaccttga	taaattagct	169732297
gtagatatag	gcgtcttgca	gttggcatgg	gaaagcaatt	taatttccaa	169732347
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tggccaaaat	tgtaagtca	gggtacccct	agaaatgaag	caagagggga	169732647
gagagagagg	gaggtgaggc	agtcatacat	caggcccaca	agcaagagag	169732697
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agagagaaca	gacatttgtg	aagcatcttt	tatgcaccgt	gctgagtact	169732847
tcacattcat	gattgatgat	acaatgcacc	ctgtaaaaaca	aacactgtga	169732897
ggctcacttt	ccaattgagg	aaactgagat	tcaggaagat	tataataaact	169732947
gccc aaagtc	atgaacaagg	cagattcaaaa	ctcttgtttt	cctgagcttt	169732997
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gtagagatga	atgagaggcg	ggtgcatttg	ctgagaagga	gctgtgccgg	169733647
tgtaccagtc	tcccttctgt	tctgcttttg	catagtgacc	agttcaagga	169733697
tcgctgcaac	catgggtgtg	ctgggttcca	gttgggctg	tgatgagcta	169733747
tgggctggaa	agcatagatt	taggcagggt	ccagctggcc	tcgtggctct	169733797
gtctgtcttg	gcagtgccca	cagcagaacc	tttgtgggac	attttcagat	169733847
ccttctgctt	ggccatcacc	cccacatcta	ttgagacttc	agaggtgtgg	169733897
ccccagggag	tcaattgaga	gcctgggctc	tgtgatggaa	aggtatctgg	169733947
aagcatctaa	caagctctca	atagttgacc	ttgacctgct	tggcattttc	169733997
cactttttgat	atggggtaaa	gacaagaaca	ggattcccag	tggttagagt	169734047
gttttcttga	gcaataccac	ctagatttga	attccagctc	tgctatttgc	169734097
taacttctgc	cttggggcaa	gttaaatctt	ttccttgtgc	ctccattggc	169734147
tcattgggtga	aatggagata	ctaataataa	cctcaaagga	tggtgttact	169734197
gttcaatgag	ctgtgcctgg	aaagatcctg	gcattcaggt	aggtgttcaa	169734247
caaatagctag	cccttattac	cgtaggaat	gatagattct	tgcacagcaa	169734297

FIG. 1.7

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gtgatcagct	aaatatatgc	ccaaatgaaa	gtggctccat	cttgctatag	169734347
tgagttattc	atccaaagag	gtgttgctgc	aggttgctcat	tgaagagAAC	169734397
tattgtagaa	agagtgtgac	tgtgttctcc	ccgacaatac	ttctgacacc	169734447
acgtaagagg	gttttcttcc	cccctactga	taccaactag	tttgacacacc	169734497
aactgggtgt	cctacaattt	aattcaattc	tgacactaac	taccagaggt	169734547
tagctcagac	cccacagggt	aagaactcag	tcccacaaga	ctgcccccat	169734597
tcaaatgcca	gccaccaata	gggtgtcctg	actatccaca	cttccacctg	169734647
actgacagaa	cattcctaca	acctccccta	cacctccaga	taggatataa	169734697
taatttacta	gagtgatcca	cagaactcaa	aagaacattt	tacttactat	169734747
tgacacttac	tattacatgt	tgattacaga	ggatataact	cagaaacagg	169734797
cagacggaag	agacacacag	ggcaagggtat	gagggatgca	gggtggagggt	169734847
gcagagtttc	cgggccctct	cccagcacct	tgacgtgttc	accaaccag	169734897
aagcccccca	aaccctatta	tttaggggggt	tttatgaaga	tttactaca	169734947
taggcatgat	tgttaaacca	ctggccattg	gtgattaaac	tcaacctcca	169734997
gcccctcttc	cctctgcaga	ggttgccggg	tagagctgaa	ggttctaact	169735047
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cccctaaagg	acctctgtac	caaagaccaa	atatctttct	gtgagacaac	169735197
agagagttca	agcaccaaat	ataaagtgga	gaagcactag	atgatctcta	169735247
aagtcttact	ggcacttgga	gaacaagtgt	ttgtatttga	acatgcggaa	169735297
tcaaagggga	gttgagtaaa	aggggctcca	gaattgacac	aggaggagga	169735347
ctcagtgcag	caatctcatg	gggcgtgggg	acagaagaca	catcccaaag	169735397
cttcatgtgc	ctctcaagcc	cctgcttttg	ttttatgtgt	actggggata	169735447
ggggagggtg	gtatggaatg	atggagatta	tgggagaaca	gagtccatct	169735497
aagccacttt	tgactctgca	actgggggag	atgcagctgg	cctgggaagg	169735547
aatcacaAAC	gtgggtccagt	actcagttta	gagttgttgg	ctttgcttcc	169735597
atataacctcc	ctttctcatc	tcccaaatcc	tttgaggaag	ttggctggtg	169735647
aaaatgtact	tatgtaagtg	gggaggggaga	gttgtgcaaa	gctaggaaga	169735697
agctgagttc	tgcatcagag	gtgacatgag	aaagaaccag	gaaagcactg	169735747
tggagaggag	gatgacccat	caactgactc	atctggggga	caggatctgg	169735797
gagccagagg	tgatggagaa	aactaaagcc	ctcctcctgg	ccccagtggt	169735847
gaatctgatg	gagcctgggtg	gagagcctca	catttctaca	gggcacgggtg	169735897
tgggaggggc	ctggaggcct	tgtctctgga	tgactagggc	tggcagttct	169735947
gaagcttttc	atcatcagga	cccttttaca	tgcttaaaaa	atattaagga	169735997
tcctaagagc	tttgggtgat	atgggttata	tctattaaca	gttaccattt	169736047
tagagattag	aactaagaat	ggtaaaaata	tttaatttga	atttacttat	169736097
tttaaaaata	taatacatcc	attagttgct	aacaaaaata	acataatttt	169736147
ttgaaaaaca	attatgcgtg	gcaaaaagta	tattgggaga	agtgggtattg	169736197
ttttacattt	ttcacaatc	tctaattgtcc	agcttttagaa	aggcacctag	169736247
aatctcattg	ctacctcggc	attcagactg	ttttaacaat	gcatgttaca	169736297
tgacctctgg	aacattccat	tgcaactctca	taagagaatg	aaaatgaaaa	169736347
aggcaataaa	tgtcttagta	ttattatgaa	cagagttttg	actttgcaag	169736397
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tctctgatct	ttctttggtc	attttctttc	ccttccatgt	gacagggcaa	169736497
tggctgggtga	ggtacaggaa	ggtggcactt	tgctcaaaca	gtgtcttctt	169736547
aaatatattca	tagaattcaa	actcccccaa	acacaagacc	aattcaaaga	169736597
atactggata	ttctcacata	acagcctgtg	ctgccaatga	acaataaaat	169736647
aaatgcagtt	tgcaatgccc	tgacccaagg	agtttaagat	aaatttttga	169736697
tgagttggtg	atttagagga	ggagctggta	tcacttcagt	aagtcacaga	169736747
aaataagatt	atattaatat	ttatatgtga	ttatttttaa	tctgcataat	169736797
gctgagtcct	cactgtgaag	aaggaagccc	ctcacaatga	ttagtgaggg	169736847
gtagggaggg	agaatggcaa	gaagacacca	agttccttgc	aggcaagcaa	169736897

FIG. 1.8

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atagatacat	cataaaagt	aagtgaatt	ccagtcctct	gagatcttca	169736947
taaatagaag	aaaccctcat	ttctttcctc	ctctgggtgc	agcttggact	169736997
gatgagctga	agctctgtct	gagacctggc	actgttagga	tgtccccag	169737047
ggttctttcc	acccagttc	tggagctcag	gtggccccct	gcctctgaat	169737097
tccaccgctt	tgtctgagtt	ctggaggacg	gcacatggga	gaaccatcca	169737147
ggtgcacctc	tccaggatg	agtcactagt	ccatgagagg	acaataataa	169737197
atgatggaag	cactagacac	tcattagcag	agtggtttat	taagaactga	169737247
tgaagggttct	ctgctcccag	gcagatatta	ttgcaaaaaa	acacgtaggc	169737297
acagggtcta	actccatcat	gcctaaattc	ccattatttc	atgcttatcc	169737347
cgtgcataaa	gttctgtgag	cagcagacag	ttgtggcatt	tgctagaagg	169737397
ccagtcctta	ttgacaggag	gagaacatct	atctcaagca	aatgaaggtc	169737447
atcattaata	atttatggga	cagtgggggt	taggcacctc	cacatactaa	169737497
tttttctaga	ggaacatggc	cttttccctc	gcagggattg	tttgggtatt	169737547
ctgagtttct	gtgtatttta	gtcccaaatt	cagggtgcag	gaaaccattg	169737597
acaaaataga	ccctttaaat	cagactccaa	gttgggactt	cctttcttat	169737647
ttttcttctc	tttttaactt	aaatttttga	gataattgta	gattcacatg	169737697
aagctttacg	aaataataca	gagacattcc	gtgccccctc	tacctaatgt	169737747
cccgaatgg	aatattttaat	attttgcaaa	actatagtac	aatattacaa	169737797
ttagaacttt	cttaaaagac	tcacatgagg	acctttgaga	cttccctgac	169737847
cccagaagga	aaaaattcca	gggaatgatg	agctgcctgc	ctttggaagg	169737897
aagggtccacc	aggtaagaaa	ctggaggcca	cagggtatcc	tctgggctcc	169737947
ctggctggaa	ttggcagatg	ctgggtgcaga	tgccagggcc	tcccctcaga	169737997
actccaacct	gcatgagggc	acctgggttc	cagggtatgca	acgcagctcc	169738047
ctgcctggcc	cctgtggctt	tgagtggctg	tgtccctcag	cccttcacag	169738097
ctggctctgc	ccctcagccc	ttcacagctg	gctctgcccc	tcagcccttc	169738147
acagctggct	ctgtccctca	gcccttcaca	gctggctctg	ctgagttctg	169738197
tggttgagat	gccaggtact	ggaacacaca	gctccaggct	tgagtcctag	169738247
cccctcactt	tacagatggc	cttggccagt	tacctcttac	agcctcagtt	169738297
tttcatagta	acttagatag	cacttaccat	atgtcactat	cctaggaaat	169738347
ttacataaaa	atttgtttca	tgccaaaact	ctatggaaag	atactattat	169738397
cagtttctgt	ttgcaaacga	ggaaacaggc	acagaaagg	tattcgtcca	169738447
aagtcaccca	gcttgtgaac	agcacagctg	gaatttgaac	ccaaacagtg	169738497
cacatcccaa	gtccacatac	ttagccactg	tctctgtttg	cttctcatca	169738547
tctgtgaggc	agggttcagga	gtatctcatt	tttttttcca	aggcaaaacta	169738597
attagtagag	tgctgggcac	agaataaata	agcaccata	catgccagat	169738647
aacattgtca	gtataacttc	tggaagtttc	tgagtattca	tgacttattc	169738697
tttttttttt	tttttttttt	ttttttttga	gacagagtct	tgctctgtta	169738747
cccaggctgg	agtgccgtgg	cgogatctcg	gctcactgca	agctccgcct	169738797
cccgggttca	cgccattctt	ctgcctcagc	ctcctgagca	gctgggacta	169738847
caggcggcta	ccaccaogcc	cggctatgat	tttttctatt	tttttagtaga	169738897
gacagggttt	caccgtgtta	gccaggatgg	tctcgatctc	ctgacctcgt	169738947
gatctgcccc	cctcggcctc	ccaaagtgc	gggattacag	gtgtgagcca	169738997
ccacgcccgg	ccgacttttt	cttgttact	acaatagctc	tttttccctg	169739047
atcctctccc	tcctcctacc	tcccgcctc	caataggcct	cagtgtgtgt	169739097
tgttccccct	tttgtgtcca	tgtgttttca	tcatttagct	cccacttata	169739147
agtgagaata	tacagtattt	agttttgtgt	ccctgtgtta	gtttgctaag	169739197
gataatattt	ggcctccagc	tccatccatg	tccctgcaaa	ggacatgatc	169739247
tccttccctt	ttatggctgc	ataatattcc	atgacgtata	cgtaccacat	169739297
tttctttaat	aatgggtact	agacttaata	cctgggtgat	gaaataatct	169739347
gcacaacaaa	ctcccttgac	acaagtgtac	ctatgtaaca	aacctgaacg	169739397
tgtaccctgc	aacttaaaat	gaaagttaag	aaaaaacac	acacacaaaa	169739447
caaacaaaaa	aaactatagt	tgccatttta	aacacctatg	atgtgtcaaa	169739497

FIG. 1.9

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cattccttca	gccctcccaa	ctatccagaa	agagtccttc	ttttatagat	169739547
gaaaaaacta	agaatcaaag	agatgaaatc	gggcagagta	gagacaggat	169739597
tcaaacccaa	gatctgcato	ttggactcac	aacactggaa	gaaacttcag	169739647
acaccagcct	aacttcacac	ccagctcagg	actggccctg	ccgaatggtc	169739697
actcacctgc	tctgaaaato	ctcgcgacag	gacgctcaat	tcctacaccg	169739747
gtagttctct	ggctcgagggt	gtgccacaga	atccccctacg	cattgttaga	169739797
acacagaaca	ttgctacccc	caccccgtgc	agggcttctg	gcgtgggtggg	169739847
gctgggacag	gggcctgaga	gtgtgcattt	ctcacaagct	gccacaggat	169739897
cctgatgctg	ctggcccagg	gaccacactt	ggacagtcac	cgttcttaga	169739947
aaacttcctg	gagtgggaat	ggtaaagggt	atggcttctt	cccattttgc	169739997
cctttttcaa	tctgagatag	gcttccccag	caggctcagt	gccagagtcc	169740047
ataccctcaa	tttaataaac	aaatcctcct	ctatatcatg	acctttcctc	169740097
cagaggggtg	tttttcattt	tttgtttttt	gttttttttt	tgagacggag	169740147
tcttgttcta	tcaccaggct	ggagtgcagt	ggcacaatct	cggctcactg	169740197
caagctccga	accccggtt	cacgcatc	tcctgcctca	gcctcctgag	169740247
tagctgggac	cacagggtgc	caccaccacg	cctggctaata	tttttgatt	169740297
tttagtagag	acgggggttc	accatgttag	ccaggatggg	cttgatctcc	169740347
tgacctcgtg	atccaccagc	ctcgccctcc	caaagtgcgt	ggattacagg	169740397
agtgagccac	cgcgcccgcc	ccagaggggt	ttttaagatt	gtgtgttctg	169740447
aatggcctgt	ctctgactgg	aacccaactc	cgtccccaga	cccacttcca	169740497
tctttttctg	tgagggggac	acactctttc	aactttttcca	aaatggcatc	169740547
taccatggct	tttctgatta	aaagcaaacg	aaacacaccc	ttcctataat	169740597
caaaaattta	gaaaagcagc	aaaaataaaa	aggggataag	gaagaaaaca	169740647
gaaattaacc	accatcccac	cgctaaaatt	ttgatgagtt	ctcatgtgtt	169740697
tccttgacgc	tgattgttgt	ttggcataca	tttattaata	ttggaattaa	169740747
aaatatatat	ggcactttat	atcctagaaa	atagtaatac	tgtaaatgtg	169740797
ttctagaaat	gggagctgct	gttgctctta	ttagagaatt	caaacaaaga	169740847
agggaggctc	gctggggaca	gcttctgggg	gaggatgggt	accgctttga	169740897
gacaacaggg	agaactcagg	cacagaggtg	acgatcatcg	ttctctgtgg	169740947
ggcacatagt	gatgcagccg	gaaacaggta	tgagtcaagt	gagtggggac	169740997
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ggagccactg	tacattcttg	agcaggcaat	gacttcacaa	aaggatttct	169741097
caaagggttag	tcctgcaaca	gaagacagcg	tggattggac	tgggaagagtg	169741147
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ggcccagcca	gtcccctgtg	ccctgacaag	tggatatggca	tggatggatg	169741247
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tggcgataat	gaggaggcca	ccggtcagca	ggaagggtggg	ccagaagagg	169741347
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gctgtgtatt	tgaaatcgag	atcatgtgct	caattgccta	cagggctcat	169741997
gaagggtattg	tcagaggggtg	aagcaggcaa	agcaatgaga	tgacagggtgc	169742047
ccactgactc	ttgccttggt	gccaggaaga	attgccaggg	tgtggcaggg	169742097

FIG. 1.10

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cctgtcaata	gggagagagc	cagctgcctc	cagacaggca	gtcaccactc	169742147
cctccaggca	atggatgtca	ggccatccag	aagatctata	atagccagac	169742197
ctccaacact	ttaagagaag	ttagaaacca	gatcacacct	gtaatcctaa	169742247
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caaaaaaaaa	aaaaaagtaa	aattattagct	aaatttataa	ttgaaaacct	169742547
ttgcagtttc	aacctgtgta	cagcaaacaa	actatgttgg	caagcgggta	169742597
tttgacactg	ggatccaaag	gaaagaaaga	atgcattgaa	aagagttttg	169742647
tgccagcaga	gcattgacaca	catttaattc	tgacgttgat	tattgttatt	169742697
aggaactttc	tgccctgttc	agatgaggcc	agctggaaag	tgatgcaaag	169742747
cagtcataaa	gcggagtttt	atctggtttt	atctctgttc	tgagctgcaa	169742797
gtgtgggtgcc	cccattctgca	gcagaatacc	tacagggccc	ccatagccca	169742847
ggctccctacc	cactctgcat	cactgagggc	gagaccaggg	aatgtgtgat	169742897
tccttcctagc	acttaatttt	gccctagtga	aatcatgtgc	aagatcaaaa	169742947
tgtgtaaaac	tgagacccaa	atggcagggtg	ttgagccaga	ttccttgacg	169742997
gcctcggcca	ctccctggat	ttatatgagg	tgccaccctg	gaagctgcct	169743047
gccctgaggg	cattcactcc	agcaacacag	aggagggttg	cactgtagtt	169743097
ctcacagcct	gggaaatgca	gatgctgcac	tcagatctag	ggccccagcc	169743147
agccagggag	tagctgaggg	tggggagacg	ctggctcctc	aggaatctgg	169743197
cattcagagc	tggttgacac	tgccagggtcc	tcagtagcat	ataatccagc	169743247
atcctgagct	gacgggtgagg	gggcctggcc	tgagtctctc	caatgcctct	169743297
gactgtgacc	ttggctaacc	tagctcctta	aatagcagtg	tggttatgga	169743347
gtcagacagg	cctgagttct	gagctgtgtg	accttgggca	ctgccacaac	169743397
ctcactgggc	cttgtaaaat	gggtttgtga	ggctacctgc	ctaggagaac	169743447
tgtcatgggg	attaaatgag	atgatgcatg	taaagcactg	agcacagaag	169743497
cccagcacac	gataagaact	caaaaaagtg	gaagatgcta	ttattaataa	169743547
taatattgtt	tgacttatct	atgaaattgc	aacaacagct	ccttctttac	169743597
cttcttaaaa	agaggtctat	ggatgagctc	tgaagtagag	gcttctgtcc	169743647
atcctggggc	tagtgtatcc	tctgcctgct	cagggttcct	ctggatcttt	169743697
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gaactcacct	gctccaggct	aagactcaca	ggaaaagctg	agggcagact	169743947
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ttcacagtga	ttccagagga	caccagcta	gcctggagcc	ccagccactt	169744047
gaacccctat	gatggacata	ggcggaagga	gcagctagcc	cacaacccag	169744097
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gcagcctgct	atcagcacca	cacctgggtc	agcctggggc	gcaggggaga	169744197
ggacagcagt	ggctccagca	tgctcctcct	tcacatcctg	ctgacagttc	169744247
attcagggga	tgctcctctg	agctggcaat	ctcaggacca	gggaggcagc	169744297
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ctcaagatcc	ccagcctcc	acgccccatc	ccaggcaccc	tgcccccttc	169744597
cgtcccatca	gccatcaagt	ccggactgtc	agcatctccc	ctgctgcagg	169744647
ccacatcttg	gtcgtgagtg	cttgctgcgg	ccttggtctcc	tctgtctagt	169744697

FIG. 1.11

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aactggaccc	acacacctgt	aggctccatc	ttcccagccc	aactctgaaa	169744747
ctctgatcat	gccctaaaga	ttcccattgc	caacagcaat	aatttccaac	169744797
cttagaatca	ccttggggagc	tccatgaatg	gatctctgac	cagagattcc	169744847
accttgatat	gtctagtgtt	ggaccctagt	tttgtttttt	aagactctta	169744897
caggggttcta	atgcatagcc	aaagttgaca	tatcttgaga	catacacact	169744947
cacatttttaa	ttccatattg	tggtgatcaa	aggcctctgg	gaacagacct	169744997
tagtctgccc	tgacagcctt	ttccagctgc	atacacccca	tcatgggtca	169745047
ttttctgtag	tcagccctct	gatccctgtc	tccacctagc	ccttccctcc	169745097
gccatgcctc	gtcctatagg	catacccgct	tctatatca	cctcattctc	169745147
tatgccttgc	atcctgcgcc	tgccctgatgt	taaaagccta	atccaagagc	169745197
ctttcttttt	tttttttttt	tttttgagat	ggagtttcac	tcttggtgcc	169745247
aggctggagt	gcaatggtgc	aatctcacca	agagcctttc	tgataccccc	169745297
atcattgtca	gctggaaaac	atccccctcc	tctaaccctc	gtaacttcc	169745347
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ggctggtgaa	taaataaatg	agaggaggaa	agaaggaaac	aaggaaggaa	169745497
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aaaaaagaaa	agaaagaagg	agggaaagaaa	gggaaaaaag	aaggaaagaa	169745597
agaaggaagg	aagagagaca	gaatatgggc	caactgatcg	ctttaggaaa	169745647
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gccttgagtc	cctgggtttcc	tggggagtc	ccgggattcc	actttgagga	169745797
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caagcgtggc	actttatata	cagcgtctct	gacttgataa	cagctcttca	169745947
aggtgcagca	ttagcattcc	actttacaa	ggtggaaact	gaggaggtga	169745997
gaggctaagt	ggcctgccta	tgtttacaca	gccagttagc	ggcagattca	169746047
aaccacaggtc	tgtgtgactc	caacacagaa	gagctagggc	tggctcagtc	169746097
tcattccagc	tgtgagacct	ggtcaagtgg	ggtgatcttt	ctcagccteg	169746147
gggacagggga	cagttaggaa	caggctcaca	cacctgacag	ggataaaggg	169746197
atgtgtcccc	atccctccag	ttcagtaoct	gctgggtctg	gtcccagagt	169746247
tcctccgtgt	ggtacagcac	agcccacctg	ccggcagctg	acacgttgac	169746297
ccacaggcat	gggtactggg	gcaccttctt	gcccttcagc	tcctcctggt	169746347
ccctgatggt	ggtctcaatc	aggtggcact	tggattcctg	ggtccacacg	169746397
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cacagaacac	ccatttgaac	ccattatccc	ctgggagcct	ctagagggat	169746497
ccaggactgg	gatccctcatc	ttgtcttcag	catccagcaa	taaaggcaca	169746547
tgaccccaca	gtccccggac	acagggagga	attgtagaag	ctggatgggg	169746597
tcttagacat	tatctatatg	actggttctc	aaccttggct	actcttgcaa	169746647
caacctgggg	agcttctaaa	aagattcccg	tgtccaagct	acaccccaga	169746697
gcaagtgaat	cagaacttct	tgggtggttt	ggcccaggcc	ctgggtgttt	169746747
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cttatccata	tcgtcttcat	tttgacagag	cagaagagaa	actcagaaag	169746847
gtcaagtgac	tttgctgaga	ccttgacagga	cctgaagcta	ggtctgagtg	169746897
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cttcaccaga	ttaagagtcc	agccttgaat	cgcttcagcg	ttgtgaagag	169747047
tgaggctgca	gcaggcccg	gagaggctaa	caggttcatc	aacatattag	169747097
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agtcagaagg	gggctgtcag	ctgctggaac	gtgccagag	cacaggtctg	169747197
agacttatcc	taaggacagg	ctgggggaa	tgagtgtctt	tgttccaaat	169747247
agaacacgaa	ttaggaattc	acagcttttc	cttaaaatct	caagtgggtg	169747297

FIG. 1.12

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atatgtcatg	gagcaagggc	atggaccatt	ctctgagatt	cctgagcaga	169747347
acttcagggg	agcagatgct	ggctcaatgc	agacacatca	gaaaacctca	169747397
aacatgaaat	gtatgttcag	tgaggcaagg	agctccccgt	ctcttgaggt	169747447
attcatcagg	aggctggatg	cccacctgac	agggaggcct	cagaggggag	169747497
agaattatgc	agctgagctg	taaacatctg	caattctctg	attcctcctg	169747547
ggatcaaact	tgcactggaa	cctttgctct	gattcctttg	tatttcttct	169747597
gagaagggca	tcatgtgtct	gttaccacca	cgtcctagat	catgtgtctg	169747647
ttaccaccag	gtcctagaat	ctcagaccag	tggggctcag	ttcatcctac	169747697
cttccttgca	cttgaaccct	agaacctaa	aatgagcatc	gtcttgacct	169747747
tgctgccttg	aatgagggct	aaggagaggg	gtgagtagaa	ggccaggggt	169747797
ccttacagat	gccagaccct	taggagaggg	ttgggggggtg	ggcaggcccg	169747847
gagagctcag	taccttttct	ggtagagggg	cagcacagtc	gtgaccagga	169747897
tgtagtaggt	gatgacggca	cacaccacca	tggttacacc	caggcaaagg	169747947
gctcgtgtct	gtccccgctt	ctggggccatc	accagcttct	tcaccatatt	169747997
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atcagcccag	ttcacagggtg	atccacagaa	agagaggaca	ggtgagaggg	169748097
gaaggtactc	aactattaat	atcactcttg	tttatatttg	gagctttgca	169748147
acttccagaa	gtcttgcttt	ttggacccca	tgtaagcctt	ccctgtgcaa	169748197
ttgagaggca	attgcagata	aaagacctac	ggctcagaga	ggtaaagtga	169748247
cttgccctag	gtcacacagt	atgtaatagg	ctcagtaatg	gccccccaag	169748297
atgtctatgt	tctagtctct	ggaagctatc	aatgttactt	tatgtggcaa	169748347
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ggctcatgcc	tgaaatccca	gcactttcgg	agaccgaggt	gggcgggatca	169748447
tgagggtcagg	agatcaagac	catcctggct	aacatggtga	aaccccatct	169748497
ctactaaaaa	aaaaaaatac	aaaaaattag	ccgggtgtgg	tcgtgggagc	169748547
cagtagtccc	agctacaggg	gaggctgagg	caggagaatg	gcatgaacct	169748597
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ggcaacaaag	caagactccg	tcaaaaaaaaa	aaacaaaaaa	caaaaaaaga	169748697
taaaggctct	tgaaatgggg	agacaatatt	ggattatcca	tgtagctcct	169748747
aaatgtaatc	ccaagggtcc	taataagagg	gaagtgaagg	gagattaaac	169748797
agatgagaaa	gctaagggtga	tatgaccagg	gagacagcaa	ttagagtgat	169748847
gtgaccacag	gccaaaggagt	gcgtcagaag	ctggcggggg	caaggaaaca	169748897
tggctcatcc	cccacggcca	ctgcagggag	tgcagcctgc	agacaccttg	169748947
gtgattttgg	acttctgggtg	aaatttctgt	cgtttgaggc	cgtcagggtt	169748997
atgatcattt	gctacaacag	tcataggtcc	catgcgggtga	gcgagcagta	169749047
catgtgcata	atccatgcac	ctccttccac	ggcacttatc	tcacagggat	169749097
acttgaggta	tttctgcccc	gaaacagttc	tgtggcaggg	ctagctgggc	169749147
cgggcacagg	caggggaaagg	agaggagggc	cccagaaggc	agctgcagggt	169749197
tgtcaggaga	ggcaggagggt	ttaccatatt	ccgggtgttt	ttttttttgt	169749247
aaggaaacatt	cccctacttc	aagcaaagaa	agaagaaaga	aggcatcatg	169749297
gtggcctcag	cgactgcttt	cttattttcag	ggcttgaagc	cacctgggac	169749347
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tcttttaggca	gcaactcctt	gtttttcccc	tggacattga	ctccacccca	169749447
atgcaagcaa	agattccacc	ctccccctgt	aggctcctga	tcgctcccc	169749497
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ccgcctggag	ccacagagat	gcccagccat	ggcccccgcg	tgatttccca	169749597
tggttccgca	agctgtccta	gagcctctgg	taaatttatt	tgctgttggt	169749647
tttatttgtt	ttaaagtaacc	agagtccatt	tctacaaaaa	ataccaggaa	169749697
gctatccaatg	taatcctcca	ttttagggga	aatttttaggg	gaatttaggg	169749747
gaaatttttag	ccagatatca	gggggacttt	attctccttg	ccaggctccct	169749797
aaagtaataa	acatattatg	gtttttgttt	gtttaattag	ccagtgtccg	169749847
ggtgacaggg	cttagtccaa	agagattttc	tgcaaagtgc	tctattttct	169749897

FIG. 1.13

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gctcaggcgt	ctcttaacta	ctagactggt	tcaaattatc	agagattcct	169749947
gactccctcc	ccttagccag	gctgccctca	tacccgggca	tctccgctaa	169749997
aggggaagaga	ccagggtcag	gcaccacgga	tacccatcac	accttcccag	169750047
tgagctggtc	cacctcccct	atcgatcggc	agagggtgaca	tccaatgaca	169750097
actttttctc	ctttatttgg	caccaggagg	tgagtttctc	ctgcattcta	169750147
atggagacat	tataaaagca	caagcaagca	gaaattgccc	ccgacaaaaga	169750197
gagatgtttt	attcaactct	ttttattcaa	tccttttccct	cctgttctgt	169750247
gatcttgtgg	gaatgggaga	gcccattgct	ttttctacct	ggcgtcagtt	169750297
gaacaagact	ctccatgtat	tcacaggtaa	agcaacagaa	tcacctggag	169750347
gtaagctaaa	agccccaaca	gcctgcttcc	ccaggacctg	caagggtcac	169750397
tggcacttgg	ccccaccca	gatactgtga	gacataaatc	at ttgagcc	169750447
aatgggaaat	cccatcttgg	aagcctaggg	ctgagtggcc	acaacaaagc	169750497
cattttctctc	ctgggggaac	tggatcgcac	ctgtgggggc	ttcctgtggc	169750547
tccttcttgg	ctaatacgcc	ccccccagcg	cccaggggcca	tggcctcctc	169750597
tgctatttgg	cttctagtgc	cctctcaggg	ccctggggcac	tcctgaggct	169750647
ggtgaaggca	ggaacctggt	tttaccagtt	ttaggagctc	agaaggaaag	169750697
gaaaggagag	gcttccttgt	cacagagaag	tctggaaact	tggcttattc	169750747
aggtctgacc	cgtctctaata	ggtctgatga	gattgttgcc	tgcactgagt	169750797
gagtttatag	agtcattgata	aatcctccta	agaccatgcg	tgggggttcag	169750847
tgtagatatg	acttcagcaa	gaagttagta	ttcagcatcc	aaaggagaga	169750897
cctttggcgg	gaggaaggat	gggaactgtc	aatatcccc	aagggaacaga	169750947
aagaaaagga	agaagtgggt	ttcagctatc	ataggaggga	tttcagttag	169750997
actgtaagaa	gaacttccca	gttttgagca	tttctaaata	tctctgaagt	169751047
tccaggatat	atcttcccat	ttagaaaggt	cacttgagat	ctgggataga	169751097
ttcagagaag	atggagaagg	acaaaggaag	gcaggacttt	ggagtgtcct	169751147
gggtgacctg	atagctgggt	cgacatcctt	ttccttagaa	ggacaaggaa	169751197
tagagtacat	tggtgaacag	tttggtgggg	tgtggacagg	gcgattctga	169751247
ggtcctcaga	catggaatca	aatcctggct	ctgccactta	cacttagcaa	169751297
ccacatgact	gtgaaacgag	aacctaggta	cctgcctcag	agagttcagc	169751347
taaagatcaa	atgccatatt	gagtatcaga	catgtatcat	agcacctagc	169751397
cccaaatacag	ccccagtaa	atattagcta	ttactactaa	cgaaggaaac	169751447
cctgaaagtt	tggagcagaa	gtctggaccc	ctcttgatga	atctattttt	169751497
gtcccacctc	tctaccgggtg	acaagtgcc	gcattgggtgt	taatctccag	169751547
gctgcagcct	tctggccact	ctgagaactg	ggacctagag	ggccagggcg	169751597
cttactacca	gagtaacctg	gccactgtgc	cacctcccc	actggccacc	169751647
agaccacggg	ccctccatcc	agaaggacag	ccccgagagg	aagggaagtc	169751697
tcctgcctgc	ctccctccct	gccccgtggc	aggctgcttt	cccctgtctc	169751747
cctccagccc	ggtcttcaga	gaaatcactt	cccaagtgt	ttcaggcccc	169751797
gtactcacag	tcttcccggc	gtcctgtggg	tcttgagcag	cagacagttt	169751847
ctttctgctt	ggacccccgc	ccccaccca	aaagaggcca	cagagcttca	169751897
gcaggaagtt	tggcctcccc	gcccgtctcc	agggaagcag	cttttggtcc	169751947
ccatctgggg	caagcctcca	tgcccaaaca	tgggtcaagtc	tgagcacaca	169751997
gcctggagac	acagactcgg	agagcaggta	cccagccctg	aggaaggcag	169752047
ctgttaccca	agcctgcac	ctccatcttc	ccagagtctc	gtgggaaaca	169752097
gatttcaaac	aacaacagac	agcaagactg	agaaactacg	aaagatcagc	169752147
ctggatatatt	tggaaatatt	tcttcttctc	tctgtctctg	tgggctggca	169752197
aagatgccag	aaataggaaa	tgattctcct	tttggtggca	tgaggaaggg	169752247
tggagttggg	ctggagggggt	tgggcttgtc	actagtccct	ggcatatcca	169752297
cgtggagca	gtacagctc	cctgcctttg	gcacttaacgt	gctgtgtgac	169752347
cctgagcaag	ttatggcacc	tctctggggc	tcagtttccct	tttttggttt	169752397
tggttttact	cccaaactta	tcgttaaatg	acctcagttt	tctcacttgt	169752447
gttactggca	tttttaaaac	ctactttgct	ttagggtagt	gatgggagtt	169752497

FIG. 1.14

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agagacgggtg	gggattttatg	gcaagggggag	agaactgact	ttttaaggac	169752547
caactgagct	gaagctggga	gtagttagag	ctccacaact	gcttccaacc	169752597
aggctcagg	acagtctgct	caccaggggc	cctcccagag	accgcgaaag	169752647
tacagagatt	tcttcctagc	aataagacaa	gtgaatgtca	gcattttgcag	169752697
gcaaaaaaaca	tgctttttaga	tctctgcttc	ttcatctgta	aagtggaaagt	169752747
aaggattaaa	aatcagcaac	aaagggcgagg	cacagtggcc	cacgcccata	169752797
atcccagcac	tttgggatgc	caaggtagat	ggattgctca	agcccaggag	169752847
tttgagacca	tcctgggcaa	catggcgaaa	ccccatctct	actaaaaata	169752897
caaaaattag	tcgggcatag	tggtgcatgc	ctgtggtccc	agctacttgg	169752947
gaggctgagg	caggagaatc	gcttgaacct	gggaggcgga	ggttgcagtg	169752997
agtcaagatt	gtgccactgc	actctagcct	gaacagagcg	agaccccgtc	169753047
tcaaaaaaaaa	aaaacaaata	tatatatata	tatatatatt	ttcaacaaaa	169753097
caacaaaaaac	aatcccagat	attggggctt	tcctaagtat	caggcgtggt	169753147
ggtagaaggc	agcttatctc	cacccttcac	ttgacccaag	aatcaaagaa	169753197
cctgaaactg	agacttggag	gcttgaagtc	actggtgcaa	ccctaggggc	169753247
cagaactaga	ttcgaagctg	gcccttcag	atggcacagc	ttggtctgtc	169753297
tctgatgacc	ctggggctgc	tctgagacat	taaaaatcac	ctcgatcata	169753347
cagtaagctg	ccacctgagg	ctctggaggt	cacctgagt	ttccccagcc	169753397
cccaggggagg	tgggtgcagc	ctggccttcc	ctgctgagcg	agctcaccac	169753447
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cctccctgac	acactctcag	gcggtgagtg	cccttctcca	cccctttcct	169753547
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caggctgcc	tttatgagta	taaccgaagg	gctccttgct	cgtgatactc	169753847
tgaataagtt	attaagggtc	acataattatt	tggaaatcat	aaacaaactt	169753897
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ctgcaacaat	aaatattgac	ggtttgcatt	agtacggggg	gtcagagatc	169754147
acaaaatata	ttctctgact	cttccaacag	cttcttaagg	tactagcaca	169754197
ataggctcac	aatagaccac	tgagggtggag	atttttctac	ccatttgata	169754247
gagggagtaa	ctgagcctca	gagaggtgaa	ataaattgcc	caagcaagtt	169754297
actttgcctc	tctaagcttc	agtttgtctg	tctctaaaat	agagataatt	169754347
atacctagcc	cctcagtgtt	tttgaggaat	gagagatcac	ctaagctacc	169754397
tgacacatag	tatggagatt	gtcctttcca	aagatgggtca	caccaaatac	169754447
ttcccattcc	atgtgccctt	ttcacagtgt	ggcatcaaca	ctccaccatc	169754497
aagaggggca	ttgatgtctc	ttcccccttca	ccctgggtgg	agcttcgtaa	169754547
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ctgacagcct	cagctcagat	ctcagccaac	agctagcaaa	tctcacgggg	169754747
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aatgtttcat	gcccctgcgt	tttggggtaa	tttggttatgc	agtcatagta	169754947
actggaacac	acttgcaagt	gatttcaaag	ggggactggt	acagttgctg	169754997
gtgatagtgg	taggattaaa	ccagtgagaa	ttaaaacacc	tgagattgct	169755047
atatggagtg	ttacaggaga	gtttagaaat	gctttatcta	ggtagggcat	169755097

FIG. 1.15

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ggtggctcat	gcctgtaatc	ctagcacttt	tcgagaccaa	ggcaggcggt	169755147
tcatttgagg	ccagtagttc	gagaccagcc	tggccaacat	ggcgaaaccc	169755197
cgtttctact	aaaaatacaa	aaattagctg	ggcacgatgg	caggtgccta	169755247
taatcccagc	tattctggga	agccgaggca	tgaaaatcac	ttgaatccag	169755297
gaggcgagg	tcgcagtgag	ctgagattga	gccactgtac	tccagcctgg	169755347
gcgacagagt	gagactccat	ctaaacccaa	acaaacaaac	aaaaaaagt	169755397
ctttatctac	tcttaggtca	cacactatgg	cacaaatgga	atagaagggc	169755447
agtgatattg	gagggtattt	ttgtttatga	agcacctact	atgtaccagg	169755497
gaatgaccac	atagatatgc	aatacatata	catacacata	cacatggaca	169755547
ttcctctoca	caatccccca	caaaaggcct	tgttctttct	gtaaaagcac	169755597
aaggcaaagt	gattttccca	aggctacgcc	cctagcgtgt	gatgtgatgg	169755647
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ctgtcacccc	atgactccct	tgggagcagt	tttcaagaga	ccccagggtt	169755747
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gcatgtgccc	tctccttcca	tggcacatgt	ctcctctgtc	cttgccctct	169756697
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ttgggcacca	agggtgtttc	cacacctttg	ctattgtgaa	tagtgccgca	169757597
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FIG. 1.16

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ttagttatttt	aagaaatctc	caaagtgcct	tccacagggg	ctaaattaat	169757747
ttatattttcc	accaacagtg	taaaagcatt	cccttttctc	tgcagccttg	169757797
ccagcatctg	ttattttttt	acttttttagt	aatagctatt	ctgactggta	169757847
cgaggtgaca	tctcattgtg	gtttaatttg	catttctctg	atgattagtg	169757897
atgctgagca	tttcaaaaac	atttttctag	aaaggctata	cagttttcta	169757947
ggttatggct	aagtogggat	agatttcac	aaagccatgt	tgtcagatat	169757997
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gactgtatct	ataagcacia	agtttgggga	ccagaacagg	tggatagaga	169758197
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gcaattgggt	gaaataatta	agttttgcct	aaagagttga	agtcaacaga	169759247
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FIG. 1.17

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cagccctcag	gagaccttga	gaatatgtgc	ccaaggtggt	cagggcacat	169760347
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aattgactca	cagttctgca	tggctagggg	ggcctcagga	aacttacaat	169762847
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FIG. 1.18

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tcatgagaac	tcccttacta	tcatgagaac	agcatggggg	agacttcccc	169762997
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taataagatt	gctcctgcaa	agctcaaggt	ctacatttac	actcagagtg	169763897
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gcaacagaaa	tgtatttccct	cacagctctg	gagggcagaa	gttcaaaatc	169764497
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cagctggcca	cggctgccac	agtgtcattc	atttacttat	tcttcattca	169765397
tgtaattcat	tatttcactc	atttttcaga	agagaacttt	gaggctcagg	169765447
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FIG. 1.19

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ttattttatta	aggggtgctg	aattaggtgc	cctcgttca	cgtacgcctg	169765547
ttccatcttt	ggattttaacc	cactatatga	tttatctata	tgcggtgccag	169765597
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actttcttct	gaattttgtt	aaagtccctt	tgtgtgctag	actgtacatc	169765997
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gattcctcct	actacgccgg	ctttgggtga	ggagctcttt	gaacacagtg	169766397
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agaggaaaat	taagcttcag	gttttagttt	ttaaaatgtg	catttattta	169766747
tcagtgtaaa	tagcttaagc	acagtcttaa	aaattggaaa	ctaataaaaa	169766797
atcatctata	attctaccat	ttaataaatg	tactatgtgc	atttataaat	169766847
ttttttccaa	gatttttttt	tccttttgta	aatgggtttt	ctgtacatag	169766897
ttatcatcat	aggctgttgt	attgggtatc	cattgctgtg	taacaagcag	169766947
cctcaaaatg	tagtggcacc	agatgctcag	gattctgctg	agtgggtcct	169766997
ctgggctggg	ctaggctgat	ctcagctagg	atcactcatg	tacttgcagt	169767047
cagtcgggtcc	caggggcctc	ccttgtgtca	gggtgggtgcc	tggctatcat	169767097
gggtgacagg	ctagtgacta	tgccatgtgt	ttctcagcag	gctagacgag	169767147
cctgtttctca	tgggtgacaag	atgcagaagc	agtagggaaa	gcagaagctg	169767197
caagtcctct	agaggtccaa	gcttgaaact	cacactgtca	cttacaagca	169767247
tttgattggg	ccaagcagat	catgaggcta	gcccagactc	agtggggtaa	169767297
agaaagttta	tttcttgatg	gaggaactac	aaaatattgt	ggccattttt	169767347
gcaatctatc	aggactgcgt	gaagtttttt	acctttccat	ttttaattta	169767397
ttatcgcatc	atgatttttt	ccttactaat	acaaaggatt	catgacatta	169767447
tttgatagat	agacagacta	cagttttact	aagcatctcc	caattattaa	169767497
acataaagat	gacttccggg	tctccagcac	ataaataaag	ctgcatggaa	169767547
catcttgatg	cagacaggta	tttctgtaat	tttgattggt	tccttgggat	169767597
agactcccag	aagtggattc	aaccaggcat	aaatggtttt	tgatattctg	169767647
ataaatgaaa	gaaatatgga	ttaaataata	catatgccaa	attgccctgc	169767697
aaaattatgc	tgttttacct	ccagccacag	agagaaaagg	gattttcttt	169767747
tctttttttt	ttgagatgaa	gtcttgctct	gttgcccagg	gtggagtgca	169767797
gtgggtgcaat	ctcggcatac	tgtaacctcc	gcctccagg	atcaagcgat	169767847
tctcctacct	cagcctccca	agtagctggg	actgcaggca	ccaccaccat	169767897
gcccagttaa	ttattagtat	attttaattt	tttagtagag	acagggtttc	169767947
gccagggttag	ccaggctggg	cttgaattct	tgacctcagg	tgatctgctc	169767997
accttggcct	cccaaagtgc	tgggattatc	agcctgagcc	gttgtgocca	169768047
gctgagaaga	gggattctca	gcagcagcct	ggactcaggc	atccttgca	169768097

FIG. 1.20

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ggcctcctgg	cttctcttga	ttcattttgt	tttcoctggg	cctcatgcca	169768147
ggaagctgga	atgaagcaca	actgggcaga	cccttccttg	ggcaaaagta	169768197
ttagtgctctg	tggtcattgt	tctctgacag	tcagttctgt	ggtacataac	169768247
gattggttca	ggccctgtg	atcttcttgt	ccatgtgaga	ctggatgagg	169768297
agtctcctgg	accagtgatg	gtaacacctg	cacctgagc	tggggagcag	169768347
gtggtatcac	agacgagctc	ccatcccagg	ctggctctca	cagtcccttt	169768397
ccacagctgt	gttaccagcc	cctgctcaat	catgtttcca	tgtgattctc	169768447
atggaaacct	tgtgtgattg	gcaacaccaa	gatttgtccc	acatccagat	169768497
agagactagg	ggctagaata	cctctccctt	gcccgtttct	ccgggcttga	169768547
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ttttacttcc	tcagttcctt	gtttgtctaa	aacaccagct	aactgataat	169768647
tgcatttata	gttactatgt	tttctccta	gataacaagc	ttcattgaag	169768697
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ggatccgtgg	gtctggaagt	taaaagagga	ctggcccttt	gagcaaataa	169768847
atgaagagta	agctggagag	cttgtgtgta	tagcatttga	gggcaagggc	169768897
tctggagtto	aacacactca	gcctcaaato	acctacccat	tattgggtcgt	169768947
gtaaatgtgg	ccaagttact	tgactgctct	gtgccttgg	ttttccatct	169768997
ctaaaatgga	cataataacc	catacagggt	tattataagg	attttgacaa	169769047
gaaatggcag	gtagcaataa	ttacacctac	tgaattttaa	aagtggctca	169769097
ggcacaagag	gtgagtggcc	tgttcaaggc	agcatggcct	ggaagacctt	169769147
cagcaggggc	cagtaagctt	actagccctc	ataccagga	aagcggttta	169769197
tttctcctcc	cacatcagca	tccctctctt	cttcctatgt	cggccccaga	169769247
aggttcacac	cctctccctc	ttaggctcct	tcctcattcc	gaggcctgga	169769297
gggtccttgc	acagagagga	atctgcttcc	tgcttagagc	ttggagaacc	169769347
ccaggccttc	cgcattcatg	agggtccaagg	ccaggcagga	ggcaaggcca	169769397
tgggccc aaa	tctgtgccat	gagtgtcaac	agaagatccc	aaagctggag	169769447
accccaaata	aaaaccccaa	gagatgtggg	ggcatcagct	tcctcagact	169769497
caaccagca	ccattcagca	gccttcaaga	ccaagaagtc	catactgttc	169769547
tcttgctcgc	aagatactca	gcctatgaaa	tcctcagcta	atggagtcc	169769597
cagagcagca	tggagccttg	ggggtgattt	tgagggaactg	acactgggaa	169769647
acagcctagg	gtctgtgggtg	cgcagtgggtg	gcagcagccc	ttgcctgtcc	169769697
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ttccacacac	taagggtgggt	gcagctgctg	ggaatgggag	aaacatttat	169769897
agatctaagg	atgggcagga	atttagaaag	gtaagggtac	tgtctgcctt	169769947
ggctgatact	tttatttcc	tctatccata	agtgtacaaa	aaaaattttt	169769997
ttaaatgcta	tgtaaagata	gggaggtttg	aaatttttac	caacaatccc	169770047
aatccttgaa	cacaaagact	attatcatat	ttgtgactgt	tgaatatattt	169770097
ttaaagacat	gttaatacta	cagggaactg	catttctata	gaatgcactt	169770147
tggaaagcat	tgccctacag	tatttataaa	tttcagaaca	catttttagga	169770197
tctgccttgt	gttggtttctg	tcatcatttt	acatttgcta	gtcttgactt	169770247
ccaaccaccc	aacacgcttc	ctgagggcag	ggcaaaacttg	gacattattg	169770297
acagaacaag	tgcccaatct	gaaaatgtgt	cacattcctg	ctcagggtcc	169770347
aaacatgtca	tagcggattt	atgggtgtaa	attatactgt	ttgctcaaaa	169770397
cactacctca	tcttcagtgg	cgtagtgcga	gtgaccttca	aactatgggtg	169770447
gcactcttagc	tataggggtg	tccctcaaaa	agcatgggct	ttgttgaagc	169770497
acaacttact	ctgctgtgtg	acttaagtca	aatagcttaa	tctctctcag	169770547
cctcaacttt	cccacctgta	acctgggcag	gataatagtt	tttagcttct	169770597
agaacagatt	aagggtggta	atatgagtgg	accattttaga	gtagctcatg	169770647
agataaaaact	caaagtctag	ctgttgtcat	ttggctgtta	atgttatctt	169770697

FIG. 1.21

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gaaatccac	agtagtcaat	agtggatggc	attaattgga	ggaggggaatt	169770747
gttagataaa	agatgggttac	tagatgatag	aaggagattc	aaattattga	169770797
ctggcagaga	actgtttatg	gaagagttct	tggctcgtaa	gagcctcagt	169770847
tagatagagc	agggccattg	gagggagacc	agttgcttga	atgcaagctg	169770897
ttaatcctca	gggaatctcc	atggctcagc	cagatcctgg	tctgtaatct	169770947
gctctcacca	cgggctgact	gaatgagctc	attgtcatgt	aattttaatag	169770997
gagccaggtg	tctgtgattt	ccaagagcgt	gagcagaatc	atcctgcacc	169771047
ccaaactagg	agggggaaaa	acacctcgca	gaagcacact	tgtccctagc	169771097
tgctttccat	gtgtcagaca	gagaggaat	tgtccaattc	caaattgcatt	169771147
cctatccttc	tcgggcgatg	agagaaaagta	attggcatag	tttgagtga	169771197
atgaaggtgg	tggtttgggg	tatttggtat	ttcttattgg	cataaaggaa	169771247
aacttgtatt	ttaaataccc	cctggcttct	tgaagaacgc	tttctctgct	169771297
gtcactgcgg	cccttgtcaa	aaaaacctta	gctgaaaaga	aaaaagaatg	169771347
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gccagtgagc	aacctcagg	gctgcagagg	cgggaggggc	agtacgggga	169771597
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gccctcatgc	catctcctga	agttgaaatc	tcaaacttgg	ctgtgtcacc	169771797
actgtcctcc	ttggctggga	gtgggttcat	aattttacaaa	aatccatcag	169771847
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tgccctcagg	gattagacct	ggggtcacaa	tgtgtgcaat	gtgggtgtga	169771947
actcatgtgt	ccagttgctc	tcagcaagcc	aacaagttca	agtcacttct	169771997
ccatcccacg	gctttgctct	tgtaacttgg	gaacaaacag	taccccatga	169772047
ataagttcac	agaggcaggg	ttgtgcagta	gtgacacgca	caggctcttg	169772097
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ttgtgtggct	tatggcccgt	tccagagctc	caggccaaga	tgacaagggg	169772197
ggcccagcct	gtgccactct	actaagccat	ggtccctgga	attccaccga	169772247
cagcagggtg	tcttatgcca	gttctacaaa	gtattcacat	gggcgaggcc	169772297
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tcagtgtgcc	tcagtgtctt	tccctgtaaa	atgggcaaca	taatgtattt	169772397
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tctaagatcc	agtgtaaacta	tcaggaatcc	tgggcaaaagc	catcagagtg	169772647
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cgcagacada	gtgcaggtgc	acctgggtcc	cccatgcagg	gtattgcaga	169772947
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caggggcacc	tgcatgttgt	tcttgacccc	tgaaatggaa	taggaaggct	169773047
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cccaggctga	gctctgcacc	agaggtcagg	gcaggattaa	taagggaagct	169773197
ataaatacaa	acaatggccc	atgtctctgt	gggcaatgtg	ctctgggttg	169773247
ggaggaaggg	agaaaattaa	attataatgg	gaaaatataa	attatttgga	169773297

FIG. 1.22

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tcaggataaaa	aaggaagaaa	tcagtggtgt	ctgaatgaat	ctcagtgat	169773347
ctgtcagaag	agttgtgagg	ttggctcagt	gtaggtgcac	aaagatgcct	169773397
aggaggatgg	tggaaacagg	ccccacacag	acgcaggtga	aactccagag	169773447
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ctgagatgag	agatgattgt	atltgtcaga	ttttctatca	aagtaaata	169773547
agatgggtcac	ccaccagtg	aatgtgattt	tagcaccttc	cctggtgcag	169773597
accctcccag	gtactggagg	tttagaggga	aacagagcca	gctctatgtt	169773647
gccctcaagg	agcaccacaga	catatcatgt	ggccaagatg	attgcatcca	169773697
agcgatgcta	attgattgca	gccttgcatg	gacctggcca	ggtgctacag	169773747
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ctaggggggca	aatgtcatta	tgatgcccac	tttacagata	aggaagctga	169773847
ggttcaaaga	tatgagggga	cttcctcaca	gccaatatgt	ggcagagtca	169773897
tggttcaaac	ccaggggttc	gtaccttcaa	agaccaagtt	ctcatccact	169773947
gtgcagacaa	atgttctgac	agaggacagg	caggggacag	agagtgcag	169773997
aaagagagag	attgtgtgtg	tacatgtgtg	cacatgtgta	tggcagtggc	169774047
tctgtgtcaa	cctggaaggc	ttcttgagg	tggatgtgtc	tagtggaaac	169774097
ctaaaggaaa	ggtcttaaat	gctacactaa	ggaatttgga	ttttatcaac	169774147
atlttttttt	ttttttgagc	agaattcaga	catgattata	tcccccaac	169774197
aaatctatat	ttaataagca	actccaaggt	gccagacaat	cttctaggtg	169774247
cagagagggg	tgcagacact	taatataaga	tgtagtctct	gccctttcct	169774297
agcttcagtc	tagctggaga	gatgaaacac	agattttattt	agaagataat	169774347
aagtaacagt	gtcaataaac	caatgccgag	cgccaaataa	aagtgcagtga	169774397
gtaggtgagt	ggaggtcaga	agaggggggca	gtctgggctc	tgggttggtc	169774447
aaggaaggct	cccagggtag	atggagagag	agaggttgga	ggggttatgg	169774497
aagattccag	aaaggggtgca	ctttgagggc	tggggcctag	tgtttggcag	169774547
tactagttcc	cccatgctta	gcagagggcc	tgcccatagc	aagtgcaggt	169774597
gcatgctggc	tgaatgaata	aatgttggtg	ccaatgaaaa	gaaaggacaa	169774647
acggttgaga	gatgaggcat	aacaaacgga	ctgtgggttg	cagggatgtg	169774697
tgaccactga	gcctctaccc	agcccaccaa	tacagtttag	ttgacttggt	169774747
gccccaccag	tcagatgacc	ttccttggtc	ttccattttt	ttttaggtca	169774797
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gagaaaagat	gggagaagcc	ttgggtgaca	gaaggaggaa	gccttgaatg	169774897
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tggccctcca	aggggggaaag	aggaaaaatg	ctataggaga	gggtttcagg	169775047
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acttctggag	atltgcccc	agatcgtgga	acaagtgtga	agaaacaaaa	169775147
acaaacaaaa	accagcaaaa	tgccctcctg	aggctccttg	agtgcgtgtc	169775197
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gccgacctgc	attgcggagg	actgcggggg	cttggtagat	gaagcctggc	169775797
ctgggtcttt	cagggccctc	tggctggggc	caggaggcac	agctgcagtg	169775847
gacactttca	aactcatcgt	gcctggcctt	ggcactcggt	gggctcattt	169775897

FIG. 1.23

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ctgggtcataa	tgacaccttt	ctaaacatag	ctacacaaaa	ttaaaatgtc	169775947
acagtgc aaa	tgctgcagct	gtgtgggtact	agaaagaaca	ctaggtcttg	169775997
agtcagaaga	gatggactca	aatcccaa at	atcaagccat	ctctctcctg	169776047
ggtgtgacct	tgactttctc	tgagcttcag	tttcttcata	tgcaagatgg	169776097
gaatgggtacc	agtagctgtg	tcacagactg	ttgtgaaggc	cgaggaatta	169776147
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tggtctcctc	caccagccca	gcctccccct	gtcacagtga	gaaggagcca	169776347
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aaccacaacc	atztatgaat	cctgcatgtt	cccctggctc	tgtccaactg	169776447
tatctgctac	cattcctgag	tggaagttaa	aaaaaaaaaa	aaaaaaaggc	169776497
agagcaagtt	gaagatggga	aagaggtgac	ctaaggtgac	aaagagtcaa	169776547
tgtagaaggc	agatatgtct	catcctcgca	gtgactaaga	ttaatgggca	169776597
tggagtgtca	ggagccctgc	cttaggaaga	actctgagac	tggctccaga	169776647
attctgtaaa	tccaatcaag	agtgttgcaa	tcagttagca	atgtctgcct	169776697
caggcaaggg	agaagaaact	atgggtctgta	tgtcatatct	aatattctcc	169776747
cttatatcta	aggtaccctc	tgctgtgaga	catgcaatca	acccgatgaa	169776797
gcttttttagg	aaaaagtcta	ttgtttacatc	aagtttaacg	taaagctgcc	169776847
tccttacata	ttttaaggtc	agcctaaagg	tttctctgca	catcgtgaac	169776897
tatagcaagt	agagatgtaa	acagactgta	gcctacactt	gtgccgatca	169776947
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agggcaaatg	ctgagctata	accaaccacg	ctgtttctgt	ccctcacttc	169777047
tgttctctgt	gcatcacttt	cctttttctg	tcataaatc	tttttccacc	169777097
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tgaagttttt	cttttatcac	tctattaatg	ctagatgttg	actattgaat	169777247
ggatccaagt	ttcaggaact	tacaaaatgt	gtgtgtgttt	gaaagaagga	169777297
aatcattact	tgctatccct	tctctatcaa	aatctacttg	agcttttcaa	169777347
ctaaaaatc	aatgcgtatt	ctttggggta	taaataaatg	tgctgaatct	169777397
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tccaatgcc	agcatgtagt	aggtgctcag	caaatgtttg	ttgaatgaat	169777547
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cccacgagga	cgttggtttca	ttctttctga	gtgaggggat	ggggctgata	169777747
gaggaagccg	gggaggggtt	tgccctgctga	tttcttccctg	cttttgtgtt	169777797
tgtgtttgcc	gtctgcctgt	ccctcacatt	tcctcagtg	tgttcctatc	169777847
cttggatccc	taatcctaca	gccacaggact	ttctacaacg	gtactactga	169777897
cattttggat	gggataattc	tttgctgtgg	ggggactctc	ctgtgtgctg	169777947
tgacatttag	caatatccct	ggcctctacc	tactggatac	cagaggcacc	169777997
ccccaccccc	agccgtgaca	actaaaaatg	tctcaagaca	caccacccag	169778047
gtgagaacca	ctgcttagcc	tccccgggga	acatggctgg	ttccttcttt	169778097
ctgaacagtt	tcagaaggaa	catcaagtct	gcaacaagtc	ttctgacttc	169778147
atggctccaca	ccagtgtcag	gccaccgcgc	ctatcaaccc	tcaggctca	169778197
tgtctccaag	gagctctctg	atcattccct	gggtgtctctc	tcgtttgctg	169778247
tctgccccctc	tcccctgggc	tatgagcgcc	acaggagttt	tttctatttt	169778297
gattatctct	ctatccctgg	ggcccagaag	tccttggcac	tcaatagggt	169778347
ctccagtggga	taaagggtgag	gacgaggtga	ctggggggagc	ctccctgtgg	169778397
agtgacgtct	ccatgccatg	aaattgccag	ccctgggaag	tcatgaggaa	169778447
gaacactcca	ggcagagggc	acagtcaccg	cacagctctc	aggcaggaac	169778497

FIG. 1.24

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aggtttgcct	tgtggaaggc	tgctggggag	gagaggggag	cgggattgga	169778547
gaaggggtgct	ccaagagcca	gaaaagctag	tcaggaggcc	acagtgaggg	169778597
gtgcaaactc	agttccagga	gtgacaacaa	gccctctgga	aacctcccag	169778647
atgtcccaag	gtccacccct	ggccactct	cactctcctc	tctccttgct	169778697
gccagcctc	actctgggaa	ggctggggag	gattcctaaa	tctgggtctga	169778747
actcctgagg	ctgaagccag	agctgggtgtg	gcccccaagt	catatctcag	169778797
gggtgggagag	agtccttcca	tcaaggaggc	aacgctatga	gggcagctca	169778847
gtgctcagcc	cacccctcta	accctcatgg	gcgggccctc	aatcagaaac	169778897
cacaaattcc	aggtcagtc	agggaaggcc	tggatcctcc	acttcgggct	169778947
cctcccgga	gtcagcttaa	agaaatgatg	cggaggaatg	atcactgaag	169778997
agactcgtca	ttcctgggtca	aacctatgctg	gaggtcaggg	gtttgttaac	169779047
tcagccttgt	cacaggggcc	ttcccttcca	cctcaatgct	acgacagagc	169779097
tggtgttgaa	ggctcttgac	gaaaaagcta	catttctgca	tttaaaatgg	169779147
agaagatcag	gccactcagt	atctccggtg	taagaagaca	tttggcaata	169779197
gtaacagcta	atTTTTTTT	atacttaccg	taactcattt	taccattttc	169779247
ctgcctagaa	aaaaaaaaaag	tcagctcac	tgccagcact	catttcttgg	169779297
ggcaaacagg	aaataagtta	atcttaacaa	caacctgtga	aggtgcatag	169779347
ttttattatc	atccccattt	tacagatggg	gaaactgagg	cagtgaagtt	169779397
tagtaatttt	cccagattca	ctaaaatttc	taagatatgt	ttaacaaaga	169779447
aatccaccct	ttaactctta	aataatatcc	tcttttttaa	attaatgcta	169779497
gaatatgggtg	caatatcttt	ttaattgagt	gtatcttttg	ccccagcaat	169779547
tctaccacta	ggaactgagc	ctaaggaggt	ataaatattt	agttagaagg	169779597
atgcagtatt	atntagtatg	tggaaactcaa	tgagaatctc	cactaagagg	169779647
ggttatTTTaa	ataaactgtg	atgcctccat	ataaatgtag	ctggtcaaaa	169779697
tgacatctgt	ttgtatgtac	caacataaaa	agacatctaa	atcatatatt	169779747
ttaacagaaa	agtcagaaat	aatcacattt	ttgtaagcag	tcatttttgct	169779797
tgaggactgg	gatttctatt	gacttttaat	ttcttatTTT	cacgtgtcta	169779847
tagtctctaa	tttttctaca	atgaacatgt	actacattta	taataagaaa	169779897
gaaactcaat	aaaagttatt	gagtaaaaga	ataagcagcc	agaaatctgt	169779947
ctcttctggg	gaattagtga	gcctcttct	ccttgagagt	agacgctatg	169779997
gctgctttgc	tggaaaccttc	catttgtccc	aaatgctcca	ctctctgcca	169780047
atgggagacg	gggtctatat	tcacctgggtc	ccttctgcgt	gaggccacct	169780097
tggcagaagt	cactgcccc	cccaaggcat	ctgacctgct	aaaacctct	169780147
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tacagatagt	aaaagctctg	ctgcctgggc	cctggTTTTa	aatgccccct	169780247
gggtgttttct	ctatacgcca	ctgacacctt	gatcatgagt	caaataccct	169780297
gaacatagag	tagcatctgc	ttcctgttga	gaatccaacg	aatacattta	169780347
cctgattttgc	tctctcttct	tttccctaagt	cctaacttcc	taaaataaaa	169780397
tgactctcca	attcacctgt	ccaccttggc	cttctctcct	tatacccagt	169780447
cttgcacct	agacgtcttc	gtttgggcaa	ccacacagct	tataagcctc	169780497
ctgatgccca	ccacaggagt	cttatTTTTgt	gctgccacgt	taaattctct	169780547
cttccatgag	cacctctct	tcactttcca	ccactccaa	acctgaaaat	169780597
cacctttctc	cacccctcct	ttaatTTTTT	acatctcatc	agtgcccaaa	169780647
acttctgaaa	tcaacctcag	taatgtttcc	ttcaaataac	cccttcccgg	169780697
ctgggcgag	tggctcatgc	ctgtaatccc	agcatttggg	gaggccaagg	169780747
tgggtggatc	acttgagggtc	aggagtTcaa	gaccagcctg	accaacatgg	169780797
agaaacccca	tctctactaa	aaatacaaaa	tttagctggg	cagggtggca	169780847
tgcacctgta	atcccagcta	ctggggaggc	tgaggcagga	aaattgcttg	169780897
aaccaggag	gtggagggtg	cagagctgag	actgcaccac	tgcgctccag	169780947
cctgggctac	aaagtgagac	tctgtctcaa	aaaaacaaaa	caaataccct	169780997
cttcccatca	tttctccagc	ccttgccctc	tcaagtctc	ctgactgggt	169781047
tcccttgggt	ccctgcttcc	ccctcagctc	gttatgtgtg	acttctgggt	169781097

FIG. 1.25

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aaaggttctt	aaaataacaat	tcagatccta	tccagtcccc	tactcaaaac	169781147
tgtgcccattg	ggatcaaaac	caaactctgc	aacattccat	tcagagcttt	169781197
aagagtactt	ttcagcctga	ggtctcctcc	tcaccactaa	cacccttccc	169781247
tccaatcaaa	ctgatccatt	gtacctacaa	aaagcccgtc	ccacctocta	169781297
gcctttgttc	acactgggtt	ctctgctgga	tcaccatccc	tccacatttc	169781347
caggtgtccc	tcaagactac	tcagcagcag	ctatccatac	aagttcctca	169781397
accctggctt	tcttgccctc	aagtaaccag	ttcatcctcc	ccagtcatat	169781447
agccctctat	ttacatttct	tttctggaag	ctatcatttt	tcacgtgcca	169781497
tttgagtga	tgtcctcgct	aagacgatat	tttctttgag	ggcagtaacc	169781547
tttcttatat	gtctctgtat	cccatgaact	tagcaaaaaa	caagggacag	169781597
aacaggtgca	aagtctacgt	ggttagtgaa	tttaacagat	cttcctaacg	169781647
tgtaaacgtc	ggtgtccagg	tgaatggaag	aagtgaagctg	agatagaggg	169781697
gacagacaga	gtcagtgctc	agtgtgacc	tctgaaatgg	aaaaacatgg	169781747
ccagtcctta	ggaggctgca	gaggccaaga	ccccagtgag	gtttgggggt	169781797
tccacagcag	aggaggagct	gtggaccaca	gcaggacccc	gatgccatca	169781847
gcaggggagg	aagtaatcag	agaggtggag	gaagggaagcc	aagggaagtc	169781897
aagtaaacac	caaataattcc	ctcccgggtc	aatgctgtga	cctgcataag	169781947
ccaccactcc	cccagtcctag	actctaccca	tgggaagaagg	aagaagatag	169781997
aactctggat	ttgaatataa	ttctaaaata	accaaattta	tctgaaaatg	169782047
actaggctga	gttttctgct	tcaaccagaa	atggagcttg	gagtcagaaa	169782097
ttatgtgaaa	ttatagaaga	gaaagtcacc	atcttccatc	tctgagtcgt	169782147
atgatcattt	tagacataaa	attgtgcact	tacgatgtac	caagtgcctta	169782197
atatacgtga	tctcatttca	ccaggggaaac	tgtataattc	attgctttaa	169782247
ctgacaaaat	tctgcaactg	aagaagggtgc	tgttaataat	tgcattggga	169782297
cgcaggcctg	agcaggccat	gatttgtggc	tgtcctacat	ctgaccctca	169782347
cagtatccat	gggagaaggc	agcatgttta	tgccccctga	cagctgggga	169782397
aaccaacact	taaagtgatt	aagtcacaag	tccaaaataa	atgacagagc	169782447
tgcagttcaa	gcccagggtg	tcatttacca	aaggccatgc	tcttttctact	169782497
ttgcatggga	ctgtgaccgc	tggctctacc	cagcttccca	gtgcgaccct	169782547
tccccgccca	ctgtttctct	tctctggcca	acggaaacac	aatgagacca	169782597
catatgtaac	attacatttt	ttcatagcca	cattgaaaag	aaaaaggaac	169782647
caggtaaaat	ccattttta	atgatatttt	atttaaccca	atacagttga	169782697
ggcttgaaca	acacagggtt	gaactgtgtg	ggtccgctta	cacatggctt	169782747
ttgttcagtc	tctgccacc	ctgagacagc	agggccagcc	cctcctcttc	169782797
cgcctcctcc	tcagcccact	ctacatgaaa	acaaagagga	tgatgatctt	169782847
tttgatgac	cactttcact	taataaatag	caaataatag	ttctcttctt	169782897
tatgatttct	cgtaataaca	ttttcttttc	tctagcctca	tttactgtaa	169782947
gaatacagca	tattcccagc	tactcaggaa	gctgaggcag	gagaatcact	169782997
tgaacctggg	aggcccgagtt	tgcagtgagc	caaaatcgca	ccattgcact	169783047
ccagcctggg	caacaagagc	gaaactccaa	ctcaaaaaaa	aaaaaaataa	169783097
aaagaataca	gcgtataatg	catgtaacat	ataaaatag	tgttaatcaa	169783147
ctgtctatgt	tatgggtaag	tcttccagtc	aacagcaggc	tattaggagt	169783197
taagtttctg	gggaatcaaa	ggttatacac	aggattttga	cggcatgggtg	169783247
gttggcactc	ctaactccca	catcgttcag	ggtcaactgt	atattcaaaa	169783297
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tcagtgggta	ttttaacctt	acagcatatc	tcaattcaga	ttactcacac	169783447
tctaaggact	caatagccac	gtatggctgg	ggtctgccag	ccggacagcg	169783497
aggtctagcc	ctgatctgag	caggagccat	ttgattgggt	tgttggtaca	169783547
ctgccatctg	gtggacagat	gttccttgct	tgaaaaacca	cctcgaagga	169783597
aagtatcagc	atcaggggaca	atagcacagt	gggcctcagg	atcagctccc	169783647
cggaaagagc	ttgggggttg	agggggtgtt	gttgctgagg	atgtccccag	169783697

FIG. 1.26

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agaagatgta	cagccatgga	gcaaactcaa	gtcacttatg	atgtcggcaa	169783747
accttggccg	tggtgcactc	ttgtttcctg	gttgcaaaag	gatttagcag	169783797
aaaatggtaa	ctctttttca	gaaggcatat	ttaaagcagc	tctttaaaaa	169783847
gcaggagttt	ctttcacacc	cagtttcgcc	atgtggttgt	gtgaagggct	169783897
tctccccaga	aatcatgtgg	tctctctttt	aattcacagt	aaaaaccttt	169783947
cttctgtctt	ggcccattat	ggctgctata	acaaaatatc	ataagctggc	169783997
cttatatacc	atagaaatgt	atttctcaca	tttctgaagg	ctgggaaatc	169784047
catgattaag	agttggtgtc	tggtgggagc	ctgctttctg	gttcaactgat	169784097
ggcgtcttct	tgctgtgtct	tcaccgaggg	gtagggacaa	ggcagctctc	169784147
tgcagcctct	tttctaaggg	cactagacct	atttgccatg	gttccagcct	169784197
catgaactaa	tcatttccca	aagtccccac	ctcccaacac	catcatcttc	169784247
atgattagat	ttcaatatat	gaatttgagg	gaggatagaa	acattgagac	169784297
catagcatct	gccaaagtgt	gtcttcctca	ctcaaattgg	gtaggtgtgg	169784347
ttattccaga	gtttcagtga	accaagacgt	atttttccaa	tgtgaataat	169784397
taattaagaa	cacttgatta	gggtcaatgt	tattctggac	ttctgaatca	169784447
ctcccacatt	tgaaggggag	ttttaaacac	aactttgtgt	gaataaaatg	169784497
atgtgtctgc	atctctccag	gaagcagtgt	ttggagctga	gatgacttgg	169784547
cagggagaag	aatccactgg	gacattcaat	aacttggcat	tgagagtgtt	169784597
ttcagcacca	tgctgtcctc	agaatagtgt	tagaatttat	ataaacacag	169784647
atgtgacttg	tgccctgaag	gagaatacag	tcttcccagg	agagacatgc	169784697
aaaaccatca	tagacaaaca	gcaagaaaac	agcatcaagg	atgtacatgc	169784747
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gagcaagaga	cagtctggac	aatttatgct	tctagaatgg	ggagacaaga	169784947
agaaaagaaa	gatagatacc	caaggacttc	agtgactggc	tcaggaagaa	169784997
ttactcagca	gtgagggggc	cagcatgagc	ccaggggcaa	gaagccggga	169785047
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cgttaatagg	caaaaattgt	tgctttaaag	aacctagaat	ctaaaggggt	169785197
ctttgacata	atacagaata	acaggtccca	gagattattt	tacagaatgt	169785247
tagtacctca	tgatattaat	agatatataa	caaaacagac	ttctttgcc	169785297
caagacttct	cagtaccttt	aacattttat	gattttccca	aaggacaaag	169785347
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tggcatgtgc	ctgtagtccc	agctgctcag	gagggtgagg	tgggaggact	169785547
gcttgagccc	aggaggtgga	agctgcagtg	agctatgttc	acaccactcc	169785597
actccagcct	ggacgacaga	gcacaaccct	gtctcaaaca	aacgaacttc	169785647
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ctagtcttga	cttttttatag	ataggggaaac	tgaaaagcta	agaggcaagt	169785747
ccaaatttca	caaagatagt	ggcagagcca	agattggatt	tttggctctt	169785797
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tctaagttgt	ttcaaaaaca	aaccaaatac	cccacttggc	ccagaagagc	169786147
aaagattaaa	agccagcctc	gaggatcccc	agcttggcta	cctgcagctc	169786197
acagcatatt	ggaaaaattt	tatgaatcgg	tgaacttttt	cattctcaaa	169786247
tgggctcttc	agatgggtta	ttaattctgt	tagatgcggg	ggtgcgtctg	169786297

FIG. 1.27

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gctttattct	gtgtggaatt	tttggatgaa	ttcactgcct	cacccccctcc	169786347
cctccacagg	ccagatgggg	agccgggtgc	tgtataaatg	tttaattgtg	169786397
gctcagtaaa	aatatttgct	ttcagtagct	ggaagctacc	aaacggaggt	169786447
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aaggctgatt	aaatcaaatt	ccccatagt	tagaaccact	taaataaatg	169786547
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ccattaggct	ggacataaat	cattcatcgc	catcactgcc	gtcaaagcag	169786647
cactggctct	ttttcttctg	ctgctgacat	ttccattact	agggagcttc	169786697
tcagacatgc	tcttgggttc	cctgtcctta	cccaagtgcg	gggtagcagg	169786747
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tgaggcctat	ggaaatgaag	tgagctgccc	ccagagtagg	gaatacagcc	169786947
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agaatccttt	cggctggggc	taggggtggg	gcagggtaga	tactgatcca	169787147
aaggatttgg	actccttttc	ctagtccaaa	tccccatcgt	ctctcccctg	169787197
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attatgtcat	tctcctgctc	aaaagcctcc	aatggcatcc	caccactcct	169787347
agaataaagc	ccaacctccc	accatggccc	tcaaggcctt	ttatgatatg	169787397
gcccctgcca	acatttgctc	attcgttcc	accccactcc	tttatctggg	169787447
cgtcttggt	tctttctggg	cttcagacac	aataagctca	tgccctaccta	169787497
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agcttcaacc	tgtcattcag	acctcagctc	caagtcactt	cctcagaaag	169787597
gccctccctg	taccctggat	tgaaaacagc	cctcccctgc	acacgctcca	169787647
caccatagct	ctgtttcatt	tacttttacag	cactgaacac	tgtctctatt	169787697
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gtagtaagt	ttcaataact	attacttaaa	taaagtgaatt	aacttgtctc	169787847
attccttttc	ctgcattcca	agttgggtga	acctgacct	ggccccttga	169787897
aagagacaat	ttgattctga	aaaccaattc	ttacctccag	gctcaggccc	169787947
catgcaggag	tctttctcca	ggtggcctgg	ccatgcagg	gatggcagtc	169787997
atggggggag	gcagagagct	gctggagaaa	agctaggagg	ccctttgggg	169788047
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gttcttgaat	tggctgcaac	tccaccctcc	ctcctgcaag	tgctcttcc	169788247
tctgccacgg	aagcctctgt	gccatgaaga	agaccaccag	acctctccag	169788297
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aggagccacc	ttcctgcagg	caggcaaggt	cctggaaata	taaggttgtc	169788397
tgtggccatt	gaccatccta	ctgcttccctg	gtgacagaaa	atgttgcatt	169788447
ggtggcagcc	atggggacag	cttccctggtt	cctgaattgc	agcactggtc	169788497
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gcatgcttgg	gaaaatgttt	gctaattgctt	tgtgactcaa	aaggaatcac	169788797
acacacacac	acacacacac	acaaacacac	acacacagtt	tttaatatta	169788847
tcagtcatat	cagccccctg	aggcagctgc	tctgttccag	acaaaccctg	169788897

FIG. 1.28

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ttaataacat	tottatcctc	tttgtttcat	tttccagctc	aatttggaag	169788947
cctgaccttg	tcttgctttg	cctcctactg	agagttaata	ctgggacata	169788997
ctgaaggcg	aaggcttgag	tcacaaagtc	acagggataa	atcctagatc	169789047
cagcagttac	tgtctacatg	acactaagca	gattagttgc	cactgggact	169789097
cagttttacc	agtctgcaaa	atggagctat	cagccgcac	tagcactagg	169789147
ggcgctgtga	gcattggagg	cagtctgcac	acagaggctt	aacacagtgc	169789197
ctgagcttgc	aggtgcttgg	taaattggcaa	ttgctgtcag	cattgtctga	169789247
tttacctgaa	ggaacagttc	acactccacc	cagattttca	ctgcagcagc	169789297
caagaaagaa	cttctgggaa	agcatctgct	tccacccaac	tcccaagagg	169789347
ggttcgtaga	gggtggagct	gagagcccg	ctcccctacc	agcctgcaga	169789397
aagaaagcca	tgttttggcc	tcaggggagga	gaaaccacga	taaaaaccac	169789447
cccatgtgca	gcctttgctg	ggccacagga	ccagctccac	aggagagagg	169789497
aagaggcg	gccgcaggac	cagctccaca	gggagaggga	agaggcctcc	169789547
tttcagggg	ggggagctga	gggcaagaca	gaccttttct	gactcagccc	169789597
aaggagggct	ggagcagggg	ctgcaggttc	cctgctttct	gctacaacac	169789647
agggtagggg	agagtcattg	cctcccagag	cctctgcagg	ttcacctgcc	169789697
aaatggaaat	aatagcatcc	tcctctgcaa	gtcacagcct	taaagagggtg	169789747
ctgagagtca	ctagtttagac	ccaagccagc	tgtttctggt	gcattaggac	169789797
tatcgaccag	aacccttgca	ttcccagccc	ctcctgcggc	ctccaacgac	169789847
caggagagaa	aggcgtaagg	tgtaagactc	tggggccagg	tctggcagct	169789897
tatggccact	cttttcttgt	gtctggacag	gagcattata	gctacaacca	169789947
tctcatctaa	tctcactg	tgccctatga	ggcgggcatt	cttatttccc	169789997
cagttttgag	ataggcacag	aaaggggaag	cgacttccca	ggttcacatt	169790047
gccagtaagt	ggtaggacta	ggccctgaaa	agcacagcct	gccatgggga	169790097
agagaattca	tcccagctg	agaaccactg	tatcctcacc	caggggttcc	169790147
cagccaatgc	aaacaggggac	gtgaccagtc	tccactggtc	ccctgtacca	169790197
ggtctccacc	ttgcccggcct	gctgctgggc	cccaggactg	ctcccaggct	169790247
gcacctgtgg	ggtctgccc	ctcctccact	tccttttgag	aagctgctcc	169790297
caccctctcg	ccttcatctc	aaaggaaagt	gtgctgccag	gcagctggag	169790347
ccagatggcc	caagacaaac	tcttcccact	acacttcctg	cagcatctga	169790397
gtccaacccc	caactccaga	gctggcaagc	tgcccagagc	ctcccagagg	169790447
aggcctatgg	gttaacttca	catttagtat	tttcagcata	tggtagaaag	169790497
aaaatagtgt	tgtttagatgt	acaagtgtga	tttccccttt	ccagaatgcc	169790547
ttcctctctc	ctccacgtgg	tgagctccta	ttcatacttc	aaaaccatgc	169790597
tcaactattc	cctgcccacc	tgtttccctc	cactcctccc	cttctaattgt	169790647
gggtgtgtcc	caggggacaac	atctgtgttc	ctcagtgaag	ttgagagaag	169790697
cctaaatttg	ctctacataa	gaaaaaagaa	taaggaggta	aactggaaac	169790747
gggaggaggc	tgggaaacgc	agggttggtg	gaaggacttg	tggggatgtc	169790797
gtggcagcca	cctgagggtg	aggaacgtga	cagccagagc	agctatgctt	169790847
aaggggcttt	gccacagtgc	gaaagatagg	atacaaggtc	ctcttcagtc	169790897
tctccatgaa	aaccacagtc	aaagtacaca	ttactcacc	atgcttttga	169790947
gctagatttg	ggcttaattg	tgtctttttt	tttttttatt	aaaacaatat	169790997
tccaggctga	tggaaattta	caacaaggaa	cataatatct	gacacaaaca	169791047
tagcctaagc	cttgatattt	atcatcttat	atagcaagag	atcagggtgt	169791097
tgagaacttt	agagcagctc	cgttatgtcc	aggctctggg	cggtttctgg	169791147
gattctgtct	gctgtcccat	cagtactcac	gggggtggctg	tgtctgtctac	169791197
agacatcata	gcctcacgaa	accacctaca	ctaaagccaa	taggaagaaa	169791247
ggtgtgtgtc	accttcacct	tcccaccctt	tatgggggag	gaaaatatatt	169791297
gccaaagtgc	ccacctttcc	cttctcaatg	cccctttgat	caaagcctgg	169791347
ttctatgtcc	ctgccagct	gcgggtgggtg	ctaggaaaga	aggtatctgg	169791397
ggtttgacag	tctgctgtga	gggctaaata	aaaagggcgt	gagaggtctg	169791447
ccctctgctt	gtactcctct	gctgaggggag	aacttgctgc	ttctggatac	169791497

FIG. 1.29

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caccctttcc	catcgtatga	tagcctgaag	tggtcagaac	ttttccatt	169791547
aatcacttg	aaccgggag	gcagaggtg	cggtgagccg	agatcgccg	169791597
actgcactgc	agcctgggca	acagactgag	actctgtctc	aaaaaacaac	169791647
aaacaaaatt	gactttctcc	cactgagccc	aaggtgcttt	cctggtaact	169791697
tctctttgac	ccagtcctgc	ctcctgcac	ttccttcagc	aaccctgttc	169791747
tccacatcag	ccaccagagg	gaacatctta	aaacacaggg	ctagactggg	169791797
catgccgttg	tctctgctaa	accctcact	gagtcctccag	tgtctacagg	169791847
ataaaatcca	agcttcacgg	cattggaggc	tcaccacagt	cctacttcag	169791897
cctagtctct	cttccttatt	cttcccctac	atatatatgt	atatatatat	169791947
atattctcat	actgtaggtg	aagcaactga	aatgcttttt	attcccctga	169791997
cactttttgt	ttttcaaatt	cttggtgtac	aaatttatgg	gggacatctg	169792047
cagttttgtc	acatgcatag	attttgtagt	agtgaagtca	gggcttttag	169792097
ggatccgtc	cccacaatga	cgtatattgt	acccatcaac	taattttctca	169792147
tcatccactc	ctccccaca	ccctcaccc	tccaagcctc	cattgtctat	169792197
tatccactc	tctacatcca	tgtatacagg	ttatttatct	cccatttatg	169792247
gggtgggaaca	tgtgatattt	gactttcttc	acctggcttg	tttcacttaa	169792297
gataatgaat	tccagtttca	ttccagttgc	tgcaaaagac	gcctcacaga	169792347
attttaaatg	cttatatata	tacatacacc	ccctttgtat	ttgcctacac	169792397
aaaactaaca	aacctttgtg	aaatgtaacc	tacaggaaat	atgatcatgt	169792447
ctaagtctgg	acatgaagca	gatgcaatac	acaaatccat	gaggtagacc	169792497
caggtatttc	agatcctgac	cttgatctca	ggtttactta	ttagaccaca	169792547
gaccaaagac	tccactgat	gtccccacag	atttcaccac	ttattcctct	169792597
tgtcccacac	actctactcc	aaagtcaccc	tcctctagag	gatagtcacc	169792647
tgagatactt	cagcgaccct	gctcaccttg	gaaaatcagg	tgacaggaat	169792697
catcagttaa	gcctgtggac	agtaagcatc	tggttggtctg	gatgggtgtg	169792747
tgggcggaag	gtaggaccca	ataggggctt	ttcatgggtc	cagcccaaaa	169792797
cctctgacca	tgccagtgca	tgctgaaggg	ccccattcca	tttatgggtcg	169792847
gggcccacatg	atttacattt	actgtctcag	gttcttcttg	taacactgtc	169792897
ttctccaatt	tttgataagc	caatgcccct	gacacttcta	tgttttgttc	169792947
aaattgttct	acttgcccag	cattctcttc	caccttctcc	agctgtcaaa	169792997
ctcctacaca	cccttcaaag	cccagctcat	gggtcctctc	cctgacaatg	169793047
attccagctg	aaggagatga	cattgctact	tccttggtc	ctatcatacc	169793097
cggataggct	agtgtagcac	ttaacattgc	ttggtgcttg	gtgacattcc	169793147
caaacgttca	tctgtcctca	aggatgggaa	cgtcctcatt	tcccatcatt	169793197
taggaagtgc	ttgctaacc	aaagactcag	ccctcatca	ggaaccagt	169793247
aaggacagag	ctgggaaaga	gttgtcatgg	gcatggggac	tatgtgaggt	169793297
catacgagct	tcctgggtca	cagaggtgac	ccacgaatgg	tagctgcagc	169793347
gttgattgtt	gcccctacta	ttactgtgtt	attactgatc	tcagcccttc	169793397
tcttaagtga	ccccttcaact	agtctcatag	atgagcggcc	agcctgcctc	169793447
ctggatccca	gaatttgctc	actgtccacg	acttctgtc	atggctggga	169793497
acattcaggg	aggatctggg	cccactcgta	ggaggggaag	acaaagagt	169793547
ccatccctcc	aggccctccc	ctcctgcagg	acagatcatc	ctgcctcact	169793597
ccatctgcag	atgctggcaa	agcacattcc	agccctcgcc	tctgaggcag	169793647
agaaacagat	tccaattaag	ggacttgccg	aaagtggctt	cattttacaa	169793697
gcaattgggt	tgtgaattga	agcgggcatt	aaagtttaca	agctaggctg	169793747
gcggaggagc	cagaaggcct	tgctgccact	gcctgtcagg	agacatcttc	169793797
tccagttact	caacaattgt	gtggagtgag	tgaggagtgc	gcacgaatcc	169793847
tgccctccat	ggctgatggg	ggaagaaatg	tccattcatt	cgtcttctta	169793897
aaaccaagga	tcaggctgct	ggaggggcaca	ggatcatctc	tctcctgata	169793947
ggctttcccc	ttctctagcc	ttatgtgaga	atctggggga	ttttaggtgg	169793997
tggtgagaaa	atggggaaag	aaatcacatt	cgttgacctc	tgcttacagc	169794047
tgggatcccc	acgcagctga	gaaattttcca	ggaaattacc	tgggttcaat	169794097

FIG. 1.30

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ggaggaactt	aacacttcaa	gctgtcacct	ggtgggaaag	ggtggtggca	169794147
agaagtaaca	agatctccca	aatggatcca	accagagaga	aggcctcctc	169794197
atttccttct	cagccaagcc	cacggggggc	ctggaagaca	gaggttgccg	169794247
gggcatccag	ggtctacacg	ggctgagctc	cccagacctg	gtgcaagggg	169794297
gccaggcatt	cccgccaaag	ctctgccacc	taccagcag	gacccatgag	169794347
ctcagcacct	ttctggactt	gaggagatgg	gtctgggttt	ggccttttcc	169794397
ctccagactt	ccttctgtct	ctgcctctcc	actgacacct	gcctctgctg	169794447
tccccagga	cattccactc	tcttctctaa	ggctcaggcc	tgaggggttg	169794497
ctggtgggca	gattccatct	catggttgag	ctgtttggcc	tcaatggcat	169794547
tttatctctc	tctctctctg	tgtctctctc	tttctctttt	tttttttttc	169794597
acattgagcc	atcttcttac	agctgaggtt	ttcatataaa	aaagcaagtt	169794647
gctggtttct	ctttaaaagt	agggcaatct	ggcagttctg	ggcttggtga	169794697
aaaacaattc	ggtagagcta	aaaacagggg	cttctgataa	agcctgagct	169794747
cccagcagcc	aaaggactta	tcacccca	aaaaaatccc	ttcctgcact	169794797
catttatatc	aaccctgcc	cctgcagaca	cgtattgtag	gttttaacta	169794847
gaaacaagag	gattagcttt	atttaaacag	caaaactgct	taaatgagat	169794897
aatatatgta	ttgggaatgg	tgcctggcac	ctaacctaat	ccttagttaa	169794947
ttaatattta	ttgagcaaat	catcttgatt	attaaaaaga	caggccagct	169794997
ggacacaata	agaatgctag	ctcagagctg	gcacttgagg	gttcggtaga	169795047
atattcatgg	cttggagggtg	ggggctatga	tacgagccca	tataatcaga	169795097
gaagttcaga	tgggaaatga	gaaccacttg	gtagcctaaa	ttcagagaaa	169795147
ctaaagccag	cctaacgctc	tgaagctggc	aagtgttcat	ttttggaaat	169795197
cagaaagtga	tgatgtgtta	tccaagaga	ctcctgggac	aagatgcagt	169795247
gagcagccat	tcacaaagac	taccttgaac	cgggctcttt	ccctacattt	169795297
tggtattata	tcctcgctac	aaccttctga	ggtggaaatt	aatatcccca	169795347
ttttacagat	gcataaactg	tctagtggag	gtgacagata	gtattgacat	169795397
gaccagaaga	ataaatataa	atgagataaa	ttctctctga	aggaaaggaa	169795447
tagggattta	caatggtgta	aaacaaagga	agtggggcct	ggtctaagcg	169795497
atcagggaat	gtctctttta	agaagtgaca	tttaagctga	ggtctaaagg	169795547
attagatgag	tgttaaatat	gaggagactg	ggcaggaggg	aaatcttctc	169795597
catggctctc	aatccagaca	cacaatttga	accacctgag	gttcacaaac	169795647
acaaagaaag	tatcgtgacc	tgatacagtc	ccagtcta	taaatcagta	169795697
gaaccaggt	gccgatgttt	ttgtttcttt	ttattttatt	tattactatt	169795747
ttttgagatg	gagtctcgct	ctgtcaccca	ggctggagta	cagtggcaca	169795797
atcttggtct	actgcaaccc	ctgcctcctg	ggctcgggcg	attctcctgc	169795847
ctcagtcctc	tgagtagctg	ggattacagg	cgcccaacat	cacacctggc	169795897
taattattct	attttttagta	gagatgggat	ttcaccatgt	tggtcaggct	169795947
ggtctcggac	ccctgacctc	agatgatccg	cccgcctcgg	caccccaaag	169795997
tgctgggatt	ataggcatga	gccactgtac	ctggctggta	ccaatgtttt	169796047
taaaagcttt	atgggtgaac	cactgaaatg	aaacaaaaag	taaatccaaa	169796097
gctcatatac	tctagccaaa	caatagccat	taatagctat	taagtaaata	169796147
gaggagatgc	tcagtgataa	tgagcaggta	gatcatcagc	atccttgtca	169796197
tcaccactac	atctgcctcc	tccagatcat	ttggtagcca	agtccaatgt	169796247
caaaggaata	aaggaaatct	gcctctgttg	agggttgct	gtatgtcacg	169796297
cactatgcta	aattcttcac	tgtttcattt	aacgtttacc	gaaaccctta	169796347
ttatttttaca	aatgaggacg	ttgaggctca	gaacaaggca	ccaatttacc	169796397
caggatttca	cagctcatcg	gggcagtggg	ggacctctt	ccaggccccc	169796447
ctggctgtag	agaccacact	ctttcctgtc	tccatgcaga	ggggcctcct	169796497
gctcacttta	gctcccattt	cccagcctga	ctgccttgat	tgggcgcgat	169796547
ttctttgttc	tgacctcaaa	aagagttttg	tagatttgtg	cccacttttc	169796597
tcatcacgct	taagaaaagt	gaccaaagct	gaaccaagct	atctagggtc	169796647
aaatgctgct	tactggctat	cggggcccaa	actatctgtg	gaacttcttt	169796697

FIG. 1.31.

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gagcctcaat	tttttgtttt	ctataacatg	ggaataatat	cagtacctcc	169796747
ctcataagtt	tcttatgaag	attaagtatg	tatgtgttaa	gattcatatt	169796797
aagtgagaat	tacgcatgta	cgcataatac	tacaagatta	agtatgtatg	169796847
taagcatata	tatatacaca	cacattttaga	atagagcatg	aaatatagcc	169796897
agtgttcagt	taatgtcaag	tattgttaat	attatcctat	gggctggagt	169796947
gagaggcctc	ctgggggtgtt	tgctttccag	cccccaatcg	ggtggcatcc	169796997
tggatagggg	atcatcatac	ctctccccag	gagatcagga	tagggaattg	169797047
taagagcact	cagggtggag	gtaggatgtg	caccaggga	gctcaggcag	169797097
gaagctgctg	tctttcctgg	tctctgcaga	ctaggagcag	cagccaggga	169797147
cctgggttga	ctgggggacg	ggtcgggtggg	tgggggtgaga	tgactatcac	169797197
acctcctcta	aaaacaagat	ggggcctggg	gcgctggctc	atgtctgtaa	169797247
tcccagcact	ttgggaaggcc	gaggcggatg	gatcagttga	ggtcaggagt	169797297
ttgagaccag	cctgggtcaac	atgggtgaaac	cccatctcta	cttaaaatac	169797347
aaaaatcagc	cgggctgggt	ggcacgagcc	tgtaatccca	gctactcggg	169797397
aggctgaggc	aggagaatca	cttgaaccca	ggaaggggag	gttgcagtga	169797447
gccaaggctc	tgccactgaa	ctccagcctg	ggcgacagag	cgagactcca	169797497
tctcaatcca	tctatcagta	aaatacagga	tggaaaggga	cgcccagctc	169797547
tcagtcaagt	gccagcccac	ggccttggac	gccactgatg	tgagcctgtc	169797597
tgggctgggg	cagaaggggc	cagcgtcagg	tcctcagaca	atttcctcct	169797647
ggtagcctgg	cctgaggccc	acccaaccca	gggagccggc	cctggccagt	169797697
tgagccaggt	accacctggg	gccagcaga	gggcagcaca	ggccacaggc	169797747
tggctttttc	taggtgaaat	tttgctacaa	cgtgtagcct	cttgggttcg	169797797
gtgtctcccc	tgtacttctt	tgaggccggg	agaagtcccg	gacattatca	169797847
cagacacctt	gcctcatccc	cagcttctga	ggtctttctg	gactctgtta	169797897
gcatatttca	gagggttact	gcaaaccaga	aacgggactt	tgagcttgtg	169797947
ttccagggca	gaggggccca	gcgcctgtag	gtgcagacag	cgcaccccca	169797997
acacccccga	gtttccgcct	cctcatctgg	agagcggggc	tggacaggat	169798047
ggtttttggg	gcttttttgc	aagctcaccg	gggccaagtg	agctatttcc	169798097
ccttgccatt	ctctcccagg	aggagaaggc	ataagatgat	gctgaaggca	169798147
caggctctgg	aagaggacag	ggccatgctt	attcctgcct	tgttatgtga	169798197
ttatggacaa	gccttcactg	acccttggag	tgatggataa	aatccgtacc	169798247
ccacagggtt	acaggagaag	taagttaggg	accacgtgca	cggagcccag	169798297
caagggtgct	aggaaacaat	gctattgttt	ttcagggtac	atcttgggga	169798347
gaccacccag	aggaccttct	ttcaaggaca	ggtacctgga	atttctctcc	169798397
ctttcctaca	tcatcttctt	gttttcatgc	gcaggggaggc	caccactacc	169798447
tgagccagac	cactcccttc	ttaagccagg	gcctgcaa	tgctgcagca	169798497
ctgccccctc	gatctcaatc	agacaccac	attcctgccc	accatgcccc	169798547
aagcccttca	ttgaccaaga	ccctggcctc	gtcccaatcc	tctgtaaagt	169798597
acacatgogt	cttcaatcca	ccctacagga	ctgtggagcc	gagaagatgt	169798647
ggggctgagc	atttaccttt	ccataagttc	tccagggggg	tctgaggccc	169798697
acagaatcaa	agagccactg	ctctaggcaa	tgagatagta	ttctaaaaca	169798747
attaatgaag	gcccattgat	gggacaggag	agccattatg	caaattccgg	169798797
ccattcgagg	ttattaattt	gcaggagaga	ctgtagacgc	tgggtaaaga	169798847
atgccacaaa	tattaggcag	tcaggaggct	accctgcagg	gcctgttcct	169798897
gctccgcctg	gtgagcagaa	aggtctcagg	gaccagcttt	aaaggatgac	169798947
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gaaggcgatc	gcccattcgg	ctcagtgggt	ctcagtcttg	ggtcagcact	169799047
ggaatcccca	ggagggaaca	cggaaacccc	gagagctggc	tccgccccta	169799097
gagctgacct	cagtaaatct	gagatgaggc	cagagaaatt	gcatttcgac	169799147
aagttcccag	gtgttgcagc	gcagggtgtg	gcatgcatgc	atgcatgtgt	169799197
acttgtgtct	gtgcccgtgc	atgtgtgtgt	tcccctgttt	tctgctttct	169799247
gcagtgtttt	agctcagact	tcctgattgg	ggtcccatcc	ttgaccagag	169799297

FIG. 1.32

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gcccagtcta	gacctagaag	aatactaata	catgcccagc	tgttttagagc	169799347
ccacaagccc	tctcatggcc	cttgtttcca	ggccccataa	cagccccata	169799397
agtttgtttt	aaaagtgcac	ctgtagggga	gaaaagattt	ctttcctcat	169799447
ccatcactag	gttcatggct	gaggcacctg	taacaaaaga	cagactcaca	169799497
agagaaaagc	aaccaagtaa	tttaagtttt	gtgtgacatg	ggagccttga	169799547
gaaatgaaga	cccaaagaaa	cagggacatc	tatgtgattt	tttgccaagt	169799597
ttgatgaaga	agcagataat	tgtggagaag	tataatcgga	aaatgggggt	169799647
atgatttgat	ggtaatgacc	taagtggcat	ttggaaggcc	tgtttcttca	169799697
gattcttctc	tgcgtctctg	catcttcata	gagaaggact	ttccttccct	169799747
gtgggtctag	ggaaggcacc	tcttaaataa	aggtttcatg	accacttga	169799797
gaataaatcc	aggaaattct	tttatggcct	gcttcagggg	agaagggcag	169799847
gagaaggcca	gagagcgacc	ttccttcttc	tgtgggtttc	tcaaatacca	169799897
agggtggcaga	tctgggacag	tgtgtcctga	actccctcac	aaccatggct	169799947
gtctgcaggc	cagtcactca	acggccatga	atgtgtattg	acttgtgaga	169799997
tcctccaaac	aaaccttcaa	atctctgctc	acccccattt	gagagaccag	169800047
agatgagcca	agagacatga	agcaaccttc	ccaagggagc	agagccaaga	169800097
tttgaaccag	ggctgttggg	ccagtgcaga	agggtctgaa	atccagtcca	169800147
gcacagggtat	cttctcagc	aggctcagag	acaggagggtg	gaccggccgg	169800197
agcagaacgg	accctcccct	tcaaagcggg	actctgccct	tgagccctga	169800247
gcagccactc	tggacagggt	ccacagagga	aggcaatcct	ccagcccggc	169800297
atgcttcctc	tgacctcttc	cctctctcag	atggaactgc	aagaagatcc	169800347
caaaccatcc	agggttcccc	tacctctggg	cctttgcaca	gccttcagag	169800397
cagccctgag	gtgatctcct	gggccatcag	cacatgaccg	aacaaacctt	169800447
gggccaccaa	gctccttccc	cggagtgggc	tctgaggcca	atcccccgat	169800497
ttcacaccat	tttaccatcc	ctagccttgg	tccctccaca	gagccccctg	169800547
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catgcagaga	ctcaaggctt	ggaggactgg	ctttatcgag	aggctctgga	169800647
aggctctctg	accccagtg	aatttggctc	tctccgtccc	tccagatggt	169800697
actcaggccc	caaaccttgc	ccagccttgt	tagtggcttc	tccttcccac	169800747
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agcttttctc	gtcagcccct	tgggtcactg	cagacaaggc	tctagtgttc	169800847
aaactctggc	ttgagctcag	agcaggggcc	actctgggct	tgaaaatacc	169800897
tcgtgtgggg	acagcagggc	acactggaga	ggtgaggagg	gtctcctgtc	169800947
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ttgcccacgg	acctgcccag	cttaaagctc	ttgcaaggct	gctcttgacc	169801097
ccagcatgaa	acccaagctc	ctctccatcc	tggctgcaca	ggccccaagc	169801147
cactcgccca	gcccaccagc	ctcaccacac	tcccatagac	ttccccactc	169801197
ttgggtgggg	gtgggagggc	tacacgaagc	tctaaagtca	gcccgtgctc	169801247
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ccctgtatct	gacttcgaca	tgtttcttcc	tccaggaagc	cctccctgat	169801347
gccccattcc	ccctccaagg	actgcccagc	atctggagca	ccctgtaccg	169801397
agcggcacac	tgtgggtgctg	gaaacatcct	tgttgtactc	ctctgtgcct	169801447
ggacactgca	tgtgggcctg	tccatacgcc	accagaccc	ctcgggtacc	169801497
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taagaatctg	ttgggaagaa	aatattccct	ctctatcaac	ttagatccta	169801597
gtggtagggg	ggagggtctac	aatcaactg	acaatggaca	gattcacagg	169801647
agaaaaaac	aatcagttgt	actcacatgc	ctggggaaga	ctgaacagct	169801697
gggaataagg	gcttctatac	ccacttaata	aaccgggtga	actgaatggg	169801747
gttagggctg	ctgtggaggc	ccaggaatca	atcagaagcc	ttcagctttc	169801797
acctcccatc	ccccgttccc	tgaccccatg	ccaccagatg	caaataagaa	169801847
ggaaacttta	attccacaaa	ttgaagcatt	tatgaagctc	agcaggcaac	169801897

FIG. 1.33

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ctggcaggca	ggcaggcaca	agtgaggaac	aagggccccc	ggctgggctg	169801947
ccttccaggc	aggtcccctc	gacacaggcc	actgcagctc	tctcctgcaa	169801997
tgtgtcagga	gagcctggca	caatgtgggg	gacgggggcg	gggggggtgcg	169802047
gagcttgcca	ccacctgggtg	gtctcagctg	ccactccaca	cgtaggaggc	169802097
tggatgcctg	ctggggcaga	aggcggaatc	cagcctgacc	acttagtggg	169802147
gctcatctac	gcaagccttg	ggagcagtgg	caggctgctg	tgagggggcgc	169802197
gctagcctga	ggaaccctca	gcctcagtac	tcttgggtcg	agctgcagga	169802247
gcaggcctgg	caagtcccta	aggcttccag	caacattccc	cttccccagg	169802297
cttggcagtg	ccagcccaca	actcagtcac	gggacaccag	gtgggctcct	169802347
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gagggggatt	agatcctgga	ggagaggccc	atcccttcct	tcatacaacc	169802447
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taagacatag	acacacacac	aaaggtaaga	ccacgtgaag	acacggagaa	169802697
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tttgtttaag	ccgcccagtc	tgtggcacct	tattatatca	gcctgagcaa	169802847
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tttaaaccac	aaatacacag	cgggggtccc	agatcccaga	gcagggtctc	169802947
agttatttca	cagatcacaa	aactgaggat	gctgaggaag	ggggcctccc	169802997
caaggccaca	caacaacttg	gaggaaacac	ggaactgaag	gaaattgatt	169803047
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ttccaggagc	atgaggatgc	tgagactaca	ggactacaga	tggagggtgt	169803147
ttcatggctg	agtgaagggg	tagaagccag	gcgagtatga	cacaggatcc	169803197
ctcttgacag	aattagaaca	cagagatctg	gagttcccat	catgccctca	169803247
ccacagatto	atggtggaaa	cttgggcctc	atctgcttat	ctctgaagtg	169803297
cagaaattta	tagcacctac	ctccaggggag	agttgggggt	taactgagat	169803347
cacgatgtac	aaacctgtaa	gctgtaaggc	aatggaaaag	tggagggtat	169803397
gtccttggtg	gaagcttccg	ctctggacag	catggaggac	ccaggagtca	169803447
ggctgggctg	ctggctcaca	gggtgtctct	ccccctggcc	caatgccctg	169803497
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gtaacaggca	tgaatttttag	tctctgcatg	ctcagggtgtg	taagaaacat	169803647
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cacagatctg	tctaaaatct	aactagtagg	aagcagttag	aacttggtgc	169803847
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tgagaagccc	aggaggcaag	aggcacctgc	agccctagag	cccactgcag	169804147
attttccttg	agggccgtat	atccagaacc	atcccagggc	ttggcttttg	169804197
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aactagctgg	gcatgggtggc	gggcacctgt	agtcctagct	actcgggagg	169804397
ctgaggcagg	agaatggcgt	gaaccagga	ggccgagctt	gcagtgagcc	169804447
aagatcgtgc	cactgcactc	cagcctgggt	gacagagcga	gactccatct	169804497

FIG. 1.34

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caaaaaaaaaa	aaaaaaaaaaaa	aaaaagaatg	aacaactgct	gactactgtt	169804547
tactacaata	agcatagctg	atactctatc	caggaagagg	aagccaccac	169804597
tcagtgcctc	agccaagatt	gttctcaagc	ttttgtccgt	cccaaaccct	169804647
tatgaagcat	cctcaccac	tgacatgtgc	agtacttaag	acgggtgcacc	169804697
ctggagtcaa	atcccagctt	ggccccacat	gagctctgag	gcccttgagg	169804747
agacagcggt	gcaaagaccc	cagggggccga	gtaagcagag	gcctttcaga	169804797
gatcagagaa	aaggccacat	agctgggagc	ctttgtgaaa	ctggagaggt	169804847
catcggggcc	agatcctcag	gggcccagtg	gccctggaaa	ggaatctggt	169804897
cttgtaccta	gaaatggtgg	cattaattat	gtgactttgt	ccaagtctgt	169804947
gtcctattct	gagcttcagt	tttcttgtct	gcaaagggct	ctggaccaaa	169804997
ccatctagga	tccaccctga	ccctgggcct	tcatgtcagg	ttaaggagag	169805047
acagggcctc	gttctgctgt	caggatgagt	ttctccaggg	aaaggccttc	169805097
tagctccgcc	ctgccctgtc	tggctctggg	gaccacgcag	gactctcaag	169805147
acactaggtc	actacactca	ggagtctccc	atctctgcca	agacaatctg	169805197
gagaagacat	cacccacttt	gagtcattag	atgtcctcaa	cagcaccttc	169805247
tagagtgcag	atctttttgc	tgctgtgaga	gaggggctta	tgcagaatga	169805297
tattgtcagt	gtagacatgt	ttcacacaga	ggagaactca	ggacagggga	169805347
caggaatgga	ggcaggaact	cgatctatta	gaacaagttt	tctgatgtgg	169805397
ttatgcatca	gggatgtaga	atcctgtgcc	ttcaggattt	ctgggattaa	169805447
agacaatccc	agaaaacagg	cctggacagg	tcctggaaac	agccccaggc	169805497
ctatttggtg	aggggattct	gggggtcctc	taccagagag	ctggtctaga	169805547
cagaaggagg	gagtgggctc	tgggtgggca	aacccacctt	ggccctttcc	169805597
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tggcttggtg	caccaccgag	gcacagctga	gtgataagtt	gatgagcagc	169805747
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tggaaaccaa	atcaaccttg	ggaaaaggag	gtgcagaggc	caaggtcaaa	169805947
accaattcat	ggaagtggga	agaaagcagg	gctggcctca	accttttcac	169805997
tattagagag	atggccatgt	aaagttagtg	gcctcctgtg	gaaggcatat	169806047
gcaagaacag	gtagaatgat	tatttcttag	gggttttgta	gaaaggattc	169806097
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ctgagttctc	ctctgtgtga	aacatgtcta	gactgacaat	gtcattctgc	169806247
ataagccctt	ctttcacagc	agcaaaaaga	tctgcaccct	agaagggtgt	169806297
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gaaatgggca	ggaagtggaa	ggaagagaaa	gggagtcagg	cccagggcag	169806447
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cctcccaggt	gggtgtaaat	ttgcaaacc	aaatggttaa	gaagatatat	169806547
ctgttaatgt	agaacatttt	gtattttaacc	agtaattgac	ttgattcata	169806597
actttaagta	tgcatagtgt	gtaagtggac	ctcagtatta	gcttcctatt	169806647
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ttcccacttt	aaagccagct	gattgacaac	cttaatccca	tccacaacct	169807047
ctgtgaccct	ctgccatgca	aggtaacata	ctcacaggca	tagggatgag	169807097

FIG. 1.35

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gatgcggatg	tcttttagagg	gccactgttt	tgcctaccac	agcttccatt	169807147
tggattccttg	tcccaacccc	tacaaaagt	aggcatataa	tttgttgaat	169807197
tctgaataaa	atgctaccag	tgtctacaaa	ttatatTTTT	tctTTTTTTa	169807247
aaaaaaaaaa	aaaaccttct	tccccaagtc	tggtttcctt	tagacctcag	169807297
gactaagtac	ctgagaagat	ctgcgggcaa	ggatagttat	gtgattatct	169807347
ggacagaatg	gcatttctga	ttgacattgt	tgcattactt	tggctccaga	169807397
tgcagtggcc	tgagagcaga	aataaaaacc	cctccagctg	cctcagocca	169807447
ccctttgcag	agggagaatt	gagttggggc	cacacgggtg	gaagcactaa	169807497
tcctcagtc	acacaaaccc	tcgctttcca	attattttga	tggaggtcat	169807547
gaaagagcac	tcagctaggc	attattaatc	cattttttca	attcagcaag	169807597
tattgattga	gcagctaccc	tgtgccagtg	aggttggaaa	cacaaggggtg	169807647
atgaacaagg	tacatgtgcc	tggccgtcac	tggccagctc	tgtcactgca	169807697
ggcgggaact	ttccttcctg	tggggcccag	ggttttataa	tcacatgagc	169807747
acctacacat	ccggtacaga	gccccgttaa	gggggcaggg	cctggcctgc	169807797
ctccttcact	gttgtctcca	attgcctcag	atgcatgtgg	atgctcattc	169807847
gttgaatgaa	tgaatgaata	gatggtcctt	gctgatcgga	gagtcaatga	169807897
ctgtatcagg	ccaactggaa	aagcagaggg	caagccaaga	gaagacttgg	169807947
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ggattcctgg	ggtggcagct	actgtttaca	aagcactttg	ctgggtattta	169808047
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tgcaaataaa	gaaactgagg	tactgggata	aaacttgctg	aagaccacat	169808147
ggctagtaag	tgtcagagct	tggatgtgaa	cctgaatgct	cgctgaggag	169808197
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ttcatccggc	aacaattaac	ctctcccttc	tcactatccc	ccgctccctt	169808297
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gccatactac	cgagggttaa	gaagggtgaa	gggctgcatt	gggcaacatt	169808397
gttccttcaa	tcctaactct	ttaatcctaa	ttcatcactg	cacactctgc	169808447
tccttccctt	gggtgaagac	agtttgattt	gccagctatc	cagaaagttt	169808497
gtgctaagac	aagggaaatt	gccacatggc	tctctgtttc	attcagtcct	169808547
tcataagcat	gcagcctgac	ctggagaaac	tgacagtgtg	aaatgcatgg	169808597
agcagctcct	gtccctctct	ttcctaccct	tgagcactct	ctaagcagta	169808647
gctggccgat	acagtgcgcc	aggaagtctc	cctgtagctc	ggccgtcagt	169808697
cattaccctc	actggcagca	cgggacagag	aacgggatat	gttctccctt	169808747
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ttctgaaggt	tgtgtctatt	gagtgtgca	gtgagactgg	gtttgaaggt	169808847
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cccacttcta	tcttctcccc	agttctaggt	gaggcaggac	ctgccacatg	169809347
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gatatctctc	ccatttgatg	tttcaccccc	ttgaagctca	ggtgaatctc	169809597
catcttctta	ttcatctgaa	tattcctcat	gcctggcatc	acgcctcact	169809647
catagagtag	gaattcaaaa	acatccagct	aggagctggg	aaagctccta	169809697

FIG. 1.36

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ctgcatgtct	tgtacatctg	ctgtatgcc	gctgggaaa	ctcctactgc	169809747
aagagagagg	caaaccacaa	aggggactaa	ggggaagaat	tgggaggggg	169809797
gcattttattg	ccccaaatga	ctgaatttgg	gtcaaataac	aggaccacgg	169809847
gcactcacat	gttcaagtta	tgttcaggaa	tcttcctgtt	ttctttatga	169809897
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acagggccag	tttcgtcatg	ttatttcaag	gggtgtctct	ggcccgtagc	169810247
ctctgaattt	atttttagttt	ctcagagatt	tcagtgggcc	aacgaatgtc	169810297
acttaatcga	tcccttttct	gcttggagga	gccagactcc	gtgtttgttg	169810347
cttacaatatg	agaccttgac	tgagacaagt	tgtcttgagt	ttccagttga	169810397
agtcattccta	ttccctttca	ccttgaggcc	tttgccatg	tcatttctct	169810447
cacctggagc	aggcattcac	cctctttttg	tgactggatg	actcctaccc	169810497
agtcattccaa	gggtcaggct	tgaagactct	tcccctgaga	agccctccca	169810547
gatcacccca	aatctgggct	cccacaccac	cctgcatgtt	cctcttagta	169810597
gcattcctgac	cctggatttt	actgtttatt	tctgtgtttc	ctcactattc	169810647
tgtgagctgc	atgaggacag	aagtgcattc	atttcattcat	tgttagtagt	169810697
agttagtata	gttgcccagc	ctattgatat	tgttgaatga	gtggatggat	169810747
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cccaaaatag	agttgcctca	tttcacttct	accagcatgt	cttgtagatc	169810897
tgctgtacgc	caggccccgt	gtcctcttac	gccacatcc	cagatcctgc	169810947
aggtagaagt	gtcacattg	ctgtgctccc	ttttctctga	ccagccatgg	169810997
aggccctggg	ggcttggagg	agtggctgct	tactccctgg	gggaagtgtg	169811047
ggctgcaagc	cccttgagtg	ggcaggttgc	catggtgatg	ctaattggaga	169811097
gacttgccctg	aggaatactg	accacccaaa	ggaacaatta	ccagagaagg	169811147
cccatttctt	tagcaatttt	caagaatggg	caagataaaa	agccacaagt	169811197
gaaaaggcat	tgcaaacaaa	taatagtgtg	tgagctggtc	tggacccaac	169811247
aaggcctgtt	tcccacccct	ctttccctct	ggttgtagt	aataaagcca	169811297
tacttttcag	tgatttataa	ctgttcaaaa	atgactcgtt	tccatatctt	169811347
ctttcatcta	cccagcaccc	attatgtacc	aaatgcctaa	cagacactta	169811397
aaataactc	tataattatg	aaaacaacc	tacaaggtaa	ttgttcccgt	169811447
attacagatg	agaacactga	ggctcaggga	gtgtaaggga	cccgtctagg	169811497
gtaacgcagc	tgggaagcac	atgcagcact	ctacttcatg	cttaattcaa	169811547
ggaagcgaat	tctccttgtg	ggtaaacatc	atcacagtgg	caattccagt	169811597
gcctccataa	gaaagtgtcc	ttggaaatga	gacactagcc	ctctcctgtc	169811647
tcatctgcac	aatatcctat	tgccatctat	ttagaagaga	ggtagtgagt	169811697
tggttcattc	attcattctc	catttgttca	ttcatacaca	tttattacac	169811747
tcaaacttct	agggcaaaac	cagcaagccc	cgtactggac	acttcagact	169811797
caaagatagc	aacttgctaa	gttacaggag	cttcctcata	attgctgagc	169811847
ttctaagctc	tttgtcccaa	ctcctgaaaa	gtagccctca	acttccaaac	169811897
tgtgcttcgg	gcactgacat	tccctgagct	ccacacaccc	ttggaccaca	169811947
gttttctgag	gccagatga	gcacaatgtg	cagggcagag	cctggcactt	169811997
ccagggctcc	aaggagtcca	gagggaaatc	gggcagggtc	tgaatcaggc	169812047
tgctgtaggt	tgaactcctg	ccccacttag	cagctggatg	atgtgcaaat	169812097
tgctcagcct	ctctgtgctt	cagtttctct	acctataacc	tagggctaaa	169812147
aattagaagc	acctactcca	tacagctatt	gtgctgatac	aatacaataa	169812197
tccacataag	gaacttagaa	cagaacagtg	ccggcggtgt	atgttaaagt	169812247
ctgagtggac	accagttggg	attagaagta	gcagcattgc	caggtactcc	169812297

FIG. 1.37

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tgagcaatgg	gtcagctaata	tccactctac	cctcagaccc	caccctcctt	169812347
tgagttcct	tctcctgctt	tgataactag	aagcagtcac	atagggcctg	169812397
gggtctctac	ttgtaggagt	tcagtcaggg	tggtaggaaa	aattataaaa	169812447
attatagaaa	gactcaaacc	ttcttggaag	gccgggaggt	tttgcaaaag	169812497
ttttgggaaa	ggatttgggt	gaaggcagct	gaattttctc	agagtaaata	169812547
acaaggaagt	gtaagggaat	taatctagat	aagttagttt	acttaggcct	169812597
tgaaacatgg	cctttaataca	tccatgctca	ggactgctct	cttgggggaa	169812647
aggatcgccc	gacccccccac	cccaccctca	ccccaccccc	tgccaccatg	169812697
ttaattaccc	acaagtgtgt	tgactcaaag	cctttgtcat	taaattctgta	169812747
ctgaatatat	gccacacagca	ccagcttgct	aaggctgcag	ctgctgactc	169812797
tttacagcac	cctcctcggt	gcctgtgagt	ggcccagtc	cttagccgtg	169812847
cagccaggca	aaaaatctgt	gtctgcatac	attttttcat	ccatcactca	169812897
gccagggtct	gcggttggga	ccccgcattc	actcacaat	caagatgttc	169812947
agttccgcc	ccccccctg	tctgtcttcc	tttctcacag	tcactctgta	169812997
ggtgtatcct	gaaaatgtaa	atcagaccac	agcattccct	agctgaaaac	169813047
ccttccgtgg	ctccctatta	ctcaccatag	gctaaattcc	gccagactc	169813097
ctctgaaggg	cttgcaaggc	ctcctgtgtt	ctagctcctg	cctgctatcc	169813147
accacacccc	ctcattcctg	cccctgtaaa	ccccttgtag	ctctcacatc	169813197
tcaagaatta	aagatttgac	ccagttgctc	cgaccacctc	cgccccgatc	169813247
cccagaaaca	gtttccccct	tctctttctc	tggccaactt	ctatcggttt	169813297
tcagaatgtc	tcccctggcc	acgcaggatc	ccttccattt	tgaggctgat	169813347
aaaatcctgc	ggatcgcaag	ctgagcgctc	atcacacccc	atcgtgatta	169813397
tctcccctgc	aaggccaggg	gctttgagag	gggtgggactg	tggctgacac	169813447
gttcagtgct	ccagtcctcat	cacctgacac	ttgccataga	gaagggtgctt	169813497
agtatttaga	agagtgtgtg	cgattaccga	gagcatggat	atgaagaagg	169813547
ggatcacaac	cttgaaaaag	ttgtttgctg	agaaagaggc	aagcagcccc	169813597
aactgacggg	agctggcctg	gtcctcacag	tttgtctcct	gttgaacaat	169813647
ttcacagaac	attgacatca	gacaaggcta	ttctgactgt	gttggagcaa	169813697
gacaaaatcg	agagcacttc	gtagtcatgt	ctaaacgcag	ataaaacaag	169813747
aacattgtct	aaaccacaaa	aatgaccaga	catcccgcct	ttttgggcta	169813797
atgggagtaa	ctgtttacca	atgtttataa	tggtggccct	gcactagtcc	169813847
ttctacctta	tagataagat	tataggtacc	caattataga	atgattccta	169813897
ctgcctgatg	gcattccaatt	gaaccctccc	tagtcactta	acacaagccc	169813947
ccatcctttt	gtaagttctt	cgtaacaccc	tctcacaag	acccctcact	169813997
gttccccaca	gtgcacaatc	tccttgctgc	aatgagccaa	taaaccagc	169814047
tccgttcaac	tgcaggtgtg	ttcctggctc	ttggctaaag	ggcattgaca	169814097
ccaccatttt	cccagaaaacc	tgaacttgca	aaaaaaaaaa	aataccta	169814147
taaacaattt	ctgcaagcta	attgatagt	agaaatgtat	ttctgatagg	169814197
gagcatcagc	tggagtagac	aactttgtac	atactatatg	ttttccggac	169814247
agttgcttca	gcttctcctg	cattgtgtgt	gtgtgtgtgt	gtgtgtgtgt	169814297
ctgtgtgtgt	gtgtgtgtgt	ttgcaggggg	aagatgcaag	ccttgctgtc	169814347
ctgggtgtcc	gtgactgggc	atgtctcatc	tggaaagaga	tcagctaata	169814397
ttccttgaga	aaaagaatgt	tatcactgga	tgattacatc	tgcttccaga	169814447
gaggtaagag	catgcagcat	ggagcagaca	ctctctatcc	caggagctgc	169814497
cctgcccagg	cctgggctgg	tggctattgt	catggagtgg	taactgtaag	169814547
gccatcctca	taagtccctg	tgatatcact	ccaatccatg	gacacccctg	169814597
tgactccgtc	tccattcctc	aggcctgctt	cccattggaa	gacccagagg	169814647
gaaacgtggg	tgggtggcatt	ggggactgag	aacagaacaa	aattcaggct	169814697
ttgagtgtgg	attagagacg	cactgtgtgt	tgcttgcatc	acctctgaca	169814747
gtggttgggt	aatgggctga	atcacccaat	ggagacagaa	tgccaacaga	169814797
tggttagttga	ggaggatgat	taatctcctt	cttcgaaaac	tcagagaatc	169814847
tttattggca	acgttgaagt	caagataggg	cttctcctta	gcaaccggaa	169814897

FIG. 1.38

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agcgcctagtg	gtgcatggct	acagaattca	atatgaaact	cagatgatga	169814947
aggtagccat	gggcacctct	gattgcccac	tgtaaatttc	tgcctggaat	169814997
gagggtctggg	gcctcataaa	tgtcaacaaa	agctggtgat	gggtccagag	169815047
agggatgtta	ggccagcctt	gatggatgag	gaagtttcat	ttaggggctc	169815097
ctgtcacttc	ccatcttcag	gccaaagtga	catccatggc	tgtaaaattg	169815147
tcaccccttct	cctttgcctc	tcaggaaagc	aaaacttctt	tacgacactt	169815197
ttaatcaaat	ctgtcttttg	ccacttctct	ccccacctg	ctccctctgc	169815247
cctttatcctg	acaaagaagc	gaactgttac	tctctgtcag	ttattttgtct	169815297
gagtaatttc	ttgatgaaat	tgcaactata	attgaatttt	ctgaaaacca	169815347
ggaattcaaa	tgaggcgaca	acagaggaaa	cagcgtgatt	aaggaattgt	169815397
tattcactcg	ttgtacatca	ttaccaccca	gaattcatcg	ctggatcggt	169815447
cacagatgga	gttgctgaac	tatgattata	ttttagaaaa	tgaaggggga	169815497
aaaatctaaa	aaggcaataa	aacatattag	aagccttctt	gaggaacagg	169815547
attattactg	attaagtata	ttttgcatga	aaaatgtgct	agcactttgg	169815597
cagtttaaat	tatacgtccg	tgcaagtcaac	atttttgtctg	gtctcaaaat	169815647
tctttgttag	tttggtcttc	taatcacatt	cctcttcacc	ctccaaattg	169815697
acgacttgaa	agaacattag	aaatgatcat	tcctgaagga	gcatttgctc	169815747
tcaaaatgca	tttacgtcca	gcagccatta	aaaggatatc	atccagtcac	169815797
ttagtttctc	aatttaactt	taaaggaaaag	ttgccttatt	agagaagtgg	169815847
cctctatttc	aatgtaatgg	tctttgtcac	atcttccaat	gtgctggctt	169815897
agtgtgaag	gatgggggaaa	ggcagttttc	acatattgca	gccaccatac	169815947
caccaaagaa	aacaggtgca	cttccaggca	tcatttagcg	gggtaccaca	169815997
ttcctgggtc	cagttttcctt	tttagaaaaat	ctgaaagtaa	cctttggggca	169816047
tatcttttaa	ggagtactcc	aacacgacta	gtggacagac	cctaaattaa	169816097
ttgccaatca	gctctgcctt	ctgggtattta	cacctttatg	taataacctc	169816147
cacttgaagg	tagatgagat	ctgtgacttg	cctctaacca	gtggaatatg	169816197
goggaggtgg	tgggacgtta	ctcctgtgat	tacattacat	catgtggctc	169816247
cctttatgatg	gaagattcat	gctagagatt	ctccttgctg	acttgacaaa	169816297
gtatgtaacc	atgatgaaga	cttccacgtg	gcaaggagct	gtgggaagcc	169816347
cagggtgctga	gactggcatc	cagcaaacac	ccagcaagaa	acagacgtcc	169816397
ttgggttctac	acatacagga	aatgaattct	gccaacatcc	tgagtaaggc	169816447
tggaaactaga	ttctcccca	gttgagcctg	acaagtaaaa	tacagaccag	169816497
ccaacacctt	gattgcagtc	ttgtgagacc	tggggaaaag	gacacagctg	169816547
aaccgtgtcc	attcttctga	cccacagaaa	ctgtcacatc	ataaaggtat	169816597
gttagttggt	acacagttta	gaaaactatt	acagctgctc	aagaaggtta	169816647
gctagctcca	gatttcaatc	cattcacagg	aaagcaagct	ttattcctag	169816697
aagaataatt	catgctttgc	aaaaagagga	aaacgtcctg	cagttttaga	169816747
aggctttttc	tttctcaaca	cacccaaatt	tctttaaaat	cctcaagaag	169816797
tgcatttggt	ttcatgggtg	actcgaagaa	gtgagtataa	ttaaactaca	169816847
aaaggtggga	ggaagggaca	aattaaattt	tggtatgcat	acaggtagct	169816897
tcttccaagt	gataatgagc	aatgtgaaac	aaagagattg	gcattaaatg	169816947
taatgaagga	ctagaggagt	gtacctaacc	ctgaaacaaa	ttccaagaag	169816997
tggccttgac	ctaaaatggt	tgcactcctg	cagagaccct	tacttataag	169817047
tcaggagata	cctgatgccc	aggagaactg	gtttttgtac	tctgtcttac	169817097
acagactaag	aattaagaat	gcaggtgaga	agtttagaaa	acttcctgat	169817147
gatcatatga	aaagacatta	aactttacct	ggtaaaacta	tgaaatgttg	169817197
cctgtagatt	tctaagaaaa	atgagtagga	agttggaaat	atttcagaat	169817247
taagaatggt	tttatataat	tagaactcct	taagctatgt	aattctgaaa	169817297
tctgtgtgac	agacttctgt	gtaaacataa	agaactagtt	atttttacag	169817347
attatctagt	ctgtgtattc	atttgatggt	tctattactt	ttaccctcac	169817397
tacaaagtcc	aatgaagggt	aaaaaaatat	tgttcttaaa	aaaagaagag	169817447
ataaacctgg	agtagctatt	tcaatgttag	acaaaatgga	ttttaaaaca	169817497

FIG. 1.39

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aaaatgttaa	tacagataga	aagggacatt	ttataataat	aaaagtatca	169817547
aaatatcagg	aagataccac	aattataaac	aaatatgctc	ctaaaaatag	169817597
aatctcaaaa	tacataaaac	aaaaactgac	aaagttgaag	ggataaataa	169817647
ataggcagct	cagcaatatt	tagaaacttc	aatacctcac	tttcaataat	169817697
ggatagaaca	actagacata	agatcaacaa	gaaaatagaa	tatttttaaca	169817747
aagctataca	ccaactaggc	ctaattggata	tctatagaat	aatccaccca	169817797
acaacagaag	tcttcctcct	cctactttctc	ctcctcctcc	ccttccccctt	169817847
ccccctcccc	ttctttcttct	tccttcttctt	ctttctcctt	ctccttcttct	169817897
ttcttcttca	acaggatctt	actctgttgc	ccaggctaga	gtgcagtggg	169817947
gtgatcatgg	ctcactgcag	cctcaacttc	ccaggctcag	gtgatacatg	169817997
ggcctcagct	tcccaaagtg	ctgggattat	aggcacaagc	cacatgcctg	169818047
gcccacatat	tcttctttaag	tacacatcaa	acattctgta	gaatagacca	169818097
tatgctaggc	cacaaaacaa	gcttcgataa	tttaaaagga	ctgaaattat	169818147
acacaatctg	ttccttggcc	acaaagaata	aaattagaaa	gaacttttgg	169818197
aaactcacaa	ctatatagaa	attaacatac	ccataagtaa	ccaattgggt	169818247
gaagaagaaa	tcacaaaata	aatgagaaaa	tactttgaga	tgaatgaaaa	169818297
ttaagacaca	acataataaa	atttatgcaa	tatagctaaa	gcaatgctta	169818347
gagggaat	tatagctcca	catacctaca	ttaaaaatgg	agaaagttac	169818397
actgttgggtg	ggactgtaaa	ttagtccaac	cactgtggaa	gacaatatgg	169818447
cgattcctca	aggatctaga	accagaaata	ccatttgacc	cagcaatccc	169818497
attactgggt	atacacccaa	aggattataa	atcattctac	tataaagaca	169818547
catgcataca	tatatattat	gaggcactat	ttccaatggc	aaagacttgg	169818597
aaccaaccca	aatgcccac	aatgatagac	tggacaaaaga	aaatgtggca	169818647
catatacacc	atggaatact	atgcagccat	aaaaaagaat	gagtttatgt	169818697
cctttgcagg	gacatagatg	aagctggaag	ccatcattct	cagcaaactg	169818747
acacaggaac	agataaaacaa	acaccacata	ttctcactca	taagtgggag	169818797
ttgaacaatg	agtacacatg	gacacagggg	ggggaacatc	acacaccggg	169818847
gcctgtcgga	gggtgggggg	caagtggagg	gagagcatta	ggacaaatac	169818897
ctcatgcata	tgggggttta	aacctagatg	acagggtgat	aggtgcagca	169818947
aaccaccatg	gcacatgtat	acctgtgtaa	caaacctgca	cattctgcac	169818997
atgtatcccc	aaacttagag	taaaattttt	ttaaaaaaag	aaaaaacatc	169819047
tcatatcaat	aagctagact	tctatcttaa	gacgctaggg	gaaaagcagc	169819097
aaactaatcc	taaagcaagc	agaaggaaga	caataatgaa	agtggaaatt	169819147
aatgaaattg	aggacagaaa	aacaatagag	aatatcactg	aaacccaaaa	169819197
gtggttcttg	ttttctttct	ttctctttct	ttctttctct	ctctctctct	169819247
ttttctttct	ttctttcttt	ctttcttgtt	tcttttgaga	caaggtctag	169819297
ctctgtcact	caggctggag	tgcagtgggt	caatcacagc	tactgcagc	169819347
ctcgatctcc	tggacttaag	tgatcctcct	acctcagact	ctcgagtgc	169819397
tgaaccaca	ggagtgcacc	accatgtcca	gctaattgtt	tcaatttttt	169819447
gtagagatga	ggtttcccta	tgttgcccag	gctgggtctca	aattcctagg	169819497
ctcaagcgat	cctcctgcct	cagcctctca	aaatgctgag	ccaccacacc	169819547
cagctgggta	tttcaaaaga	tgagcaaaaag	tgacaagctt	ttagctaaac	169819597
tgaccaagaa	aaaaagaata	cttaaattac	cataatcagg	aaagaatgag	169819647
agaacattac	taccaacctc	atagatacaa	aaagtataga	ggaatacaac	169819697
aagccaattg	atatgccaac	aaattaaatt	acaaatgaaa	tggacaaatt	169819747
cttagaaaaga	cacaaactac	aaaaactgac	tcaagtagaa	atagaaaatc	169819797
taaataggta	tttaaaaaag	attattaaac	tgagagctga	agacagggca	169819847
gcaaaactgc	agggggccacc	accaccacca	ccacatgtca	ggaagagtac	169819897
ggagaggccc	tggaggggca	taacgactgc	aggaataaat	taggagagcc	169819947
aagagaaccc	acagaccctc	tgaaggaagt	ggattgctcc	tgcaggacct	169819997
gggagacacc	tcaataactg	tgctggtatc	tgtggctgag	aaacccacag	169820047
atgggttgca	tcacaggact	ctgtacagac	aacccccagt	accagcctgg	169820097

FIG. 1.40

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aacctggtag	acatcctggg	tggctagatc	cagaagagag	ataacaatca	169820147
ctacagctcg	gctctcagga	agccacatcc	ctaggaaaag	ggggagagta	169820197
atacatcaag	ggaacacccc	atgggacaaa	agaatctgaa	caacagcctc	169820247
gagccctagg	ccttccatct	gacagacact	acacaaatga	ggaggaacca	169820297
gaaacccaac	tctagtaata	tgacaaaaca	aggttcctta	atacccccca	169820347
aaaaatcaca	ctaggtcacc	agcaatggat	gcaaaccaag	aagaaatccc	169820397
tgtttcacct	gaaaaagaat	tcagaagggt	agttattaag	ctaatacagga	169820447
aggcaccagt	gaaaggcaaa	gtccaactta	aggaaatcaa	aaaaatgata	169820497
caacagggtga	agggagagat	tttcaatgaa	atagatagca	taaataaaaa	169820547
acaatcaaaa	cttcaggaaa	caatggacac	agttatagaa	atgcaaaagg	169820597
ctctggaaac	tctcagcaat	agaattgaac	acgctgaaga	aagaacttca	169820647
gagctcaaag	acaagggttt	agaatgaacc	caatccaaaa	aagacaaagg	169820697
aaaaattata	agaaaatatg	aacaaagcct	ccaataagtc	tgggattata	169820747
ttaaattggcc	aaacctaaga	ataattggca	ttcctgagga	agaagagaaa	169820797
tctaaaagtt	tggaaaacat	attcggggga	ataatcaagg	aaaactcccc	169820847
cagccttgct	agagccctag	acatccaaat	acaagaggct	caaagaacac	169820897
ctgggaaatt	cattgcaaaa	agatcattac	ttagacacat	tgtcatcagg	169820947
ttatctaaag	ttaagatgaa	ggaaagaatc	ttaagagctg	tgaggcaaaa	169820997
gcaccaggta	atctataaag	ggaaacctat	cagattaaca	gcagatttct	169821047
cagccaaaac	cctacaagct	agaagggatt	ggggccctat	cttcagcctc	169821097
cttaaacaaa	acaattatca	gccaaagaatt	ttgtagccag	tgaaactaag	169821147
ctttataaat	gaaggaaaga	tacagtcttt	ttcagataaa	caaatagctga	169821197
gagaattcac	cactaccaag	tcagcactac	aagaactact	aaaaggagct	169821247
ctaaaccttc	aatcaaatcc	tggaaacaca	tcaaaacaga	acgtctttta	169821297
ggcataaatc	tcacagaaac	tataaaacaa	aaatacaatt	aagacaacaa	169821347
caaaaaacaa	ggtatacgga	caacaaatag	catgaagaat	gtaatggtac	169821397
ctcacacctc	aatactaaca	ttgaatgtaa	atggcctaca	tgctccactt	169821447
aaaagataca	gaattgcaga	atggcctaaga	attcaccaac	cagctatctg	169821497
ctgccttcaa	gagactcacc	taacacataa	ggacacaaat	aaacttaagg	169821547
ttaaggggtg	gaaaagacat	tctatgcaaa	tggagtaact	attcttatat	169821597
cagacaaaac	aaattttaga	gcaacagcag	ttaaaaaaga	caaagaggga	169821647
cattatataa	tgataaaaag	ccttgaccac	caagaaaata	tcacaatcct	169821697
aaatataat	gcacctaaac	ctgaagctcc	ttaattttata	aaacaattac	169821747
taatagacct	aagaaatgag	atagacggca	acacagtaac	agagggggac	169821797
ttcaatactc	cactgacagc	actagacagg	tcacgaagac	agaaagtcaa	169821847
caaagaacaa	tggattttaa	gtatatcctg	gaacaaatgg	acttaacaga	169821897
tatttataga	acattctatc	aaacaactgt	ggaatataca	ttctattcaa	169821947
ctgcatatgg	aactttctcc	aagatagacc	atatgatagg	tcacaaaatg	169821997
agccttgata	aattttaagaa	aattgaaatt	atatcaagca	ctctgttaga	169822047
ccacagtggg	ataaaaactgg	aaattaaggc	caaaaggact	ttctaaatca	169822097
tgcaaatata	tggaaatttaa	ataacctgct	cctgaatatc	actgggtcaa	169822147
aatgaaatc	aaaatgcaaa	tttaaaaatt	attcaaactg	aatgacagta	169822197
ctgacacaa	ctatcaaaac	ctctgggatc	cagcaaaggg	gatgctaaga	169822247
ggaaagtcca	tagccctaaa	ggcctacatt	gaaaagtctg	aaagagcaca	169822297
aatagataat	ctaaagtcac	acctcaagga	actagagaaa	caagaacaaa	169822347
ccaaacccaa	attcagcaga	agaaaggaaa	taaccaagat	cagagcagaa	169822397
ctaaatgaaa	ttgaaacaaa	aaaattacaa	aagataaatg	aaacaaatag	169822447
ctgattcttt	gaaaagataa	atacgattga	tagaccatta	gcaagattaa	169822497
ccaagatagg	aagagagaaa	atccaaataa	gctcaattag	aatgaaatg	169822547
ggagacattg	caactgaaaa	ccacagaaat	acaagagaac	attcaaggct	169822597
actctgaaca	cctttatgtg	cataaacttg	aaaacctaaa	ggagatggat	169822647
aaattcctgg	atagatacaa	ccctccttgc	ttaaatcagg	gagaattcga	169822697

FIG. 1.41

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taccatgaac	agaccaataa	caagcagtg	gattgaaatg	gtaattaaaa	169822747
aattaccaat	aaaaaagtcc	aggaccaggt	ggattcatac	cagaattcta	169822797
ccagacattc	aaagaagaaa	tggtaccaat	cctactgaca	ctattccaca	169822847
agatagagaa	agaaggaaac	ctccctaaat	catoctagga	agccagtgct	169822897
atcctaatac	caaaaccagg	aaaggacaca	accaaaaaag	aaaactacag	169822947
accaatatcc	ctgatgaaca	tagatgcaaa	aaatccttaa	caaaatgcta	169822997
gctaaccgaa	tccaacaaca	tatcaaaaag	ataatccacc	atgatcaagt	169823047
gagtttaata	ccagggatgc	agggagggtt	taacatatgc	aaagtcaata	169823097
aatgtgatac	accacataaa	cataattaaa	aacaaaaatc	acaggatcat	169823147
ctcaatagat	gcagaaaaag	cattcaacaa	aatccagcac	gcttctatga	169823197
ttaaaactct	cagcaaaatt	ggcacacaag	ggacatacct	cagtgtataa	169823247
aaagtcattc	atgacaaacc	cacagcctac	ataatactga	gaactggaac	169823297
aaagatgccc	agtctcacca	ctcttcttca	acctagtaat	ggaagtccca	169823347
gccagagcaa	taagacaaga	gaaagaaata	aaaggcatcc	aaatcagtaa	169823397
agaggaagtc	aaactgtcac	tgtttgctga	tgatattatt	gtttacctag	169823447
aaaaacctaa	agatgcctcc	agaaagctcc	tagaactgat	caaagaattc	169823497
agcaaagttt	tgaatacaaa	attaatgtac	acaaatcagt	agctcttcta	169823547
tccaccaact	gcaaccaagc	tgagaatcaa	atcaagaact	caacctcttt	169823597
tacaatagct	gcaaaaaaaaa	taaaataaaa	tacttaggaa	tatacctaac	169823647
caaggagatg	aaagacctct	acaaggaaga	ctacaaaaca	ctgctgaaag	169823697
aatcataga	tgacacagac	aatggaaac	acatccaatg	ctcatgtatg	169823747
ggtagattaa	atattgtgaa	aatgacaata	ctaccaaag	caatctacaa	169823797
attcagtgca	attccatcaa	aatactacta	tcattcttca	cagaattaga	169823847
aaaaaacagt	cttaaaattc	acatggaagc	aaaaaagagc	ccacatagcc	169823897
aaagcaagac	taagcaaaaa	gaacaaatct	ggaggcatca	cattacctga	169823947
tttcaaacta	tactataagg	ccatagtcac	ccaaacagca	tggtactggt	169823997
ataaaaaatag	gcacataggg	ttgggtgcag	tggtcacac	ctgtaatccc	169824047
agcactttgg	gagaccgagg	caggcggatc	acaaagtcag	gagattgaga	169824097
ccatcctggc	taacatggta	aaactccgtc	tctaactaaa	atacaaaaaa	169824147
ttagccagggt	gtgggtggcag	acgcctgtac	tcccagctac	tcgggagggt	169824197
gaggcaggag	aatggcatga	acccgggagg	cagagcttgc	agtgagctga	169824247
gatagagcca	ctgcactcca	gccggggcga	caaaacgaga	ctccatctca	169824297
aaaaaaaaaa	aaggcaaata	gaccaatgga	acagaagaga	gaacgcagaa	169824347
ataaaaccga	acgcttacag	caaactgatc	tttgacaaag	caaacaaaaa	169824397
catatagtg	ggaaaggaca	cctcattcaa	ggaatagtgc	tgggataatt	169824447
ggcaagccac	atgtaggaga	atgaaactgg	atcctcatct	ctcaccttat	169824497
acaaaaatca	actcaagatg	gatcaagggc	ttaaactctaa	gacctgaaac	169824547
tataaaaaatt	ctagaagata	acattggaaa	accccttcta	gacattcgct	169824597
taggcaagga	tttcataacc	aagaaccaaa	agcaaatgca	ataaaaaaca	169824647
agataaatag	ctgggactta	attaaaactaa	agagcttttg	cacagcaaaa	169824697
tgaacagtca	gcagagttaa	cagacaaccc	agagagtggg	agaaaatcct	169824747
cacaatctat	acatctgacc	aaggactaat	atccagaatc	tacaacaaac	169824797
tcaaacaaat	tagcaaaaaa	aaaaaaaaaa	aaaaactacc	aaaaaaaaatc	169824847
atcaaaaatt	gggctaagga	catgaataga	caattctcaa	aagaagatat	169824897
acaaatggcc	aagaaaaata	tgaaaaaatg	ttcaacatca	ctaatgatca	169824947
gggaaatgaa	aatcaaaacc	acaatgtgat	accacctcac	tcttgcaagg	169824997
atggccataa	taaaaaaatc	aaaaaataat	agacactggc	atggatgtgg	169825047
tgaacaggga	acacttctac	actgctgggtg	aaaatgtaaa	actagtacaa	169825097
ccactatgga	aaacagtgtg	gagattcctt	aaagtactaa	aagtagaact	169825147
accattttgat	ccagcaatcc	cactactggg	tgtctaccca	gaggaaaaga	169825197
agtcattata	cgaaaaagat	acttgcacac	acatattttac	agcagcacaa	169825247
ttcgcaattg	taaaaacgtg	gaaccagccc	aaatgcacat	aaagcaacga	169825297

FIG. 1.42

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gtggatatat	atatatatata	atggaatact	actcagccaa	aaaaaggaat	169825347
gaattagtg	cattcacagc	aacctggatg	agattggaga	ctattattct	169825397
aagtgaagta	actcagcaat	ggaaaatcaa	tcatcatatg	ttctcattca	169825447
taagtgggag	ctaaactatg	aggatgcaaa	ggcataagag	tgacacagtg	169825497
gactttgggg	actcaggggg	agaggggtggg	gagtggatga	gggataaaag	169825547
accacaaata	tggtgcagta	tatactgctc	gggtgatggg	tgacacaaaa	169825597
tctcacaaat	caccacaaaa	ggactcactc	atgtaacaaa	acatcacctg	169825647
ttccccaata	acctatgaaa	ataaaaaaaa	taaaaataaa	atttttaaac	169825697
taccaaataa	caaagaaatt	gaatttgtca	ttttaaaact	tcccacaaag	169825747
aacagcttaa	gccagacag	cttcactggg	gaattataca	gaatatttaa	169825797
attaaagaat	taatgtcaat	tcttcacaaa	gtcttctaaa	atgtagaaga	169825847
agaggggaca	ttttccattt	catttttgtga	ggccagtatt	atcccattac	169825897
caaaccatac	aaagccacta	caaagaaaac	tacagaccaa	tactgcttat	169825947
gaatataaac	ataaaaatcc	tcaacaaaat	actagtaaac	tgaatccagc	169825997
agtctgttaa	aaagactaac	accatgacca	aataggattt	atcaaaggaa	169826047
tgcaaagttg	gtttaacatt	tgaaaattaa	ttaatataat	acataattca	169826097
atagaaaaga	gaaaaaaaca	catgatcatc	ttattagaca	cagaaaaatc	169826147
atttaacaaa	atccaaactg	acgtcatgat	aaaaacactc	aacaaactag	169826197
aaatagagtg	gaactttctc	aatgtgataa	aggacatcta	ccaaaaatcc	169826247
acagctaata	tgataaataa	tggtaaaaga	ctgaatgttt	ttcctctaag	169826297
atcaggaaaa	atacaaggat	gtctgctctc	agcactttta	ttaaatattg	169826347
tactggaagt	tctagccaga	acaattaggc	aaggaaatga	aataaaatga	169826397
actcaaattg	gaaaggaaga	aataaaaacta	tttcoggatg	ataccacctt	169826447
atatagagac	aatccataat	aatccattat	tagaattatc	agaactaatt	169826497
aacaagatca	gcaagggttac	aggatataaa	attaaaattc	ctatacacta	169826547
gtaatgaata	atccaaaaat	aaaattcaaa	aaacaatccc	acttacaata	169826597
gcatcaagaa	aataaaaatcc	ttatgaataa	atttaacaga	agtctaaaac	169826647
ttatatatac	tctaaacacg	acaaaatatc	attgaaataa	attaaagatg	169826697
gaaataaatg	caaagacatc	catgttcatg	atcagaagac	ttatattggt	169826747
aagatggcaa	tacttaatat	tataaagtga	tttacaatt	gatttatagg	169826797
ttcaaagtga	ttcgatgcaa	tctctgtcaa	agtttcatag	cattttttgc	169826847
agttatttat	actgcaaagt	gatttacaga	tttaatgcaa	cccgtgtcaa	169826897
aatccccatg	ccatttttgc	agaaatggaa	aagctattgc	tgggaattcat	169826947
atggattgca	agtgaaccca	aatagccaaa	acaatcctga	taaagaacaa	169826997
agctagacaa	agtcocatct	gcacttcctg	atttcgaatc	ttacttcaaa	169827047
gctatggcag	tgaaaacatt	gaactgagta	cggtaatatt	tatcatctca	169827097
aaacctcaca	acaatgcagt	caagtggaa	cactgtctca	gtatttcaga	169827147
tgacagagccc	aggctcaaag	aaatatgggg	aattgcttga	ggtcagagag	169827197
ctgggttaacc	acaaatgcgg	gtccacattc	agatctgccc	taagtataaa	169827247
gacattgcat	cctctcagcc	actacctaca	ccactcttga	gtttcttcga	169827297
cacaggacct	gtgaacagac	agcccaagac	gcttgggaa	catggaattc	169827347
taacccccaa	agcctggctt	aggacctca	tccagcgacc	agacagggcg	169827397
tggttgctc	catccacatt	tctgaaagt	tccactcagt	ggacagcctg	169827447
ctttctagtc	tctgccctac	tggcttgagt	gtggatgccc	agacggttag	169827497
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ccacaagtgc	tctctgtaca	catgctccac	ctgttctgat	gatctttcag	169827597
tctttcaact	tccaagccat	gtgagggatc	cttcagggaac	atgagcactg	169827647
ggacatgctg	gacgctggag	agagatgcag	acaccagag	ctggctgagc	169827697
taacatgcta	cagtttgtga	ggaggagaca	caaaatttca	tacagatgat	169827747
aaaatttttc	tgtacaacaa	accttttgcta	tagatcctac	aatatatcca	169827797
ttattctcac	tagaatgtga	acatgattct	gcaaattcct	aggagaaaaa	169827847
cccagcctgc	cccttatcag	aggctataaa	ccacctgttt	ttctttccat	169827897

FIG. 1.43

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cctccttccc	ttgcttccct	ctcacacatc	agtccttttag	agaaaactga	169827947
gctttttccaa	gctgttattg	ctcaaagaaa	tgtcttcatc	caagggaacc	169827997
aagggatgtg	aagggcactg	gcctccgaag	catttgccat	tgtcaacttt	169828047
tattgagcac	ctactatgta	ccaagtactg	tgctaggttc	tgacgacact	169828097
gaagaaacaa	aaaaatagat	acttcctaata	ctcaaggggac	agtcactctgg	169828147
tggagtcaga	ccttcatcac	gcacacacac	aaacacaaag	agagagacag	169828197
aaagagagag	agagagagtg	agagagaaat	acatgtattc	agatactgct	169828247
ctgaacctta	tctgggtccg	gagggcagag	aaggcttctt	gaactaggac	169828297
ctaagaaatg	ggaagaaatt	tgctagttaa	gcagggtgtg	ggggaaggct	169828347
ctcagaagaa	cattctagaa	caagtgcgaag	gtcccaagag	ggagggagat	169828397
ggtccattcc	tgcaactgaa	agaagaccaa	tgtttctgaa	ccacatggag	169828447
caggaggaag	cagcaggaga	atccaacagg	gggagggtca	gaaagcccat	169828497
gtttgttaact	aaccggaacg	atgaatgtgg	tttggaagac	aagtgagagg	169828547
atgtgtacca	cgggccagat	gtgggagacc	aaggagggga	ctagtgcatt	169828597
ttccagtaaa	agaaataata	gtgcttgggg	ctagggaggc	tcaaattgag	169828647
aagaagacaa	gtggggagggt	ttaagagaga	tttctaaatt	aaaatgtaca	169828697
gggaatagtg	acagatgatg	catggggtag	agagagagaa	ggcaatgtca	169828747
agagtgactc	ccaaatctgg	cttgcaaaaca	gaatgaacgg	tggtgtcatt	169828797
cactgagaaa	ggacacccaa	gaggaggatg	tgattagcag	gggagagagc	169828847
aggagttcaa	gctgatatgt	agatccacat	taatattgtct	agtcagaatg	169828897
tggatacgtg	ggtttggggc	ttagaagaaa	ggtctggggg	gaagatctaa	169828947
ccctagcagt	catctgcaaa	gagatggtaa	taaaataaat	acaattttta	169828997
aatggatgga	atttccaggg	aaaaagcaga	gggtgaaatg	agtaaaggat	169829047
ctagggccaa	ggctaaaaga	aatccattat	tagaaacaga	aaagggtgtct	169829097
tagtgcattc	aggctgctat	aacaaagtac	catagcctga	gtggcttata	169829147
aaccacagaa	attcatttct	cacagttctg	gaggctggga	agtctaggat	169829197
caagggtgcaa	gtgagagtct	gccttctggc	tcatagatgc	tgcttctctg	169829247
ctatgttctc	acatggtaga	ggatgtacgg	aagctctctg	cgacttcatt	169829297
tatgaggacg	ctaattcccat	tcatgaagac	tccaccctca	tgacttaatc	169829347
acctccccaa	atccccacct	cctagtacca	tcaccttgag	ggttaagatt	169829397
tcagtatatg	aacttttaggg	gtcacaagta	ttcagtctat	agcaggagga	169829447
atagccaaga	aggatgaatg	aaaatcatac	aaggatgatt	tcatggaagg	169829497
caagggagta	caatgtctca	aataaaacca	gtcctgagtc	aaacattact	169829547
gagaatgtga	gtgtaataaa	accgagactc	aaaagtaggc	attggatgtg	169829597
atgacatgac	tatcactggg	taccttaggg	agagaagtgt	tggcggaggt	169829647
gacaagcaca	gtcagatgga	atgtgctggc	ggatggcaaa	gatggggaaa	169829697
tgaagatacc	cagtgtagac	agcttctgaa	agcagctggc	cgtgagtcag	169829747
aggtagacag	gaaagtgact	aatacagtgc	agaggctcgac	gttttttagct	169829797
ttattgtatt	taagagagag	acctgagcac	atttaaaatg	ctgatgtgac	169829847
attgtccaag	ctgagaggaa	acaattagat	ctatatgaga	gaaaagaatg	169829897
atgaatatca	ggcaagtatg	gcaaagacca	ccattacttt	tgaccaacc	169829947
caataagaaa	ggttgaggat	cttcacaaaa	caaagggtgt	tttggcctga	169829997
gtggggagga	ggaacagctt	ctttactacc	agtggaaaga	aggagaggct	169830047
ggtgcagggg	caggagggta	gcaggggagca	gagggaggcc	ccatccacgc	169830097
tcagggttctt	agaatgagga	agatgacatt	ggcaggacca	taggtgagca	169830147
tcttctaacc	caagggaagat	ttagaactaa	gtataggctg	ggcgcggtgg	169830197
ctcacgcctg	taatcccagg	gcttcgagag	gccgaggcgg	gtggatcacc	169830247
tgagggtcagg	agttagagac	cagcctgatc	aacatggcaa	aaacccatct	169830297
ctactaaaaa	tacaaaaaatt	agccagggtgt	gttggcgccct	gtctgtagtc	169830347
ccagctactc	aggaggctga	ggcaggagaa	tcgcttgaac	ccaggagggtg	169830397
gaggttgtag	tgagctgaga	tcacgccatt	gcactccagc	ctgggcaaca	169830447
aagtcagatt	ccatctcaaa	aaaaaaaaaa	aaaaaaaaaag	gaaactaagt	169830497

FIG. 1.44

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atagaagtat	ggaatagaac	tatatctctt	ctattaagat	atttgtgctt	169830547
tgaaataagc	tatgtttaca	cacttgtaat	gtttaagaat	ctgtggcctt	169830597
tcagagtcac	atatgaactt	tcccttctaa	tataaaatgt	ttaacggagc	169830647
aattgacttt	gacatcagat	tctaagttga	aatcttactg	tatttaaata	169830697
agatttgga	cctgtaaaag	aatttaagcc	ttgccgtctt	tagaagttta	169830747
atgaattaga	tttataacaa	ttacttaaat	atctgagaag	gtttgttaga	169830797
caattgaagt	acttaaaaag	gaattaaaat	atattaagcc	tataaatgca	169830847
gtttacaatg	tttagagcaa	tttaattaaa	aacatttgta	aatgagacga	169830897
aacatttctc	aaaggtactc	ttaaatgtga	ttgttaaaat	ttgctagacc	169830947
tataaataaa	taataagatt	cgtaagctga	atttcaaagc	ttatggagga	169830997
acttggttcc	atatgaattt	gttactttta	taaattgaat	gttaattttg	169831047
aaaaacaaag	aaacctttca	tcaatatttt	tggcgcctaa	gagctgctct	169831097
tgagggcatc	taattaatag	tttttttatt	atttaaaaaa	tatcattagg	169831147
ccaggtgcag	tggctctctc	ctgtaatctc	agcactttgg	gaggccgagg	169831197
tgggtggata	gcttgagccc	aggagtttga	ggccagcctg	ggcaacatgg	169831247
agaaacctta	tctctactaa	aaaaaaaaacc	acacaaaaat	tagctggatg	169831297
tgggtggcaca	ccgctactta	ggagactgag	atgggaggat	cacctgagcc	169831347
caggaggtgg	aggggtgcagt	gagccgagat	cgcgccctta	ccctccagcc	169831397
tggaagacac	agtgagaccc	tgtctcaaac	aaaatttttt	taatggctat	169831447
aatgaaaaaa	aaaaatcaac	cagtatgtaa	ggaaaaagct	gaagcccttt	169831497
gccccatttc	ccagaggtaa	ccatcattac	aagttccttg	tgtttctgcc	169831547
cagaaatggt	atttgcataa	gcatagaatc	tctccccagc	cccatTTTTa	169831597
aacaaagaga	tatatctctg	atctaacatt	ctgtactgct	tttgtgctta	169831647
acaagataac	ttgagccggg	tgtggtggtt	catgcctgta	atcctcaagc	169831697
tttgggagct	gagacaagag	gattccttga	ggccagaagt	tcaagatcag	169831747
cctgggcaac	atagtgcagc	ccgatctgca	aaaaaacatg	taaaattagc	169831797
tgagctaggt	ggtgtacacc	tgtagtccca	gctatttagg	aggatgaagc	169831847
aggaggatca	cttgagccca	ggaattcaag	gctatagtga	accatgatca	169831897
cgccctgcac	tcctgcctgg	gcaacagagg	gagaccctgc	ctcaaaacaa	169831947
acaaacaaac	aaaaaacaat	atatctttaa	aacatgttca	tgtttcccat	169831997
aagaataaag	attaacatcc	ctctctccct	tcctcatcgc	ctttgggggtg	169832047
tggcctcatg	cctccctctc	gggttgtgcc	caaacttctc	tcaagagtgg	169832097
atcctctcac	tgtctctact	tcctgcctcc	ccagctactg	actgtacca	169832147
gactgtgctt	tctgagggca	ccaatgcctc	ccaccttacc	aaacccgcta	169832197
gaggcttctc	agttctcata	tctcttactc	tccggctttc	aacacgtgag	169832247
ccatcttttc	cttgctgcat	tgcaaagcca	ccttttatcta	gcaatgaatt	169832297
cccatttgta	tctgggtcta	tttctggcct	ttccattctc	ttccattgat	169832347
ctctctgtcc	ttgggtgcaa	gttttctgat	gacctgactt	gattcatgga	169832397
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ataacaattc	tttcaataga	gcttttctct	ctttcttaat	aagagatagg	169832497
gacagcagag	gttcacgtat	ttcctggcaa	ggcccagaat	gccgttatcc	169832547
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tgtgtgaaaa	tggaagagcc	aatctgagct	gtcgccccat	tcctacagaa	169832647
ctagctgccc	gtctttgaat	tcccagtgct	cattcaggcc	tctgcacttt	169832697
cacttgagca	catctggccc	ccactttctc	ctttcctcct	ctcttctact	169832747
aaatagtaaa	agagctcttc	ttcacatctc	agctcagggtg	tccccttgcc	169832797
caggaaacct	ttcctgagge	tcctccctat	gccccacatt	agccactctg	169832847
ggcttccctc	tgccccagcc	cttaacacaa	cagaatcaac	atgcctgtaa	169832897
cagaattgcc	ctatgcccc	tctcccttag	accaccgtga	gctccccaag	169832947
ggcaggacct	gtctctcagc	agacttttac	tcttgttacc	gaactgatct	169832997
tgggtctgcc	caccgggcac	agtgcagcca	aacactgata	ttgggattgc	169833047
agccagagaa	agtgaggcat	ttattgcagg	gcgccaagca	agcagaattg	169833097

FIG. 1.45

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ggcagctcat	gcttaagatc	agaactccct	gatggcttac	aggtaagggt	169833147
ttttaaggt	agagggggag	aggttacagg	caaaatcata	aattaatata	169833197
tggagactat	gtgttgggtt	ggcctaaaaa	ggcaaagcat	cttgaagcgg	169833247
aagtttggga	gtgtggcaag	tgaaagggtg	attcaaagat	ttttcagtgt	169833297
tgtgatgggt	taaggagggt	aagttttgtc	taaaattttg	gtgtaggcag	169833347
aaaagaacgt	tagctcttgc	cogtgggcat	gatctcttcc	aggccctca	169833397
gcaagaaact	taggagaaag	catggtgggt	ggagttcggt	cctcagcttc	169833447
cccttatcca	aggctctctgt	gcctgcagat	ggcactttcc	atttggtgga	169833497
ggtctgggtt	tctgaaacac	aactcagga	cgtagggttg	gatgttatct	169833547
ttagtctcta	caggaaacca	aatatcctat	gactctaatt	tccttggcta	169833597
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ttcaaggctt	gctacgtgcc	tgggaatttct	agattttcct	ttatttccat	169833697
gcttggggag	aggagtgcct	ggcaggctcc	taagaggggt	ctgtgctcca	169833747
tctcgccccc	tatcttgaac	tatcggttgg	gtgctctaga	atctgtatgg	169833797
ggtggaagt	ttcattcatt	ttctgtacaa	aagcaatcaa	tgcttattgt	169833847
ggaaaaccca	aataagagag	ttgctctaaa	caacaccctc	cccagtccca	169833897
ataccttgct	cagaagaaac	cactgtttgg	tgagtatatt	agtcaatgtc	169833947
tgcagaccag	atcggtatgac	caagttttcc	ataaatggat	ggccatccac	169833997
ttcccttcaa	gggcgagggt	agtttgttct	gatccatctc	ccttttcaca	169834047
gctcagggag	ggaggaagac	ccaggaagga	gagctgccac	agttactagt	169834097
ggcccagctg	ggatttaaa	tccgccgtga	ctgaagcttg	gctccacatg	169834147
ccagtctgca	aggccctgag	tgccctcagc	agtaattcca	agcaaagcag	169834197
ggaagcagcg	ggccagggtgc	tgaactgaac	tgctgctcag	ggctcctgag	169834247
cctccccctg	cctcctccct	ctcttctcca	ccctggggcc	tctctctctg	169834297
tcctacttcc	ctcctttaga	tctcttttcc	cctgaaccca	ctcattttatc	169834347
accttttgat	gagttccacc	aggcagacca	tgtcaggaag	tttcttgggtg	169834397
ttcatttttaa	taaaacttaa	ttattaagac	agcctcacia	gtcatgatac	169834447
atttactggt	tcatttttca	catctccgtc	agaggcctcc	tggcagccac	169834497
gtgggaggca	tgaaggctat	ggggtggaag	tgtcagagcc	ttttctggcc	169834547
tctgcagga	gctgggtttg	gggaagcagt	tcctgaccct	tcctctgccc	169834597
gcccaccccc	gttattctcc	agacgctgag	gatgggatgg	aatgagcacc	169834647
aaacatggag	tcaggagacc	tgggactcaa	tcctcctcct	gctgcagact	169834697
atgctcagac	cctgctgaag	gaaggcatcc	tctctgggcc	tcagctgtct	169834747
catgtacaag	atgggaatca	tctcagtcca	aaccagacag	agccactgtg	169834797
agattcagaa	gaaagctctc	gcaatgagag	gcctccccag	gcagatggag	169834847
gcaaaaactgc	aagggtggat	tgacgctggg	gcggcgccctg	ccccacagtc	169834897
ctgtaggtcc	gcccgcctgg	gtaaggggatg	gggtgaaatt	gggggtctct	169834947
gatgatcaca	gtaataactg	acttttttaa	aaattttatt	tttccatagg	169834997
ttattgggtg	acagggtggg	tttgggttaca	tgagtaagtt	ctttagtggg	169835047
gatttgtgag	attttgggtgc	accatcacc	caagcagtat	acactgcact	169835097
ccatttgcaa	tcttttatcc	ctcgccccc	tcccaccctc	ccccccaagt	169835147
cccaaagtc	cattgtatca	gttttatgccc	tttgctcct	catagcttag	169835197
ctccacaca	tcagtgagaa	catacgacgt	ttgggttttcc	attcctgagt	169835247
tacttcactt	agaataatag	tctccaatct	catccaggtc	actacaaatg	169835297
ctgataattc	attccttttt	atagctgagt	agtattccat	tgtatctaca	169835347
tataccacag	tttcttttate	cactcggttga	ttgatggaca	tttgggtcgg	169835397
ttccacgatt	ttgcaattgc	gaattgtgct	gctataaaca	tgtgtgtgca	169835447
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gtgggattgc	tggatcaaat	ggtagttcta	cctctagtac	tttaaggaat	169835547
ctccacactg	ttttccatcg	tggctgttct	agctgacatt	ccaacgagca	169835597
gtgtagaagt	gttccctgtt	cactgcatcc	acacctacat	ctactgtttt	169835647
ttgatttttt	attatggcca	ttcttacagg	agtgaggtgg	tgtcgattg	169835697

FIG. 1.46

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tggttttgat	ttgcattttcc	cttatcatta	gtgatgttga	gcatttttttc	169835747
atatgtttct	tagccatttg	tatatctttt	tctgagaatt	gtttataaatt	169835797
gacattttatt	aagtgccttg	cagacgctgt	gccaaaggatg	tcatgtttgtc	169835847
atatgtatta	gctggctaaa	tctcacagtt	gctgtacttg	ttactaatat	169835897
tgtaaaatgt	gtaccagtgt	tatgcccatt	ttatagttga	gaaaactgag	169835947
gcataggggag	gcaaaagcaa	cgtgcccga	gttacaaagc	cagtcaatgg	169835997
tggaaaccaga	attagaactc	tggccaactc	cagagtctac	cttcttacca	169836047
ataaagtcac	cacccctgag	aaatcagggg	ggggccagga	gttttttaata	169836097
atcaaagcaa	cctcacaccg	aagtctaagg	gaaagcagag	gttcggctga	169836147
gcaccagggc	ccctggcagc	tcagcatggg	ggccgtcagt	gacacctgca	169836197
ctcatgatata	cccacacctg	tggtcttcca	aggggacaga	ctgaactctt	169836247
gccacttcat	ccacaaagcc	cccctctatt	tcctcctttc	cctcgactgc	169836297
acttccttga	taacagaccc	aattttgttc	agcaattcac	ccccagggaa	169836347
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aaataattag	actgcgttgg	gcgtcaggac	acaccactcc	aaaatatgac	169836547
tgtaggcgac	caggaatctg	ccacagcaaa	atctactttg	gcatttttca	169836597
agctagtatt	tatgagaaac	tgcagacaca	ggagtagctc	tgaaaagctg	169836647
tccttttgta	aaagaaattt	acatctataa	aggaaatcca	cattagtaaa	169836697
acaatctgta	tcaggaagag	ggctgctcag	agacagcttc	tattacccga	169836747
gaggcttttt	atctttataa	cgagacaacc	tttacttata	atacattttcc	169836797
tccccttacc	ctccaagaac	tccaccatct	ccgagaaacc	caaagcacc	169836847
ctattccttt	ctgtagctca	ggatgctaca	ttagcttcaa	tcactctggcc	169836897
ctactttgag	tctcatgtat	tgtgggaacc	cccgcctccc	atacctatgc	169836947
aagtaattat	aaatgttttt	gcttctgcta	atctgtctta	tgtaaaattta	169836997
atttatagct	cagtcaaaga	acctagaagt	gtgggggtta	accaccgttc	169837047
cctcccctgc	aagaggattg	gtctatgaga	gaagtcagct	tccattttatc	169837097
gagcacctag	taagcaccag	gccccagacc	ttaagcttta	catgtgttat	169837147
ttctgattoc	catagactcc	tctagcttca	gtgggtattac	ttgcatttttg	169837197
ctgatgaata	aacggagggt	cagagagggt	aagtgacttg	tccaaggtca	169837247
cacaaccagg	aaacagcaat	gctgcgagtg	gaacccaggt	gttgtgtccg	169837297
tgggtctgtg	gtctcgctga	cttcaagaat	gaagccacca	gaccttcacg	169837347
gggagtgtga	cagccctcaa	agggtggcaag	gacccaaaga	gtgagcagca	169837397
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gggacccac	tgggttgccg	ccgctgggtca	gggtagccag	ctttttatttc	169837497
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caattgggtcc	atttttacaaa	gtgctgattg	gtccacttta	cagagtgtctg	169837597
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attttgacag	agcactgatt	ggtacatttc	acaaacctct	agctagctac	169837697
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gaccaacctc	caagcttttt	tatttcattg	cttggtctcc	ctctctacca	169837847
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gccaggcatg	gcctaagtgt	tattcgaaca	aagcttcgga	agctagtcca	169837947
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tcctgctgca	gacccactga	gaggtgactc	ccacacggct	gtcctggaac	169838047
aagacagcag	cttttcttag	gttggttctaa	gttaagggtc	ctcactgctg	169838097
gtaagacagg	gaaatagagg	agataaaaaat	aacaaaacaa	aaggagaagt	169838147
cacaaagtta	caggaaatct	caatatatct	ttctgttctg	gatgctgtctc	169838197
caaacacaa	tgcagcaggg	cctctttgtg	gggggttctt	atgtgagagc	169838247
cacaaaggac	ctcaaagcca	aaacagactg	attatctagc	ccacctccat	169838297

FIG. 1.47

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gtcctccct	ccttccccct	acttccttac	taacagaccc	aattttgttc	169838347
aggaatccac	cccctgccga	gaagaaactg	atcctattcc	cagctcagag	169838397
ccaaatcctg	aatcatccaa	tattaccccc	ttgtcaggag	taggttgagg	169838447
ggtgacaagt	ggcccatgct	ttttctgggg	tcaggagaaa	gaaatgatta	169838497
ttagaacaat	tttggtttta	actttttttt	tttttttgaa	acagggtctc	169838547
actctgtcac	ccaggctgga	atgcagtggt	gcgatctcag	ctcactgcag	169838597
cctcaacctc	tgcagcctca	agtgattctc	ccacctcagc	ctcctgacta	169838647
gctgtgacta	caggcctgtg	ccaccatgcc	tcgctaattt	ttgtattttt	169838697
tgtagagaca	gtgttttgcc	atgttgccca	ggatggctct	tcacttctga	169838747
gctcaagcaa	tccatcagcc	ttggcctccc	aaagtgcctg	gattacaggc	169838797
atgagctact	gcaccacgcc	taaacttggt	tctaatttag	agttccaaat	169838847
ttttagatgc	tcatatctct	gactaattac	aataacagat	gatgaaatat	169838897
cgaagtgttg	aactgtcctc	tcaattccag	cgggaacaaa	cagattctgt	169838947
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gcacactgtt	gataaacaca	atatgaatag	aaaaattttt	gtttagcctt	169839097
aaaaaatagc	agtatgacaa	tttgtcttga	attttgacct	ttcagtgggtg	169839147
gcttgatatca	aagttacggg	cttgggatag	tgtcatgacc	cgctgaaatg	169839197
gctgcggggc	tgaaattttg	atcgtaaggc	aaatttttgt	acagaaaatc	169839247
gcctgtttct	gctgacttct	gcttttagaca	tccactctta	aggaaaagca	169839297
ttgttatccc	accagctaac	acatcactct	ctaccatata	tcaaagagtc	169839347
tcaagatcct	tctattcatg	aaaaatgaaa	atattctcac	cacatcctcg	169839397
cagtaatgtt	caacataaat	taccaagcac	agagacagtt	tgggaatgta	169839447
cattataaat	ggccttccct	acaagactaa	gagtgaatcc	taatgtaaac	169839497
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taaatgcacc	gctgtaatgt	ggaatgttga	agtgagggaa	gctgtaagtg	169839597
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gtgaacctaa	gactgctcaa	aaaagtagaa	gtaagtaaata	acataagtca	169839697
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aagtatatgt	tacttggacc	tgtaaattca	ctctggggat	gtgtgtgtat	169839847
atatatatat	acatatatat	tacatatata	tataacaca	tatatattag	169839897
aaagtaaata	tttcttggtta	aaatctgaga	tataactgcc	ctctaaaggt	169839947
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gtctccactc	actgcaacct	ccacctcctg	ggtcccagtt	caagcaattc	169840097
tcctgcctca	gcctcccaag	tagctgggat	tacaggcaca	tgccaccatg	169840147
ctcagctaat	ttttgtattt	tttagtagag	acacagtttc	accgtgtggg	169840197
ccaggctggt	cttgaactcc	tgaccttggt	atctgcctgc	ctcggcctcc	169840247
caaagtgctg	ggattagagg	tgtgagtga	agcacctggc	cgggttggtt	169840297
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ctttatccaa	atggacttta	ttgtagtgtg	attcatttga	taccttttgt	169840797
aagtcccttg	tttagttatt	acatgattat	cataaagttt	gggagcataa	169840847
tggtagaaa	gatatcacag	acttaggaaa	aggatgcatg	ttcctttaat	169840897

FIG. 1.48

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ttggctcttt	taatggactg	agagactatg	caacgctcat	ggctggagga	169840947
caagcttccc	cggccttcca	gtcccataag	gacacctgct	gttaatggca	169840997
gtcctgatgg	agtgtagatc	cctcgggctg	ccatcctcac	aaagggtgtg	169841047
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tgtgtccgaa	ggcttactgc	aagactgtgc	gactccacca	tgggtcagttt	169841147
ccccggggaa	ccatctctct	accaagccca	gttttccatt	gcaagaacaa	169841197
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tcatgaagca	ttagctttca	agattacagt	tcggtaggat	gttcaagatg	169841347
cttagggtga	ataaaaaatga	cagacagctg	aacacttcct	ataaatgaaa	169841397
caccaatata	gatctaagtt	tcatgcatga	ctctcaatgt	gggttaatgaa	169841447
aaggaagata	aaaaaaaaaaa	agggttgcca	tatttgcagg	gcatttgctc	169841497
ccaaatgttt	caatcctggt	ttcttttagac	tttgaaaagg	gggattgcac	169841547
gttatctgtc	aagaaggcat	caaagcagag	aaatccacaa	atgtgtagtg	169841597
tcagatagaa	ttcaagcctt	cagaaaggac	tccactcctt	tgggtactaa	169841647
gagaactagg	ggcttgtatt	tctaagatgt	cactagctgg	aggcgctgag	169841697
caggtaatgg	tctatgtttt	cctagactat	aaaatcctga	ttatatgggt	169841747
taataaaaata	agaatctcag	agttctgatg	gaaaacaagt	aaacttcagg	169841797
tcttagcagg	cactagcaga	aagcaccaga	gaaaactggg	ggagagggtta	169841847
ggactcctgt	cccaaagatc	cccctcaatt	atcctgccat	gttatcagtt	169841897
ccctctttac	atgtttaccaa	acatgactac	taattttctat	ttttttccaa	169841947
gactattaga	tgtattcaaaa	attcactcct	cttacaagga	tagagaaaaag	169841997
tgcctatcga	tgccttaataa	cccaacatat	atttaataga	agaattaaat	169842047
caccttctgc	aaaggaccaa	gaaaagctcc	atttgatcaa	ttcctttaag	169842097
acatgaagac	ttctcctttt	ctaagaatcg	ccatagtaaa	atgcaagctc	169842147
agcatgacat	accocaaagga	aaaatgtatc	tgtcccttct	gcttttacta	169842197
cagttccata	agggttaatac	cgagttgttt	tgcccacatg	ggggctctgg	169842247
aatcttggct	gtgatgcatt	ggtaggatat	ttgtcaccaa	aactgactca	169842297
gcaatcagtt	aaatatataa	caaagcactg	attagtgttc	ctgattcata	169842347
tttgtgcttt	gtttaacatt	taacttccga	attttataca	tctattaaac	169842397
aatattcctc	ttgacattcg	aacactatct	gcacaattaa	taaatcaaaa	169842447
acttattaaa	aattgaaaca	attaaaaatt	cccaacttta	taaaccattg	169842497
tttacaaaat	tatttaacca	cactctccaa	cacttttaaa	taaaaccata	169842547
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caaaaatgca	cacaaaacgt	catactgatt	gaaaaatata	tatgcacact	169842647
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ccaacattat	tgcacttgag	cttaaatgtg	gcctaagaat	ataaaaagtc	169842947
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ggaattttaa	ccttgcagtt	tgctgtcctt	acgagcacat	ttggccaatt	169843347
atccttccat	gttatcagtt	ccctctttac	atgtttaccaa	gcatgactac	169843397
taattttctat	ttttttccag	gactattagt	tgtattcaaa	attcactcct	169843447
tccttcttac	aaggatagag	aaaagtgctt	atcgatgctt	aataacccaa	169843497

FIG. 1.49

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catatatatta	atagaagaaa	taatatacacc	catatatataa	tctgccatta	169843547
aaaataatat	gaaataaaaac	cctatcgcat	ttgccattta	catcaacttt	169843597
tctcttcata	gcttcatttag	gaacttacag	ctcttcacag	actccatgtg	169843647
ttttaattga	ttatagccat	caatcttatt	tgatattcaa	aatctcagag	169843697
cttgaccaga	ggaaacctct	ttaatctagc	ttcttagtcc	ttccagaacc	169843747
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ttccaggctt	aaaccatttg	ttttacccta	ctcaggacaa	cccttcctaaa	169843847
gagccctgt	ttctttaagt	ggagaaaact	gtagagaca	aagtctggcc	169843897
atttaggggt	acaggagagt	tgtgggtggg	attagtacta	ctcctgctgc	169843947
tgctgtgct	gctgctgctg	tgtccactgt	agtgacaga	agtgaggaaa	169843997
tatttaagt	gagttcacat	tagtgttccc	agtttagcgt	gagcattgct	169844047
ccattatgtt	gttctaattgt	aaaaatgtca	aacacatttt	tctcaatgag	169844097
atacttaaca	ttttaaccct	tcatccaagc	tatatgttac	acctcacttt	169844147
tctatagtgt	tatatattaga	aaataaatat	ttatgaaata	cttgatattt	169844197
ctcatcaatc	cttgggtcact	caattgaagg	gtgtagaagt	aagggtcagg	169844247
tcaccttagt	gaggggcctg	catctaacc	tatctgaagg	ggcttatgaa	169844297
tttgggattt	attaccttga	cagaaagaaa	tattgagaat	gaccccaacc	169844347
atgctttata	gcaatcgctc	tttatagttt	atttcatagt	gacaagaagg	169844397
aactcatcca	tggtgggttt	ttccctgagt	gggtctgtatg	gtcatatcag	169844447
aactgaaatc	atcccttctt	gcttctgagc	ccccgtttcc	aagtcttggt	169844497
ctttgtttct	gtaggtagta	aagtgaattc	tttaaattcc	tgccctccat	169844547
cagctgctaa	agcattctgc	ttccctctga	taagattaac	agaatgttgg	169844597
ctgtgggttac	gggatgcttt	gcagtctatg	tcttaaacca	agccagccat	169844647
gttagcattt	cctctagtgg	tggtgtttta	ggccaattga	gaatgtgggt	169844697
gatattaata	ttttccaacc	agctgataac	aggaaagaca	cttctgcttg	169844747
gagtcactt	tgagaagaga	tttattattt	aggcagcaca	ggacacctcc	169844797
attaatcttc	ccccagcagt	gcccactctac	catcaagtcc	atatactttc	169844847
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atcaataaga	ataataacag	taaaattaca	atggccaatg	tttgaatccc	169844947
taatgtgtgc	caggcacagt	acgggggcctt	ttgcagctat	tatatcataa	169844997
aacccttaca	acagccccc	gaaattttgca	ccatgatttg	cttcattttta	169845047
cttttgggga	aaccacggat	caagtaactg	aagtgatttc	tctaggactc	169845097
acagatgagc	ggtggcagag	cctggaatta	gatataatctg	atgttagtgt	169845147
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aatttgtctt	tgctgaggct	tggttattga	tgatttaaaa	gtccccagag	169845247
accagatttc	atctgggtatg	ctgtgggagt	caagtaacgt	ccaaggccaa	169845297
gcctgtctga	gagagggttt	tattagctcc	aaaattataa	taacttccac	169845347
agccttcttc	caccaattct	gccttccact	gaaacagcgc	tggtgatgtt	169845397
tagaggtagt	agtttgggac	aattatcagg	agaagcattt	tggtgctatt	169845447
gtcccacccc	ttctgtcctg	agagggttta	tctgggtctt	cagtatttca	169845497
aataggtcat	gactagattc	catgcatccc	tagaaaacat	agcctaaatt	169845547
ttaaattaaa	gtatgagggtg	gaagaaacag	cctttcttcc	cttttgtttc	169845597
caaggacaga	tgaggtcaaa	agtggaaactg	gggcccgcag	agccggatag	169845647
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tggagctcac	tcgccctgcc	tctcatccag	gcctgaaaat	cataggtaac	169845747
tatgaggcaa	gaggaaccca	gggtgggtggg	aacaccctag	ggtgatccca	169845797
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cagatctgca	gtcaccttct	aaatccccct	aaagtggacc	tagccatcct	169845947
ctccatttta	agaccacatc	tcctgtctgc	tacagcccct	ctcgcttctt	169845997
tttctttaag	gatattctggc	tggttgtatt	gggttaacat	gcaagaagag	169846047
agtaccaatc	actccataac	ttgggtaaatg	catgtcaatg	gtgatctgtg	169846097

FIG. 1.50

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tggggccgca	aggttccaga	tggttgggac	aactctacaa	tcagtcacat	169846147
ttgggttggg	taaatcccc	actcatcttt	acagctgtat	cctgcaagtt	169846197
agtggctgcc	tgtctctgaa	cttcaccttc	cttatgggtg	tcaaaaatac	169846247
ctccatggga	taaaaacgca	gcatctgtag	attcccaaat	agggtgcaagt	169846297
agattcccaa	atagggtgaa	ataggttcat	tcgttgggtc	attctgcagt	169846347
cagggagctt	tcagttctact	ggcatgcaag	acgcaatgat	aatgagaata	169846397
cttcacaatg	agtgtgacgt	gatgactgat	gaatgtgaca	aaggagaagt	169846447
aggatgcact	tagacagcct	gggggaattg	agttgtggcc	agaagggaga	169846497
gagagtgtcc	attctccacc	tcatcacttt	gctgccaaga	gaaacaggaa	169846547
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cgcacgttgg	ggaagctgga	aagagcctgg	tggctgccgg	gcctccctct	169847047
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ccttctctct	accogtttcc	ccctccctct	ctctctctcc	tccctctttc	169847247
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cacatcttct	tccatttgcc	accctccctc	tctgtagcca	cacccagtgg	169847447
gctcagagct	gggtctttct	tttttttgtt	ttttcttttt	tctttttttt	169847497
tttttttgag	atggagtttc	actcttgttg	cccaggctgg	agtgcagtgg	169847547
cgcaatctcc	actcactgca	atctctgcct	cctagtctca	agcaattctc	169847597
ttgcctcagc	ctcctgagta	gctgcgatta	cagtcatgcy	ccaccacgcc	169847647
cggctaattt	tgtattttta	gtagagacgg	gatttctcca	tgttggtcag	169847697
gctagtctca	agctcccgac	ctcagggtgat	ctgcctgcct	cggcctctca	169847747
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aacctttgct	ccttccctca	ccacacctct	ccacatccca	aactcaagcc	169847947
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aagtgcctcc	aggaatcatc	aaggagagta	gggcagctct	gagtctccac	169848147
caggcccacc	ctccgcctct	cagggtctgag	cttcaacttc	cttcccaaag	169848197
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cctccaggct	gcctctgggc	ctggcacagg	aaggaggagg	agaaaatagg	169848297
gagcccaagg	aaagatcaac	ccagcccagc	ccaaggaccc	ccagccccag	169848347
ccccagcccc	agctgggctc	aaactaattg	aaaacagact	ggaaaaggct	169848397
gcttttgccc	ttcctctaga	CTCAGCATCA	TCAAGACTGG	AGGGACAGAG	169848447
CATTTGAATC	ATCAGACGCT	GGGCCAGACG	TCACCCACAG	CGTTTCTCA	169848497
TTTTATCGTC	CTAAGAGGCC	CAGAAGgtgc	gtaaaatggc	ctgtcccaaa	169848547
cagatgagga	cattaccttt	ctcctcttcc	tcctcctcct	tcttcttctt	169848597
cttctttttg	cttcattttt	ctttcatttt	ttcccccaga	tgttgcatth	169848647
cagagaggct	gagcgtgttg	actaagggtca	cacagctaca	aacatcaggg	169848697

FIG. 1.51

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acctgcgaaa	aagctctgtt	ccctgggtgac	aggtgttctg	tgatcctaac	169848747
acagccggag	gtggggacaa	cgtccttgca	gtaacaaagg	ccctgttgct	169848797
caactcagtg	gacatcaggc	cctgttttca	ttcattagca	ggtcagggat	169848847
tccagtgtca	cctgtgccat	gtattccagc	tgatctacct	gcaagcctct	169848897
actccccatt	ttcccagcag	cagccgcaga	caccacccaa	ctggcagaaa	169848947
tttcaaacaa	ggggttctgc	cttgcaactcc	gggtgcaaggg	ttgggcacgt	169848997
ggactcacat	gtgaccaatc	acattgtctt	tcctgagatc	ctgcattttg	169849047
accagaggaa	tcaagaacaa	aaagtgggtg	caactgattt	atccttaaga	169849097
aatccaagta	atgagttcct	gctgccaaaga	tttctgggat	ttccctggct	169849147
cctgccagtt	tctggatttg	gttcttaagc	atcttctggg	tgtgtgagcc	169849197
ccataccctt	ctcatagctt	cttcagccag	agtcagtttc	tggtttttgc	169849247
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tatacacatt	attatatatt	acacacatgc	acacacacag	acatatctat	169849597
atatctagag	agagaaagag	atctccttta	aggaattggc	ctacatgatt	169849647
gtaggggctg	gcaaattcaa	aatcggcagg	gcaagtagtc	aagggaattt	169849697
caaaattggc	agggcaagaa	gcctagggaa	aagttgcagg	cagaattggt	169849747
tcttcctggg	agagacctca	gtctttttcc	ctgaaggcct	tcagctgact	169849797
caatgaagtt	tacctatatt	atggagagta	atccactttc	ttcaaagact	169849847
cctgctttaa	atgttaattt	ctttgaaaaa	attgccttca	cagcaacatc	169849897
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cacgcaaaaat	taaccgacac	aattcacata	cogtagcata	aaatgaaccc	169849997
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atgttggttca	tgttggttca	ccttcctcct	tgcctccctt	tgactgcctc	169850497
ataaattttcc	actcattcct	caagagttag	cccttctgaa	atatcttctt	169850547
tgatcccacc	tactagaagc	acctgtccc	acctcaaact	gagtcaatca	169850597
ctttatttttc	tgtgaacccc	caatataagc	tgatgggtgc	tcctggaata	169850647
gccttttagca	aaagatatta	aaattgccta	atcaacttgc	ttctctttct	169850697
caccaaacca	gcagttctta	aattatgatt	tcagggtctc	ttgacactta	169850747
ccccatattt	ttaccatttg	atgtgcttgt	gtttccggga	agagagttca	169850797
gggttttcatc	agatcttcaa	aaggatccca	ggaagggcca	agagccttga	169850847
gattagggct	tctcgaaggg	cagaggcatg	cttcatgagt	tccttgtgtg	169850897
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gagtagtcac	atgtaggaaa	agtgtccttc	cttcaagggg	tttccatcat	169850997
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gctcccagca	gcgggtgttc	agagctccga	gaagcaagca	ggcaccacat	169851197
gttggtctca	gaaggtagag	agagactgta	aagtaaacca	aggaaggctc	169851247
cctgggggag	aggccgcatg	acatgagcga	agccaagagc	aaggactggg	169851297

FIG. 1.52

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actcagccag	atggaacaga	gccccgggaa	gggtgtcttg	agtgtgtgtg	169851347
ctggggggag	catccacgtg	agcaaatgcc	aggcctgcag	aggacccaga	169851397
gaaggggagag	aatttacaca	cccacagtcc	ctgaagcctg	gagaggactt	169851447
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agtgaggtgt	ggggtgtaat	taccaagcca	gagtgcagag	ctgagccaag	169851547
caggtaagag	tactgacccc	gagcccactc	gggctctgag	cagaaggaag	169851597
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agggcaggag	accagccagg	cggggaggct	gacccaatgg	ccccggaatg	169851697
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cgatgactcc	atctgtcacc	tcggcactta	ccccaaaaga	tggaggactg	169851797
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aggcaatcaa	gatttgcaca	ttgtcagcag	agaaggaatg	agactgtctg	169851897
gttgccgcta	gactttggcc	agggtgttcc	tgcaggtaag	ggcctcgtgc	169851947
aggaggcccc	tgggcaaggg	ccggcccttc	tcctctccct	cagtgtcctg	169851997
gaaaggcccc	agggtgccc	caaccctga	cctctctcct	tctttctcca	169852047
tattgctaga	cccccttctc	ttggtccctt	gcctcctccc	actggtgtgc	169852097
accacacact	tcagacagtt	ctgagcagac	cacgcaaaat	acaactgtga	169852147
tgttatttgc	agcaggcatt	ctggaccag	aactgtgtct	ggtcttgaag	169852197
ttgaaaggta	gcaatcactc	atactcctct	cccatgaaca	atctgagaaa	169852247
aaatggaggc	tcagggcaga	agttaccccc	tttacaactg	acgggagcta	169852297
tcctggggaa	tgaagcctga	ggctaaaacc	tatgccctat	ttccagcctc	169852347
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gggtctcccc	caggtctgcc	ctccaactgc	cccaagcccc	acatgcctgc	169852447
aggcgggcct	gggatattctg	ccatgtgcag	ggaataatga	gcctggcagc	169852497
tgcaagaagg	agatgagctc	caggggttga	gggttaagga	cattcaccag	169852547
tctcccagca	cactcatctc	caccccaccc	cagtgaatga	gactgagagg	169852597
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aatgacacag	aactacacac	atacacacac	ccataagagt	gcatataaaa	169853047
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gggtgaaggg	tgcaaggggc	tctcagtatt	attatgggaa	ttttctgtga	169853197
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gatgaatgaa	tgaatgaatg	aagaatgaat	gaagaatgaa	tgaatgaatg	169853847
caccacacaa	agtagcattc	tagcagaagt	gaaaacaagg	ttacctagtg	169853897

FIG. 1.53

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cagactttcc	cagccaggac	tcatactatt	tttaaacaca	tacacctgct	169853947
tcggtgatgt	actgaaggcc	tcaggctact	ctccccgccc	acatctccca	169853997
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ttacctagca	aatctggctc	acagtataat	atcagtcatt	tatacttcag	169854097
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aacatttttg	gacagaggcc	ttttcctgtg	ctcatttggt	cctcacagga	169854247
agccaagagt	aaatgtgcat	ctagacctac	aggggagggt	ttggcagtta	169854297
cagcaaactc	aggggaatttt	aaatatgccg	gaaactttcc	agagccctga	169854347
ggtgcagtc	cagctctgtc	actgtctctc	tgtgctttgc	taaacagact	169854397
tcgccccctc	gtggggccgtc	tgtgaaaata	gggcccagct	cgatggcata	169854447
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cccacagggt	aaaggcctcg	tcccacaaaa	ctgccccac	ttcagacacc	169854697
agtggccagt	ctcagacccc	ctgtacttct	gaccaaccag	ctataagtca	169854747
aggattccta	agactccttc	ctcagggtcta	ataatttgct	aaagaagctc	169854797
acagaactca	ggaacacact	ttacttatgt	ttactgggtt	gttttcaagg	169854847
atgcaactca	gaaacagcca	aatgaaatga	ctgaatcagg	caagatatgg	169854897
ggttggggga	tgaggcatcg	agtttctatg	ccctctccag	gcatgccttt	169854947
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tttttggtga	ccagcccaat	cctgaagcta	tcaaaggctc	accaagagtc	169855197
acctcactgg	aacaaaagat	gctcctatac	cctcatcact	cgggaaactc	169855247
caagggtttt	aggggctttg	tgctaggaat	gggagacaga	gaccaaatat	169855297
ctatctattt	atttattttat	ttattttatt	tttgagacgg	agtctcactc	169855347
tgtcaccag	gctggagtgc	agtggcaca	catctgcctc	ccaggttcaa	169855397
gtgattctcc	tgcttcagcc	tcccagtag	ctgggactac	agggtgccac	169855447
caccatgcct	ggctaatttt	tgtattttta	gtagagacgg	ggtttcacca	169855497
tgctggccag	gatgggtattg	attccctgac	ctcatgatcc	aaccaccttg	169855547
acctcccaaa	gtgctgggat	tacaggcgta	agccacctcc	ccgggcccct	169855597
ttctatgaca	ccacagatgg	gcacagtcag	aatcagagcc	tgagggtgcag	169855647
gtcaaatacc	ttagccctcc	accagtcccg	cccacttggt	ttctgtggta	169855697
gaaagttttg	tttactatct	gtatctgtat	ccccaccaa	atgcgagctc	169855747
ccccatccca	ccctgatgct	gaactgagga	cactcagggc	tttgtgtggc	169855797
tctggcagct	tgcaaatgg	gttctcagat	gaggtattcc	atgccttctt	169855847
tcttgagta	gtaagagtca	atgcttttca	gttcagcaga	aattcatgag	169855897
atattagaaa	gcacttccta	gatctgcgta	gaagttggaa	taggttgcat	169855947
atagaagcta	ggaaggttcc	atccctggag	atctttagga	agatcccat	169855997
gctctgggtg	actcagtcgc	tcattttcaat	catgaattac	aggcattatc	169856047
gagttaagtc	accatgggtg	ctggacctgc	tttctccaaa	gtccctccag	169856097
ctgcagggtg	gtgagcccat	agatgggggt	agtgaagcat	tggttggtcag	169856147
ctcaccaggg	cacccttatg	agagtgaagt	agaccgtgac	tcctctgcag	169856197
ttgggttaagg	aagaggacac	tgaacaaagt	catgtgttaa	gagtggtgtt	169856247
tggttgga	attctgatcc	atctttcagg	accctgctca	agcatctcct	169856297
cttttgagaa	gcctggcctg	gccctctccc	catgccccac	tcttctctcc	169856347
ccagggttaa	ttaaatgtct	cttctcagct	ggtgtgacct	cttggttgat	169856397
tgcaaatagt	gcatactcca	ctctctctcc	acggaactgt	gagctttcta	169856447
agggccagaa	ccatacccac	ctcatctctc	actgcctccc	tggtgccatc	169856497

FIG. 1.54

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gcaggacagg	tggggcagag	caggggcccc	gtgggtgctg	gctaaattgt	169856547
tggagggact	ggctgggagc	ccatacatca	cagacagcag	ataccccagg	169856597
gactggcagt	gtgggaacca	ggtgagaagc	cccagttctca	ggtctgcagc	169856647
cttcctcagt	ctcctcactc	agtagccttg	attcccagca	aaccacatca	169856697
atttctcatt	gcacaccctg	ctcaatgctc	atctgcatag	tgtcctccat	169856747
ccagagcagc	cctgagctgt	gggcacgaat	actaatggat	catgcaaattg	169856797
ccagcctagg	gcaagagtgc	cctggactgt	caattagctc	cccccagcac	169856847
cagctacagt	gccccacccc	ttcacttgat	acaggccagc	ccaatgcaag	169856897
aaggagcaac	agaaaaagaa	ctcggcttga	aggactgctc	tagtcaagggt	169856947
agtgtgttgt	ggcagcctgg	aaagggatct	tccatgtaga	gtgaggggaa	169856997
aagagagcca	gcctggcctc	tcaggaagag	gttcccacag	gcactcttgg	169857047
gaggaaagggt	ggtgctcttg	ggggcccagg	taataattgc	tacacgaatg	169857097
ccacggctct	tggaaactgt	gcttcactct	tttccctcca	cctggccatc	169857147
tatgtgccag	gccaccagcg	tacgtcctgt	gttgtcctct	aaaccaagac	169857197
caaagctctt	cacagccact	cttctctgac	ccagtaccaa	ctccatcctg	169857247
ggagggagga	tgacaggctc	cccgtccctt	cacctcttct	tcccaatact	169857297
gctgtttcct	cccagttcct	tctcttccct	ccactgctcc	catctgcttt	169857347
ccttccttag	tggataaaag	cattaaattt	gaaggcagag	agatcggggt	169857397
caaaccaga	ctctacagat	cactcaagct	ttgtggcttg	ggcgaattac	169857447
accatgcctc	tgaacttcag	tttgctagtc	tataaaatgg	agaaaagaga	169857497
agtacctgcc	acagtggcat	tgtgaggatc	attttatgaa	tagctaagaa	169857547
tttcaggtaa	ctcactctga	tgtaccagaa	agttactttg	cttactgctt	169857597
caatcactga	acttaatttc	tactccaagt	tcccattcct	ctcagtggca	169857647
gagaaccttc	aatcagttca	ggatgcccc	tcccagtggt	tgcctgaatg	169857697
ttttgggggtg	ggcttacgga	gcatggagcc	tgaagtgggc	tctacctctg	169857747
gtgggcagcc	ctaccattcc	tacagaaagg	cacccaaga	ggttctgctt	169857797
cctgtgcatt	ctgtggtcac	tgtgccattc	aggctgcagc	tggggcctcc	169857847
caggctctag	gaggggtttcc	tggaccgcac	cactgttggg	tgcaggggaa	169857897
gattccccct	ctccttaccg	gacttgcccc	ggagaggtag	gtcaggaacc	169857947
cctgcctgaa	aaagacacac	aagtcaagtg	ctgtgcaatg	ctcctgctac	169857997
acacagagggt	ggcaggcctt	agaggggaac	cctaggctgt	gttcactctc	169858047
ccaggctcca	ctttggaaaa	gccagggtct	gctctcagct	cccacattcc	169858097
gccaaagtct	gggggtttcag	tgccaaacag	gccaccaacc	ctcgaactct	169858147
gcctgagggtg	gaggacaagg	gcaaaccctt	cttgctcctg	ccctccaacc	169858197
agtcacatat	tcttcagggc	ctttcatctc	aaaatccaag	atgtgaccat	169858247
tgtttccgtg	ccacctctgc	cacaggtagt	gaatgccgca	gctcaaattgt	169858297
gcggcagggtt	gtgtggtcac	aggaaataac	agaaggagcc	ccggttaata	169858347
tctcagttgt	atgtggcctc	atttttgcag	gccctgtccc	agagtcaatc	169858397
ctcagcacga	gggcagctga	gactcttttc	tcccccatte	cttcctcctt	169858447
ccctcttcct	gggtttcttc	ctttttcagg	ctccaattgc	agcagcagca	169858497
atgtctgggag	cggagatcct	gggagcccg	agccagctct	gacatgttca	169858547
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ctgcgtgcac	cctggcaggg	tgataatcac	agctgcagcc	cccaggcact	169858747
aaaaggatgg	gtgggagcat	catccaccac	tcaaagggtc	ggggaccctt	169858797
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gctgcctccc	tagagaaaca	gtgctagaag	tcaagtggca	gagcagcagg	169858897
aggacttgga	gctacatgca	gagtgtgagc	tccggagtca	gaccagctga	169858947
gttcaaggcc	agctccacca	tctattcact	gtgacttcag	gaagggttgc	169858997
taacctctct	gtgccttagc	tgccctcatc	ataaaacagg	aaacaatgag	169859047
agtccttctc	tatggggcta	ttgaaatgat	taagtgagat	caggcatgtg	169859097

FIG. 1.55

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atggcacaca	gtaagaactc	cataaacaga	ggtcaccact	gctaattgcaa	169859147
ttattctatc	acctcaggag	actaaagcag	gggaggaaac	accattgact	169859197
cctggacatt	taccaagga	gattatggat	ccatgttttg	cacacacttt	169859247
agaaagacaa	ggaattctaa	ccacagcatc	tgtctccact	gcccccgctca	169859297
tttcagtctc	acccgtccac	cctcaacctc	accactgtgg	cccggaaatg	169859347
cggttgccc	gggccaactc	cacccacact	cagccctgct	ctgctcaagt	169859397
ctcacttcca	ctccttccag	ctcccatccc	tttctaccca	gctccaccct	169859447
gattttctcca	ccatgacctt	tacctctcta	gtctgatcta	gacccctgat	169859497
cttgccgagt	atctaggact	ttggtgcctt	tgaccctcag	cagcagaggt	169859547
agagagggat	ctcgggtgaag	tctgggatgt	tatagtgact	tgtttatcta	169859597
agtgcctga	gactgtgagt	tccctaattgc	aggagacatc	aacctctgca	169859647
gagagcccca	gagccctgct	caggtgtgat	gaacaggagg	cactcacttg	169859697
atgcctcac	aaagtgtga	gtgaatgaat	gaatgagtga	atgaatgatt	169859747
gaatgaagat	tagtgattat	gttaatgacc	tgcctttttc	atgagccttg	169859797
caacctcca	ggtaccacac	taaagcactt	aatgcttcc	actcatttaa	169859847
tctcatagc	aaccctaaga	cataggcgta	attattgtac	ctattttata	169859897
gatgttgaaa	ctgaggatca	gtgaagttaa	aggcacacag	ctaagggatg	169859947
aatggataaa	atcctttacc	ataacctttc	ctccttagga	caaagtttct	169859997
tcaccaactg	tccaaggctg	tgtttcactg	gggagagtct	gaaattctac	169860047
accaagcatg	agcatgtgtt	catgcagcat	ggtaactctg	ggggaaaagg	169860097
ttcacagggt	ttatcagata	cttacagttt	gttagaacat	atgtgaatcc	169860147
atccatctaa	ccaccogtcc	cctttcaatc	cacccttctg	tccaccccca	169860197
gacagccatt	tgatcaatat	tcatgaaata	tctgccttgc	gccaaagcata	169860247
gtgctggcac	ccatgaattc	cctgggtctcc	agaaatatcc	ttccccctct	169860297
ccctgactac	ccctgcccc	gcctcaccac	acacacactc	cttgcaggat	169860347
ctgggtaact	gggagggtct	taccgccagt	gtcccagctg	cgtgggtggc	169860397
tgcactctgt	ctgaactcat	ctcagctctg	gtggagactg	tggcagcgca	169860447
gaagcgtgca	gggggaatcc	tcaggcagcg	cagccatcag	gacatgaagg	169860497
gcagagcctg	tgccccggct	tccccggctt	ccgctgcagt	ctacatcagt	169860547
cctgctccct	ccagaacatg	atcaaccggg	acagatgagg	ccatgcttga	169860597
tgcataagga	tgcagccagg	gagagctgcc	tcccaaacc	aagtcctatt	169860647
caaaggtctt	ttcttcctcc	tggggaggta	ggggagaagg	tccaagcaaa	169860697
gggaactgga	aggggaaagt	gaggcatgga	gtttgtgttt	totgaatcag	169860747
gactgtgttc	cagccaggga	gacctgtgt	caggcacttt	tgtaatcacg	169860797
atcactttca	gcctcaccct	gcgacctcca	acgacattgc	tgagattggt	169860847
ctccttgcaa	acatgaggaa	attgaggggc	tcaaagggtca	aataacttgc	169860897
ccaaagtcac	aaaacaaatc	cgggacttta	agcctgatct	gcttgacctg	169860947
aaactcatat	ctacttcctt	gccctctgaa	gatctatatg	tcctatgtca	169860997
tcacttcact	gttcacacaa	ggtgatacct	ggcttctcca	agcacctgct	169861047
accctgaact	tactgcacca	ctctttcctt	cctagCCTGA	ATGCAATTG	169861097
CAATGAGGAG	ATGATTTGAT	TTTCTTCAGC	CCTAGACCTC	CAGCTTCCTG	169861147
AGAGCAGgta	ctcttgcttc	ttcttgctca	ttattgatcc	atatatttag	169861197
aatagcgcct	ggcaggtaga	tggtgcttaa	taaatattca	ttgaataaat	169861247
gaatgaatga	atgatccaat	gagcccaaaa	gcaaataaca	ataaaggaca	169861297
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acccattctt	cacaacaatc	ccctgacatg	attgggttca	tgtttcacag	169861397
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tcatatgagc	tcaggggtaa	atgatgacac	cctttccctt	gccctgaagg	169861497
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agtggcggtg	gatgggggag	gtggaggtgg	ggtatgcaaa	gcaggaaaact	169861597
cggcctttgc	tttctaaaag	ctcccagctt	atgtgaggcc	agacttatgc	169861647
atgcagaaca	tttgggaaat	ggtacaagac	agcagcaagc	atagtgtctga	169861697

FIG. 1.56

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attgcacata	atcaggtgcc	aactgcattc	ccttccttaa	ctaactctgag	169861747
tcttttaata	ccagatgggg	accctgagaa	tagattttct	atcaaacaga	169861797
tgaagagcaa	agatggggagc	cgagggaaat	gctgtggctt	actcattttt	169861847
ataccctgt	aaccagcat	gatgtctggc	ccacagcaac	aggaataggg	169861897
cagtccacct	tcaataatgg	gccactctat	gtgccaggca	cctgctaagg	169861947
gccccacaaa	catcatgtca	ccaatccctc	acagcaaacac	taccacttac	169861997
taaaggaatt	atgaaagtaa	tccacaagaa	gctgaaagca	gggttcagag	169862047
atcgtactca	tcatgcccac	agtctcagag	taaaggggca	agctcagtgt	169862097
ttgaacccaa	ttctagcagc	ctcccaaatt	aatgctctca	atctgactct	169862147
atgctacctc	tgtgcctgga	aggaactact	gttgctccata	aggatgagaa	169862197
gaaacatggc	taagggagca	ctgagtaggg	aggaaggagg	cagcaggagg	169862247
gaagaaataa	attaagaaag	aaagagatac	aaagaggaag	aaaggagagg	169862297
gggagggagg	gaaagaacag	ggcttgtgtg	ttacataaac	tcagacaagc	169862347
acatgcatgt	tttaacagga	ttcctgcagg	tctgacaate	tcactccttc	169862397
ctccctgaac	aaccttagag	gggttgcccta	aggagtccta	tatagaggct	169862447
tatggcagaa	ggaaggcctt	gcgtccagaa	ctttctgagc	tcattggattg	169862497
acactggggt	tgcccatcag	tctgcttgga	atgccttcaa	aaaatacccc	169862547
agtctgggtg	gcttatacaa	cagaaatcta	ttttctcatg	gttctgaaaa	169862597
ctggaagtcc	aagatcaagg	tgccagcagg	gttgggtgtct	ggtgaggcct	169862647
ctcaccttgt	gttgcaactg	ccttttccct	gtgtgctcac	atggtatctt	169862697
tgtgcgtggg	gggtcttttg	agtctctcct	tgtaaggaca	ctaactctat	169862747
cagatcaggg	ccccaccctt	atgacctctt	ttaaccttca	ttagtctcct	169862797
agaggtccct	tcttcaaata	cagccataca	ggggccttaga	gcttcaaacac	169862847
agggattttg	gagggacaca	aacattcagt	ccacaccggg	gtgcatgagg	169862897
gaggggtcag	agctggagaa	agtgcattgag	ctagttcacc	ttccagagta	169862947
aaggggagcaa	cagccactga	agctcagggt	ggatggggct	ggcaaggctc	169862997
ctgtattgag	tacatcatgg	gagggacaac	aggacaaatg	gctcctgcag	169863047
tcaggggtgac	tgtggggag	cttcttcagc	actccctctg	cacattcatt	169863097
ttgtcactcc	ctctctcccc	atgcagttct	ttgctctctg	ttgcaagttc	169863147
ccaggaggca	ggcagagggc	ctgttatcat	cattctttct	tcttgccctt	169863197
cacacttacc	tgtgttcttc	tacttagaca	cattctttgt	gagcatctca	169863247
tgggtgatgt	tggctgcatt	gtacagtggg	cacgtgcgta	tgtgtgtgta	169863297
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gctattgtgc	atgtaaataat	ctggtacatg	gtagatacat	gaatgaatga	169863397
atatttgttg	aataaataag	tgaatgaatg	aatcttcact	tggcagagca	169863447
tgtgtcttcc	tttaaggggc	aaggatgatc	tggtaatcat	cagtttctgc	169863497
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ggaacagcac	gtgcaaaggc	cctgaaggag	aaccacaaca	cgcattctgag	169863897
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gatctgcaaa	atggagcaag	tcattctgtac	tctgcttctt	cagtgggttg	169864147
tggggaagca	gaaatgagag	gatgacattc	tagccttttg	tgacctctca	169864197
agtgtgtcc	ttatgggtcat	tcaggtagca	tgaaaattag	cagagcccca	169864247
agggggaagt	agcttggtgc	tcacccagtg	gtatccctga	caagttggca	169864297

FIG. 1.57

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aagacaccca	gggtggctta	actttctcct	cagcaaagag	ctctcctctg	169864347
ttccctgaat	cctggatata	ccactgggtc	ctctagtgaac	cccaagcttc	169864397
agcctcgcat	gcctctcttc	cgaacagaga	aggcaggagg	gaagcaggga	169864447
ccagcccttg	ctccatcttc	caggattcca	ggcctccctg	gcctggacaa	169864497
gccctgagct	ggcagttagg	agagcagagg	ttgtgaatct	ggtgggaccc	169864547
ccagcaggtc	tttctggctc	agtgcctca	tctgtgagca	gGGGTTCCTC	169864597
AGGAGACCAC	GACAGAGGCC	TGGAACCCAA	GTTCTAATCC	CACATCCTGG	169864647
CTGGGCAACT	TCAGGCAAAT	TTCTAACACA	AGgtaagcct	caatttctct	169864697
ctggggtaat	gatcaggcac	ctgcttaatt	cacaggggtt	tggtgggcat	169864747
cacgtggaca	atgtgggtgc	acagcagtg	gcaatgcaaa	ggaaaggaag	169864797
tatgttagta	agtgcctctc	ccctgttgca	caaaacagga	cacatgctgg	169864847
gattgcagaa	aagcaataaa	tgctgcacag	gtgaagaaaa	ctattcaagg	169864897
accctggcca	agtcacaggc	tacctgtggc	cctgagggga	cagctcatgg	169864947
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ctgttttgc	gtgtgtgcgt	ctgcatgcct	gtgtgtttgt	gtgtctctcc	169865097
accttcgtgg	ggggcaactg	taggtgtatt	atgagccttg	ggtctgtctg	169865147
tgtgtacaat	agcaatgtct	gtgcggactt	aaggacctgc	gcccataatgt	169865197
ttgtgggact	ttctgggcat	gcatgcttgt	ttatgaggcc	atacatccgg	169865247
gtattctgtg	aactgctagc	atgggtgtga	tctgtgtggc	agacagaaaa	169865297
tggtctgggtg	ggattgtagg	gggcagcttg	ggcaaaggat	cctcagtgctc	169865347
aatcaaaatg	ggtctcagtg	ggaacccaag	cagctcagac	ttggggggagg	169865397
ggaagctctt	cctccacctt	ccagggagca	aaccttgcaa	ttcaacacca	169865447
caaggctttg	agtccacagg	cagggacgca	aactttgccc	attgggtgag	169865497
acgccactca	cagaagggaa	atggcttctc	aaatctaate	attgcccctt	169865547
caagcactaa	caaccctgtc	ccaggagctg	atggctaattg	aattattgag	169865597
ctggaaaagg	agaagaggta	gaaccaagga	ggaaagaaac	agaaaaatga	169865647
gagagcaggc	cgggtggggg	ggctctcgcc	tgtaatctca	gcactttggg	169865697
aggccaaggc	gggtggatca	cctgaggtca	ggagttcaag	cccagccagc	169865747
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gggcctagt	gtgggcgcct	gtaatcccag	ctactccgga	ggctgaggca	169865847
ggagaatcgc	ttgaatctgg	gaggcagagg	ttgcagtgag	cagagatcgc	169865897
accactgcac	tccagcctgg	gcaacagagc	gagactccgt	ctcaaaaaaa	169865947
aaaaaaaaag	aaaaagaaaa	atgagagtg	aaggggcccag	aggggctgag	169865997
ggctcctttc	tcctcccaaa	ctccctgtca	ctagaagggtg	ggccctgcca	169866047
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ggcagacttt	ccccctcccc	atgagttcag	gcagtggtgt	aaataagatt	169866197
tcccttgaag	tcgaatgaaa	tcacaatgca	ccacacacag	ggacacacac	169866247
acacacacac	gcacgcacgc	acatcacaca	cacacacaca	cacacacaca	169866297
cacacacaca	cacatacaca	cacacagctc	ccctgggggc	aatctactgc	169866347
cccctgaacc	tcacccatca	gccaggtgcc	tgggcccggg	tctgtctctt	169866397
agggttacat	gctcccgggg	ctcccgcaca	taccccgcca	gatgagggtg	169866447
cgcaggggtg	agggcgaggg	gctgggcgtc	ccccgcccc	accgtgcagc	169866497
cctcgcccc	gccccgcccc	tccgtagttg	cccgcccc	gccccctccg	169866547
ccgccccctc	cgccgctccg	actctcgccc	cgagcgctgg	cagcaggcag	169866597
caggcagcag	gcgggcgcgc	tgtggctccg	cgccgcgcgg	tcgggctctt	169866647
gttcattcat	gattggtact	cggccctccg	agacccagcc	cgagcgaggg	169866697
gaggggagcc	gagtgtgcgg	caggaggggg	gggcggagcg	cggctcccgc	169866747
accgcacgcg	gcgctggctc	ggcagcctcg	gccgggcggc	cgctctgggc	169866797
ccgtgtccag	tgccaggcag	gcttcagggc	accgtcctcg	gcccctgggcg	169866847
agggaaaccg	cgggcggggg	cctcgcgcg	ggaagcggtt	ccgaaggctc	169866897

FIG. 1.58

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gcggggagcg	gctagccctg	agtccctgca	tgtgcggggc	tgaagaagga	169866947
agccagaagc	ctcctagcct	cgcctccacg	cttgctgaat	accaagctgc	169866997
agggcagctg	ccgggcgctt	ttctctcctc	caattcagag	tagacaaacc	169867047
acggggattt	ctttccagGG	TAGGGGAGGG	GCCGGGCCCC	GGGTCCCAAC	169867097
TCGCACTCAA	GTCTTCGCTG	CCATGGGGGC	CGTCATGGGC	ACCTTCTCAT	169867147
CTCTGCAAAAC	CAAACAAAGG	CGACCCTcga	aaggtaagcc	accttcttcc	169867197
ttttgttccc	ctgtctgggc	ttgggggtgc	taggcgccga	ggtgggctgt	169867247
gccacctgcc	tcccttagtc	cggactctcc	tctccacgag	gagcccggac	169867297
aggtgcttgt	atccaaagga	gagagaaatc	ggcgggaggg	ctggtgtgaa	169867347
caccagaggg	agggagccgg	agtggacgtc	tgccccagcg	gcaactggac	169867397
ccctctgggg	caccaggtgt	cgggactctc	ctcctgggga	aatctctgag	169867447
agccgaagga	agcggcatgt	tcacaggtgg	gggtgaccgg	attctctggt	169867497
ggaagtgtgg	tgaagctctt	cccattccca	tgacagctgg	cgtttgagca	169867547
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tcccaggcct	catgtcctgg	tggtccggg	agtccaggag	agcaaccgtg	169867747
aagggtggc	tgcgagctga	gcttacatca	aggattaaaa	agcataatat	169867797
cgtggagtct	cttctgcctg	gacgtgttcc	cttcaccacc	tgtccccagc	169867847
cgaggcatgg	ctgatctcac	catccgtggg	agagtccctca	aatgggtcca	169867897
ggtgaagtgt	gaaccagtgt	gttgggccc	ggaggacaat	gcaggtctcc	169867947
ttaccagcag	ttcaaaagtt	agtgggttga	ataaagagac	tggaagcagt	169867997
taggaaacgg	gaaatgatgg	gttttgtttt	gtttaatgtt	caaattgtcac	169868047
tacgagtggg	aagattttta	gcagcttgac	acttaaacat	tcaaattcta	169868097
ccatcagagc	ccccatcctg	gatacaggtg	ggagttaagc	tcctacccta	169868147
caggcctgat	agtgagtaga	agtgtaatgg	ggtaagggac	ccaagtga	169868197
caataagtct	cctcttagaa	cttgggttgg	ctcaccctgt	ttagaaccac	169868247
agagatctcc	ataagtaagc	tgtccttgaa	accccttggg	agaaggggtc	169868297
ccagcttctg	gcccagctcc	caggggcctc	aggctggctg	agccccgagg	169868347
aaagagatct	ctgggtgcag	atcttaggtg	ctgaagctgg	gttggcattt	169868397
acatcctaga	acataggaag	aggctttggc	ccatttgtcc	agctgagtta	169868447
catgtcctgc	tggcaaggaa	gggactgggt	gtcctgttac	cagtcctgac	169868497
cagaacaggt	ctgcaaagct	cagcccaagg	ccttgacatt	ctaagcctca	169868547
cctctcacag	atcctgggat	gctgcttgac	tggggacaat	tttcagcgcc	169868597
aaatataggt	cttctccctc	atcatctgtc	tgaccaccat	gcggtctcag	169868647
aggccagggg	actgtgggga	caggaaagtc	aggggcttgt	ttttaaatat	169868697
tttcaatgcc	tgtggctctc	ctgggagctg	ggtgtcacag	aaagatctca	169868747
agccctagag	tcaagtggag	tctgggtgtg	aatcccagct	ccatcactcc	169868797
ctgcctctgg	gaccttagga	aagtcccccg	cacctcccta	agcctcagtt	169868847
tttcatccat	gaaattcgta	tgctaacttc	cggagggaag	ggtatgtagg	169868897
aagtagagga	aggggaagact	ctgcctcata	tactgtgttg	gctgcagcca	169868947
ccagggaccc	agaggaagtt	gttgtaagga	tgtgagaatc	aaatgaatga	169868997
tgaataggga	gctccgtgca	tagggctggg	aaaagagtaa	gagctcagac	169869047
attgctgtct	accatttcc	tctcctgccc	caaacatcca	ggaattcacc	169869097
ctggatgaat	tcctgcagga	ttcccagagt	acaaaggtct	ttgcttctgt	169869147
ctcctcggat	tctaagaaac	agaagagggg	gtactggcat	tcagtgtgtc	169869197
cctactgtgt	gcttgccata	atgctcgggt	ttttatcaac	aactctcatt	169869247
taaccctcac	aacaatgttc	gtttgaggct	catagcaggt	tcggggccaa	169869297
tgggtggact	cccaagacaa	gctatcgaag	cactgggcac	tcagcccttc	169869347
ctgcacaaag	cccactggcg	tgagttgtcc	aggggtccag	ctgcataatgt	169869397
tccccaggt	atttgcccc	gaagcacagt	catctcactg	cottgcatag	169869447
tggaatgcta	atcagcagaa	gacccttcta	tgggaggcag	cttggaacc	169869497

FIG. 1.59

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tggaggaagc	cctgggtgag	gaggctagtg	gtcagggagc	ctatcctggc	169869547
caggtcactt	ttccccactg	gggcctcggg	ttcttctttg	taaagggaga	169869597
aacttacatt	aggcatttcc	tcagggtcca	tttggttctc	aaatttcta	169869647
atTTTTatgg	ttgatgctct	caccagagct	gctgctatga	tctcagagac	169869697
gtgaggctca	gatctaatta	gaagcaaccg	gaagagagca	gttgggattt	169869747
ttcaactcag	gaatcagtct	ccctgctggg	ttcaaattca	ggctctgcc	169869797
cttactagct	gtatgactaa	gccttggttt	cctcaactat	aaaacagaga	169869847
tagtagtagt	taccatctta	aaatagctgt	tgtgtgtgtg	ggatttcaag	169869897
gatcatgcaa	gtcaagcatt	tagcacagtc	tctgctacat	aagtggtcag	169869947
caaatttgag	gtactattca	atTTatggct	ctattgtttg	gggcttccaa	169869997
atgtccagag	taaggccatt	ttcgaagtag	gcagtacatc	tgagagcctt	169870047
aacagctcat	ttctggaaac	cttatccagc	cctatccaga	taactaggac	169870097
caaaaacccc	agcacacaga	tgctcgtccc	ttgcttcaac	cctcactgac	169870147
ctctactctg	tggcttgctc	tgaaaacatc	aaagcctgct	caattaaaat	169870197
cctgaatgcc	ttgataatac	aatttagaaa	catacatagt	ttttaaatag	169870247
ggcaaaaact	ctgcatgatt	agtgcgtgcaa	gaagatatcc	agcccaacct	169870297
gggtgttcag	ggagcgtctc	ctaaaggcaa	cagaaatcta	aagtaattta	169870347
agagccatgc	cactgaataa	aaatattcag	gttcatttcc	tgtccttctc	169870397
tctgtttggg	atctttgtgt	gtctttaatt	aaaagtagga	gagccctgct	169870447
tttgggattc	agcctctgca	tcccagtcoc	agatagaatt	tctgactcta	169870497
gcagttttgc	atgtgcatga	cacaccaagg	acactgctcc	tggccttgaa	169870547
tgggtaagtg	agacaggcta	gggcattgag	gagaaccaga	ggaggaccat	169870597
acaggtgcag	ctgctgggct	tgtcagcggg	gcaggagaat	ttagggacaa	169870647
catcactaga	ccaaggccat	ctcaacagag	aattgcctag	aagcaaataa	169870697
tcccacacta	caggggtggc	tgggttagaa	atcctccatg	accgagtgc	169870747
agcatgcaga	actttctgaa	agggctgagc	ttcggatctc	cagaatagtc	169870797
atagcatagg	tgagctatga	ctcaacccca	tggctatcag	atgctttttc	169870847
taaggcccaa	cggtgagtta	atagggtact	ggttaataata	gggcaaaca	169870897
tgggaattgt	ccgatagtc	ccatatttgc	tcctagatca	atgagcacct	169870947
cagggaaactt	atggaagcag	agtgtacctg	atgagactgg	gtttagggtt	169870997
tattggtcag	ggcagcattt	tcaacctaaa	gatatgggag	agtgacaaga	169871047
gacagacagg	catagagaag	cagtagccgt	gttgtcacat	agtcctgagc	169871097
ccaaggggca	ggcctttggc	aagtcatttc	accttgtaaa	tgctagtttc	169871147
tttatctgca	aaaggagaat	cctgatgtat	agaaatgttt	gtgctttggt	169871197
ctttaccocat	ctttgcatct	ttgcctgtcc	ctttaattct	ataatgctct	169871247
cccacccac	cccttgctgc	cttgtcta	agttaaaatt	ccaccgacat	169871297
tccaagacct	cactcagcaa	tttccatatt	caggaagcct	tctccaagcc	169871347
ccagagagaa	gtgattttct	ccatctgaat	tcccatatcc	ttttaagggtg	169871397
tacattttct	tatgactcac	aatcgcgctt	ggaattagac	aatcaacgga	169871447
ggtgttaacc	ccctttcccc	accaccagag	gtcaggggtc	ttgggggtag	169871497
gagctcgtct	aactcatcct	tcacaactct	ctgcttggtt	ctgtgcacat	169871547
agtaggtact	taataaaaa	tttccctagag	taaactataa	ataatggaat	169871597
ggttggtccac	tctccattat	ttgctagaat	tgcagaccct	gcaggaaaag	169871647
ttagcttccc	accggaattt	cagttaccag	ccctctgcca	ggaatgaatt	169871697
ctgttggtcg	gtctgctggc	tttgaattga	ctttgtccat	gaaatgtacc	169871747
gaatctgttt	accatttagc	aggaaagtgc	tgagaacagt	gattctactc	169871797
ccactccctc	ataatcacia	aggatatgagg	aaccacacac	cagcaccagg	169871847
cacagttctg	gtccctcaat	cccagaagaa	gctcaatgga	gctcaagata	169871897
aacagaaaga	gagagatgga	aaagaatgga	agacagagga	gaaggactta	169871947
ctgcctaaaa	tcagtgggat	tgttttgact	tggtctctgg	aaaagggcca	169871997
aggcttagac	ctctttgtct	gcctggaagg	gccttgctcc	atgaatgctt	169872047
tgtaaatctg	taagtgaata	agtgagcata	tgctttaaca	aataagtga	169872097

FIG. 1.60

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aagatgaatg	attgaatgaa	tgggggaagc	agtaaaggag	tgaatgaatg	169872147
aagcaacaaa	tgaattatca	actgaatgac	agaaagaatg	atcgaataaa	169872197
tgaccacatg	aatgaatgaa	tatgtccata	aatgaatgaa	tgatgaagtg	169872247
ccagaacagc	tataattaac	agcctatctt	ttcacaaaga	gcattgatag	169872297
tcatctcccc	aaagttgaaa	aatataaatt	cagtcaagaa	gagtcctggt	169872347
aatttttttg	atactggtag	gtgtatagtg	tcttttgaga	aggtgaggag	169872397
atgtctctaa	gttttcactc	ttttgctgaa	acaaaagcag	ggactgactc	169872447
acagtgattc	cccttgtctt	cccttatatt	tcaggttcgt	tcacccttgc	169872497
ctgggtgaga	tcagaatctg	tatatattatc	cactcattta	tttgttcact	169872547
tagccagtc	cacaattgtc	cttcagcatt	gcttccctgc	ctaagatcca	169872597
ctctggcttc	ctcatcctcc	ctcttcctcc	atctcctcat	tcacctggcc	169872647
aactcctact	tatctttcaa	ggcctcattc	aatgccaccg	ctctgggaag	169872697
cctttcctgg	cttctgtagg	cagagcacat	ctctgccttc	tctctttccc	169872747
catagctgct	gctgcttccc	tttaactaaa	ttctgaacac	actatgaggt	169872797
tgtcattatg	ggtttacaca	tttatctctc	tgactagctt	tcaggcactg	169872847
agtcttatcc	cagggcctct	gtcaggcctg	acactgcac	caggcttgat	169872897
ggatgctggc	ggcatggagg	taaggatgga	tgggccagag	tgtgcgttct	169872947
tgatggctct	gagcgggtgtg	agaatgcggc	gggtgcagatg	aggaatccag	169872997
gtctgctcct	ggggagaagc	tctgcaaaat	tctgcataat	ggccgtggag	169873047
ctgatgttcc	cattcatcag	gcagggaagg	aacagttttt	agaaaagaga	169873097
gagagagcct	aagagtccca	gggccttcag	agaaacatct	ctttaaatgc	169873147
ttccctctcc	tccgggtagt	attttaaata	ggtcaccttc	tgggaagtagt	169873197
ggtagtcagt	tgggatattg	ctagcttccc	gtaccccagc	catgggagta	169873247
gtactttgga	ttaaatcttg	ttattcaagg	ccagactaaa	agcctcattg	169873297
gtgcgggtgg	gggaagtagg	aaccacattc	cactcaaate	aggaagctag	169873347
aagtaggatt	gcattatggc	tatgagcacc	gcgttaaaat	aagagtcttg	169873397
ggattgaact	cccttccatt	ggttcatagc	tgagcctttc	caggcctcag	169873447
tttccctctc	tataaaatgg	ggacagtggtg	ccaggatagg	tggctcacat	169873497
ctgtaatccc	agcagtttgg	aaggtcaagg	tggacagatc	acgaggtcag	169873547
gagttcaaga	ccagcctggc	caatatgggtg	aaaccccatc	tctactaaaa	169873597
atacaaaaat	tagccggggca	tgggtggcatg	ctcctgtaat	cccagtcact	169873647
caggaggctg	aggcaggaga	atcgcttgaa	ccgaggagac	ggaggttgca	169873697
gtgagccaag	actgcaccat	tgcactccag	cctggatgac	agagcgagac	169873747
tccgtctcaa	aaaaaataaa	aattaaaaaa	tggggacaat	gacagtgtct	169873797
ccctataggg	ccacgtgagg	gccaagaagg	aattgaacat	ggtgctgcac	169873847
accaggtgag	ttggcagtg	tggctttgct	gctgcctttt	gtcccatctc	169873897
aggacaggcc	ccttccctct	gccttgctcc	acttggatga	tgacggtggt	169873947
acccttggtg	atctcccat	ccctttgagc	tgtggcctct	gattccagcc	169873997
ctctgagatc	ccgagccacc	atatccatgg	tcactggcat	tctaagcagt	169874047
ttctctggtg	attcctaagg	gaagctgtca	acttttagatg	gtaaaagcaa	169874097
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cggtcttttc	ctgtgttatt	ttattaaccc	caaccctgga	ggacaagatg	169874247
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aagtgcctta	ctaaggggtca	tagagcttgg	gaatcgagga	gcctggttct	169874347
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cctggctttg	cctctggaac	cttagggacc	tgagtagaaa	aacagtcaaa	169874447
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gcttttagcc	ccatcccaac	cccgcctccc	cctagatctg	tttccatttc	169874597
atctgacact	gtggaagcct	gaatatgaaa	tgattggggg	cagaaggcca	169874647
attagcaaat	tcattaatag	gattaaacat	ctctcctctg	ctctaataat	169874697

FIG. 1.61

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ttatgtgaac	taaaattttc	tctctttgtt	atagccatca	ttgcctgtca	169874747
gtgaagatag	agtgtttaaa	tatctttcaa	gtatgttaga	attgcaaacg	169874797
ttcagaacca	gggaccagga	tcagagtttt	cacacgggcc	aggtgggcaa	169874847
ggagatcagt	cggttttacaa	gtggttatca	ctgctaagaa	aaaaacacaa	169874897
gaacttgcta	gtacattttgc	aagtacotta	ctgctcatct	cctttctctc	169874947
cttagccaca	tgttggtcca	aatcacctgc	gtatgttata	cggttgttat	169874997
gagcatacac	tcctgggttag	gcagacctag	aattcaaatac	ctggctctgc	169875047
aactcattag	ctgtgtgaca	ttgagcaggt	tacctcgctt	ctgtgaactt	169875097
tcattctctac	ataatctaga	aaatgaaagt	attgttgata	attccctccc	169875147
aggttggttat	gaggattaaa	tgcagtcattg	catgtaagat	gcagcgggtca	169875197
gcactcagaa	tgcgctaaag	gtaaattgtt	actatctggg	tctactccac	169875247
ttaaagtgtg	ctcctccaac	caacagcctc	agcatcagtt	gggagcttgt	169875297
tagaaataca	gagtcctcggc	caggcgcggt	ggctcacgcc	tgtaatccca	169875347
gcactttggg	aggccgaggc	tggcggatca	tgaggtcagg	agatagagac	169875397
catcccggct	aacacgggtga	aaccccgtct	ctactaaaaa	tacaaaaaaa	169875447
ttagccaggc	gtggtggcgg	gcgcgtgtag	tcccagctac	tccggagggtt	169875497
gaggcaggag	aatggcgtga	accaggagg	tggagcttgc	agtgagccga	169875547
gatcgcgcca	ctgcactcca	gcctgggcca	cagagcgaga	ctccatcttg	169875597
gaaaaaaaaa	aaaaacctca	actcagtgag	acctaccag	tcagaacctg	169875647
catttttaaca	agatcaccag	atggttttata	tgcccactgg	agtctgagga	169875697
atactggcct	aaagtacaga	ttatggaact	atgtgtattg	tattacacaa	169875747
aattatatat	caagccagaa	gaggcttttg	ctaagacttc	tgattttaagc	169875797
ctcattttac	aaataagaaa	atagaatoca	gagaagggtga	gtggtttgcc	169875847
cacaatcaca	cagctcaagt	gttaggcctg	acatccgaac	cccagccctg	169875897
gtcatctcat	ataaattgtt	aagaagtcag	atttccagat	ttgcattttct	169875947
gcaatcaagc	ttgtctgttt	ttctttctct	ctctttcttt	ttacaacaa	169875997
agaagtgcag	gatgatgtac	gccatttaag	ttttagttta	ctcattttta	169876047
atgttattcc	agccaacaga	gatcctgaat	cttgactcca	ccagccatca	169876097
tcttagctgt	acctccaagt	tttctgctac	ctgaagaaat	gataaggagg	169876147
cattctaggt	ctttatctaa	gttgcttcta	agaactggg	ccagaacagg	169876197
gtgcaggaca	gagccatgtg	gactgcgaact	agagacttgc	ctgcataatg	169876247
gatttcatctg	ataatgttca	gaatccaga	gcaggatggc	agcctgggtt	169876297
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aggagtctaa	acagacacag	gtagggcctg	gggaatgaaa	gtcaaatgcc	169876397
ttttccaggg	ggtctagtag	gacctctctg	ttgggtgggga	tcccccaaaa	169876447
aagtaatcct	tttatttttg	taggagtcct	gtaatgggtt	cattattatt	169876497
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agtgattagt	aagcaaggac	ttgaagtggg	tctgattgag	aggcactcca	169876597
ccacctgggc	tcctgcctgc	agctggaggg	catatccagg	acaagcaagc	169876647
ctctgagccc	caggaagagg	ctgagcagtt	acagctagtt	tcccaactcc	169876697
caggaactga	aaatgacagc	ctcctcttgg	ccccatcagc	tcctcaccca	169876747
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gtctgccaaa	tttggttttt	tcccatgttg	actacttttag	tgactttttct	169877197
gaaataaaat	gtgctttcaa	aacacaattt	ttgatgcctc	tactttgcta	169877247
gtgctttaag	catctcttga	gtgtgcctgt	gagggtatttc	agcattggag	169877297

FIG. 1.62

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ttggaaccag	acaggaaaag	gaaagaaacc	gatctgtatc	gggcacctgc	169877347
tgcattgcaa	ggactgtgca	aggtgttgac	aaaataacaa	cagtaacaaa	169877397
cataacattt	aaatcgctct	tgtgacattt	atatagcaat	ctgtgccaa	169877447
taccactcta	agcgctttcg	gtacattaag	ctaattttaat	cctcacaaca	169877497
accctatgtg	gtaggtagt	tgattattcc	catgtaacag	atgaaatctc	169877547
acactatgag	agacaggcac	tgatccccct	attttataga	tgaggaaact	169877597
gaggcttggg	aagaagtgc	ttgcccaggt	gccccgatgc	ctggtggaag	169877647
aacagtgttc	acaccagctt	tggccacttc	caaagccctt	gatgttgaca	169877697
ctccaaatgc	aggcctcact	catttcctag	aagcgcttta	tgatttgata	169877747
tgtctcagg	gtgcattata	agaggaggga	ggaaaacctg	ggactacaat	169877797
gagcattgaa	tcttgtcctg	atcttctcag	ggaccctctg	tcattcccga	169877847
ttgcctattg	catctgttct	cacctggtac	taccattccc	tcctccctgg	169877897
tttttccctt	gctaagtgc	cactctatac	gttggtccat	atcatgtagc	169877947
ctctgctgga	ggcaagtctg	gttcccatct	gccttcccct	gaagaagaag	169877997
ctgctggaaa	attagagtta	tgttggacac	agtctttgtc	cccaagggaac	169878047
ttctctctgg	tcataatcat	tatatataca	gcaaacctat	agcatgctat	169878097
gtgctagaca	cttttagcaac	ttggttttat	gtaagcctta	cagtatcccc	169878147
aggaagtgc	cactattact	agaccctttc	cagatgagga	cactgaagac	169878197
tagagggcat	aagcaaatgt	ccaatgtctc	acttctcata	agtggaaaag	169878247
ccaggattcg	aaccagatg	gtttgcctcc	agtgcctgca	tgctgaatca	169878297
ctggactagg	ctggacctga	gcatttagag	gacattatag	attatgtaac	169878347
actgtgggga	ttcagaggat	ggagaaagca	cctctatctg	aggggcaggg	169878397
gctggagaat	tagagaagat	ggccgaaaga	ggcggcatta	gagctcaaca	169878447
aaagagctag	gggttggccc	aggcaagaat	gtagggttagt	gaagttctag	169878497
gcagaaggaa	caggataagc	aaagtacacag	aggcaggcaa	caagaagggg	169878547
aaagaaatga	aaactgacag	tgatgttttg	tatgcttgtg	acttggagga	169878597
tgttaacaga	aagaggatgc	catcagaagt	gggaggcaag	gagcagagtc	169878647
aggctgtcca	tgttcaggag	aatgggacaa	ggtcctagga	ggtagtagac	169878697
agcaaggatg	aggaaagcac	caagcaagta	gggatcgaga	ctgtgccctc	169878747
tcagcaccac	ccttgtcccc	ctaagtgtct	ccccgtgatc	actgcagctt	169878797
acatttgatt	cctccttctc	ctctcccagg	gaacttacta	tttgtcccca	169878847
tgatttagcc	tttgattacc	ttgaactggt	ctatcatcat	tcctgtaaa	169878897
cacgcttgac	tctccagcaa	gagtgcacct	tcctcagaga	cctggacctt	169878947
tctttcttcc	cttctcagca	tcttcgagca	tcaccaggaca	gtactgggca	169878997
aaagactggt	acttgggtgac	ttgaactgat	atttcacaga	gatgcacaaa	169879047
gacttgggat	tccttaatta	gaattcatgc	ggcagagaaa	cttgggcatg	169879097
actttgagga	tctccccac	cgcacaacag	catattcaca	agatacgaac	169879147
atcaaagatt	gtggcttggg	gtgaaaacat	agcacattgg	aggccattcc	169879197
ataacagctt	agagctgatg	aagagaaaaa	gatatggtgt	gttgggtgaa	169879247
atagaactga	aggccagctc	tagcttaccg	tttaggagct	gtgtggtttg	169879297
aagaaattgt	ttagcccctt	tctgcatatc	agcttcttca	tctgttaaac	169879347
aataacaatc	atggtatcaa	ttcattggat	tgtcatgagg	attagtgaga	169879397
taatatgaat	gtgttttagta	agctataagg	cagtgcatac	gtggtgggga	169879447
tcagtattag	atgacaataa	tgggtcatagc	aataataatg	attttgatag	169879497
tggttggtgat	gatgtttgtg	atggtggtgt	gatggtggtg	atggggatgg	169879547
tggtattcgt	ggtggttaatt	attatattat	ggatgtgtga	gtctgttttc	169879597
acactgctgt	aaagaactac	ctgagactgg	gtaatttatg	aagaaaagag	169879647
gcttaactga	ctcacagtcc	tacaggcttt	ccaggaggca	tggctgggga	169879697
ggcctcagga	aacttacaac	tgtggcagaa	ggctaaaggg	gaagcaggca	169879747
tattttcaca	tagtggttagg	acagagagag	agcaaagggg	ggtgtgctac	169879797
atacttttaa	acaaccagat	ttcatgagaa	ctccctcact	atcacaagaa	169879847
cagcttgggg	gaaactgccc	ccatgatctg	gtcacctccc	accttgtccc	169879897

FIG. 1.63

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tcccccaaca	ttattaacta	cagttcaaca	tgggatttgg	gtgaggacat	169879947
agaggcaaac	catatcaagg	gataatattg	ttgatgatgg	cagaggtggt	169879997
gggtgacagta	atgacagtag	gggcttcatg	gcaataatga	tgatgatgat	169880047
ggaggattac	aatatttagtg	gtaatggtga	ttattatagt	ataggtgatg	169880097
ttgattataa	gggtggtggt	gggtggtgaca	atggtgatgg	tggtagtgat	169880147
gggtgatgatg	atgataatag	taatgatggt	gatatggttag	tatgacagcg	169880197
atggtggtat	gggtggtggtg	gtgatgatag	tgacggtggt	gatgatggtg	169880247
atggtgatgg	tagtagtgat	gggtggtgatt	atggaggtgg	tgatggtgat	169880297
aatggtaatg	atggttagtga	tggtggtggt	ggtagtgatg	atggtgaagt	169880347
gatagtgatg	gtggtggtta	tggaggtggt	gatggtgata	atggtaatga	169880397
tggtagtgat	gggtggtggtg	gtagtgatga	tggtgaagtg	atagtgatgg	169880447
tagtggttat	ggaggcggtg	atggtgataa	tggtaatgat	ggtagtgaag	169880497
gtggtggtgg	tagtgatgat	ggtgaagtga	tagtgatggt	ggtggttatg	169880547
gaggtggtgg	tgacgatagt	gatggtggtg	atgataatag	taatgatggt	169880597
ggtgtggtca	taatgatagt	gatggtggtg	gtgtggtggt	agtgatagtt	169880647
gtgatgaaag	gtggtgatgg	tggcagtggt	gatgatagca	gtagggctga	169880697
tggtggtgac	agtgggtgatt	atatagtgat	gtaagtagta	gtgttgttgg	169880747
aaggatgata	gtggttagtgg	tgtcaacagc	actggtgaat	ttaaggcaat	169880797
cattcccttt	gtccaaacta	tcttctttga	ctaggctgca	cagaaggatt	169880847
tccaaccccc	agaacttgaa	ttcccccagg	tgtatttgtc	aaaagtagga	169880897
aagaataaga	caaatcagcc	catgccttca	gatttcttct	cttattcctg	169880947
gttggtactt	tcagaatcat	tttaatgtaa	gctgctttct	tgacatttgc	169880997
attccagcac	gtggcacagt	gccatggctg	gtacatcgtc	aagtcttcaa	169881047
taaatatattg	tgaaatgaag	ggatgaactt	gcagaaagac	acaggctggt	169881097
ctcttggtatg	aactcatcag	agttaaatgt	ttcatctttg	aagataacgc	169881147
gggggttatc	aggcacatca	gaatatacct	gcattaacac	tattgccagc	169881197
atgagcaatt	cgataacctg	gcagggtggg	aagatttctt	ggcacctaca	169881247
ctgcccctgg	aagcccccg	atgtcagctt	ggcctggccc	ttgtaccac	169881297
cactttgccc	tcagaggtag	ggtctgttct	actgggattc	tgtgctaact	169881347
gatcacagg	aacagtggg	aaaatggcct	ctcccaccgg	ctgcttctgg	169881397
agagtccea	cctccctcct	cagtgcactt	gctgtcgccg	aggaatgaga	169881447
ggcacatcct	ggctctggag	atgttcttct	tggcagcaag	tcctcccaa	169881497
tggcaggagg	gattacagaa	gtgatttcag	gtgccagtgc	ctccacagcc	169881547
caccacccct	ctgctctagg	caagtcagag	gcacctgtag	agcctctggt	169881597
ctttgtgtgt	ggaaaaggaa	taatctcgca	ccagcattat	aaggttctca	169881647
tggttttttag	gggtgtggca	tatagtgagg	gctccgctaa	tggcagcagc	169881697
tattaatatt	ggtatcattt	attatttcca	ttactagtgg	agacattgag	169881747
ctgatatatg	ggtcaataat	gatagactag	agactttgtg	tgtctctttg	169881797
gtggaacatg	tgtggcttgg	attcaccttg	aatccctga	ttctggcact	169881847
ctggcctgag	agtgtcctct	gaatgagtca	tgtggtgcca	gcgggggtgt	169881897
tgagatagat	agatggcctg	caggcatttg	ggttcaaatg	ctgttctgct	169881947
gaataaggaa	tacgatttgg	ggaccaaaca	cccttggtat	taaatcccag	169881997
acttggtttt	ccctggtggt	gtggccctag	ggaagtattt	ctgctgagcc	169882047
ttactgtctt	cttgtgtcca	gtaagggttag	taatattgac	cacattggct	169882097
ctttgggaag	aggatggaaa	ataaagtgtg	aatggagcga	gggagggaat	169882147
ttgtctccga	ggcagcacag	gacaggaggt	aatggaaaga	ccaaagtggg	169882197
ttttggatta	gagctgcctg	cagcctttat	ctgtctatgg	agttgattta	169882247
ttattctccc	aaatcttggg	acaaagtcaa	gaaagggagg	aaggaaggga	169882297
gagagatggg	taataagagt	atggaagaaa	atgtaaacad	gtagagtgca	169882347
gacagcggct	gcctgcccat	agcaagccct	ccgcagaggg	agaattaatt	169882397
ggctgttgct	atgtgtattg	ttgtgattgt	tcttattggt	gaaagatgta	169882447
gaagagaaat	caggtagaaa	gaattcaagc	aaagacaggg	ggtgagcgaa	169882497

FIG. 1.64

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agcatgaaga	aatgaacaga	atctgggctg	aattttcttta	aggttataaa	169882547
gcactctatg	caatctgagg	caggcagtc	ccaagcttct	agtaccaacc	169882597
tgcgactcta	cgtgtcaaac	aggaggagtt	ccttaaagg	tgtttggtgt	169882647
gtgcatgtgt	gtagagggat	gaagcatgta	tacctctttg	tatacatcag	169882697
acactgtgct	gggcactgcc	cttaaattat	ctcacttaat	tgtcacacag	169882747
tcctatgaag	cagatgctgt	tattgtctca	gttttagaga	caagaaaact	169882797
gaagctcaga	gaaaagaagt	gatgaccagc	ccaaggtcac	atagctgcta	169882847
agtgcaggga	cagcatcaga	acccaggccc	gtctgtgccc	ttaggtctca	169882897
gagattctac	acctactacc	tagtattagc	tcaatctgac	ccttggggaa	169882947
attaagcccc	aggaaagctg	tttccttcag	ttgcgagcc	aacttgaagc	169882997
aatggtagac	tgaatcccag	ttctgactgc	cagctccaca	gtccctccct	169883047
ggggcctcgc	acatcattgg	aactgacaac	acaagaatct	tccatctcct	169883097
tccttctctt	cctccttttc	ttggctgtca	tccaaaactt	taggggaatg	169883147
cattataaac	caacttgaga	gacagagaaa	ggctgtagga	agatccaact	169883197
caaaaacatt	ttggtgtttg	ctttacctcc	gcctgagcgt	ccctggagat	169883247
aaaccctcct	cactctcgcc	caccattgct	ctgctatgtc	aatttcagca	169883297
gocggactct	ggggctgaca	tgcattgccc	cttctcaacc	cagacaccac	169883347
ttccttcagg	gaaggctcca	cataatggtg	aagtgcacag	actcagaagc	169883397
cgggcagtc	tggtcagaac	ctggttctgc	ctttctcggt	cgtgtggcct	169883447
tggataagtc	atctactctc	tatgagcctc	agatccttcg	tctgcaaaac	169883497
agagctaagt	cctcccttct	tgggttgctg	tggggcttaa	ttgagaaggt	169883547
atatgtgaaa	tgctgtctcc	ataatagaca	cccgtttgag	aattaacgtt	169883597
tgggttggtt	cagtgtgagc	ccatgggtct	caggcaacag	acttgataaa	169883647
tacaggttcc	tctgcaacca	caatcctagt	ccttagcaca	agcatgacac	169883697
tgcttgcat	gtgctatccc	tcccatatcc	atcagccatg	gcagacacag	169883747
atccctcatt	atgagacttt	tttattctga	gctagaatgt	gacctcagaa	169883797
tctttcttaa	cacaatgctt	caagcagtc	ctaccagttg	aacatagttg	169883847
acatggaaga	tagatgaagt	ttatttgcat	tctagtctc	accaagtcca	169883897
tggtcactgc	tccatctgct	cagtgcaggc	tgtctctctg	ctctgtctcc	169883947
cacctgcttt	tgtgagtgtg	tggttctatg	tttgtgtata	tgtgtgttta	169883997
aactcctctt	ccagagtga	agaccatttc	agtcttttgt	gtgctgattt	169884047
gtagaaatca	ttgaactttc	agaatcccat	ttgcaatgtc	atgtctgtgg	169884097
ctggggatct	ccaagtaaca	tcagcttacg	tctgggaagg	acaaggggaa	169884147
tcaaagttag	aagtcaggag	agcaaaatcc	acacacagca	tgcaccatcg	169884197
gccaccttta	ggagtgcac	aagagatggt	gtttgaatat	aaatttgaag	169884247
tctttccaaa	gatttaacac	tcctttggct	gacaaccata	atctcaagga	169884297
ggtaggccta	ggctagagca	attatacttt	agggttaacc	tagctgctat	169884347
aacaaataaa	ccccaatatt	gcagtaggct	gaaacataga	attgttttta	169884397
tcattcatat	aacttcttga	tgggccagta	gccttcttcc	atgtagtcc	169884447
tcagggaacct	agcctccttc	catcttggtg	ctcccccaac	cctaaggcat	169884497
cctctacatc	taggtgaaag	gggagcagaa	aatgtggtct	ctggcccagg	169884547
aacaactcta	gtcttgagga	agcacatgat	atagtatgga	gatcacagcc	169884597
aggcctgcca	cgggcagcaa	ttcagggtct	ggcaccagat	cagctgggtg	169884647
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gagtcctgggt	tcaccaagaa	acattattgt	aatgtgctcc	ccaggcagct	169884947
ctgcctcagg	gagagacaat	gccaggcatg	acaacttcag	cattcttgtt	169884997
ctgcatggca	gttgcatctt	tcattgtggt	ttatatgttg	gtcacatgat	169885047
ctgagcta	at	gggagtat	gcctgacaga	tgagtcctt	169885097

FIG. 1.65

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tgccagcaaa	atcaggcttc	caagccccc	aggctcactg	ccagaggctg	169885147
gggaattcgc	caaggtaa	gccacottgt	gaggtctttg	ggacacagcc	169885197
agcagcctcc	ccagggcacc	attcctgtct	cagcatgagg	cttctctggc	169885247
cagcccaatg	gcatttggga	gccacatcca	caccocacgg	gtctgggtct	169885297
gtttccagct	gcactgggac	attctggcag	attctccctg	atctctgtaa	169885347
ggaagagtac	agcaggaagg	agaggaagca	gaaaaaaatt	ccaatgctta	169885397
gagttttccc	tctaaagagg	acctcctgag	ccacttctga	acaggacttg	169885447
gaacaaagga	atcttggcgc	tttgatgatc	gtgtctgcag	cagttgttga	169885497
aatgagctctg	acactcgcca	gtgccttagt	aggaattata	attacatcag	169885547
gagacccag	gcaaccaagt	aaactgatta	gctactgctc	cgagttgata	169885597
gatttttttc	tctctaggtc	ataaataggg	ctgtgggaga	tggtggaagc	169885647
atgctgggtg	gaacaggtcg	agatgggctg	tacattcagg	aagcccaacc	169885697
aagtgggtgtg	ggcagctccc	cctgccccac	cctgccaccg	gaagagacag	169885747
tctgacaggt	gccaaggtta	gagttcagtt	ccctcggcca	gggactgcac	169885797
tctgatctt	gcgtgctgca	gagagctgtc	ctcagagcag	gctgagggtg	169885847
gctgaactgc	taggcgatgc	tctgggaagc	cctccgccag	gaaagccgat	169885897
gctttctgcc	aggcataatt	attgcatgga	taattacacg	attcagagcc	169885947
tgctggagaa	tcttgggctg	gtgccagagt	agaaaggcag	ggttccggaa	169885997
ctgcagccag	tggtgatctc	tcagagtcga	ctttgaaaga	agagggta	169886047
cattcctcct	cctaagactc	ctacctggct	gggccaggac	atggcaaacg	169886097
taaagctaag	ggaggcgggg	agttgatgag	ttctctcctc	caccocactcc	169886147
cttacaggag	ggggtcccca	gagttctgac	ctaaccctc	ttctttactc	169886197
cctgcacgtg	tcacctccct	gggacaatcc	accctgccc	attagcacat	169886247
atatgcggat	gacaccaagt	gtctttccag	ccaggcatct	gcaa	169886297
gctgggcac	tccttcacgt	gtctcctcca	gcccattgca	ctccagcctg	169886347
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agccagacat	acctaacctc	ccagacctcc	actaggaacc	caggagtcc	169886447
aacctgctag	tcctttccca	ctccctgtgc	accatccgaa	gccaggat	169886497
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ggctttcttg	tggtggcctc	ctccctggcc	tcccaccct	catccctgg	169886647
ggaccagcct	cccactgcct	ccagatccaa	tgtcttccag	ttaa	169886697
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ccaacttggc	cccttctgac	tgtcctgaag	acccttccca	agctgccaac	169886797
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aatgtagaaa	taatagtaat	aacagaacc	atccatgggg	ttgttgggag	169887097
gattcaatga	catattcatg	taaaagactc	agagcatgac	cagtgcacag	169887147
tggccatctt	atcaagtgcc	tgtgcctgt	cccaagatgg	aaacacaaaa	169887197
tgtgaaatcc	aagtgtgggt	ggtggagggg	tggtatgggg	cggggcggga	169887247
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gacatttgac	ggtggcagcg	ttaggagggg	acttctgcac	aaggccgggg	169887597
aaactttgcc	taagatttag	gccttgggct	cagcctgatg	cacccattt	169887647
actgggtgcc	tgctctgaga	ccaggatacg	tggaaagaac	ccacgcctgg	169887697

FIG. 1.66

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gagccagctg	tcctgggctt	tggaaatagc	tgtgtccgta	ggtgagacct	169887747
tgtctctgca	ggcctctagc	agagggggcta	agagcatgog	ctctgcaggc	169887797
tgccctgggtc	ctcaccacct	ctcccgcaact	tagtagccct	tggtgactta	169887847
accttcctga	gcctcagttt	tctcttctgt	aaatggaaga	tcataatgat	169887897
acctgcccc	tagagtgtgtg	tggataagcg	atagaatctg	cattaaagca	169887947
tttaggtagt	gcctgagatt	tagcaaaggc	tcaatcaaca	tttaaaaatg	169887997
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aaccctacat	acatctttgc	caattggcag	tttttccctct	agttaatttg	169888147
ggagcctgtg	acctttaccg	ccgtgtgatt	ctctgactca	gactgcagtg	169888197
ttgcagtgcc	agccaaacat	ggtgacaagc	cccttcccag	gcaactgagg	169888247
acaggcagga	gtgttctgga	atcttctcct	ggagtgggag	taaggggtggg	169888297
cagagccatg	tgatgctgca	ctgtccacct	ggttgaagga	agtaattcca	169888347
gactctgtct	ctgacatctc	tattagccaa	gggtgagggt	gttagttcgg	169888397
gtcatgttag	ctgcgcctcc	cacctgcat	cctgggccc	gaaaccacac	169888447
ccctgtgcag	ggcttctgtg	tcagagtcac	cagggaatg	ggctgctgag	169888497
gatgccagca	ccaaccaggc	tgctgtcctg	gggcgacatg	tctgccatct	169888547
tacaacctcc	cttccaatat	tcaccatgtg	ccagctccag	ctcagtcact	169888597
gagcctcaca	tcgctggacc	ccactgtgtg	ctcagggtca	tcaggcactt	169888647
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gttgtcaata	tcaactctac	gcagtagccc	atttctgtag	atgaagaaag	169888897
ggaggctaca	ggaagggaag	gcatgtgcct	gggggtggatt	cgaactcagg	169888947
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actgccatta	gagggactca	ttcattccca	tacatgtcaa	atatgcactg	169889047
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gacctggtac	aggcatcacc	ttctctggga	tgcttccctt	gtccctccct	169889647
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atcagccact	cacagctgca	gcagaaccag	gcagttgagt	ttgacattgg	169890147
ccttttaagc	tagtcacgaa	taatcagaag	acccatggca	ggctgtcact	169890197
agtgattttg	cttaggtaca	aacttgaatg	gtgctccttg	gagttctgat	169890247
gtgggagagt	cactgagctg	gacgttagca	cacacagtta	cacgctcaca	169890297

FIG. 1.67

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ggctcaccoc	agcatgcatg	tctcaaaaca	atatattttc	ctctattttg	169890347
cottggggtt	tcagttacag	caaaagtatt	ttcaaaacaa	aacaaaatgc	169890397
atcatgatac	aatctcatat	caagtaacat	tcattttggg	ggacgcactt	169890447
aaattaatag	tttcataagc	ggttggtgtc	ctgcattttac	agacacacga	169890497
caattctgaa	ggggcatgt	tattttttcga	ttatccttta	ctgcattttta	169890547
tgtgggacat	ggcatgctgc	agtgggtgtt	gtgagctgga	ggattttggga	169890597
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tcaaatagag	tttgccctggg	gcctgccctg	gaggagacct	gcctctcagc	169890697
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ggcatatatg	gagagaaggg	ttttgtggga	tgtcagactt	aatagtgcc	169891197
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aaccaactct	tctgttttaa	aggaagaaaa	gggggggtta	ttgggttcatg	169891647
taataaaatg	gccagggtta	gattaacttc	aggcagagct	gaatacaggt	169891697
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gctctcttct	gtcttggtt	cattctcagg	aatgctcta	accttggggg	169891797
tccaagagta	gtcaccagca	gccccatatt	tacagcccac	cagctcagca	169891847
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ctggcacaga	gtaggtgctc	atgggtcata	acatgtttat	tgattgttta	169892747
gatggcaaca	cagataaaat	caaaacatgg	aaggttgctg	agactcaaag	169892797
acaggattat	tattgttggt	aatgatctga	tagctaata	gtattatatt	169892847
aataatagtc	aacatgtcag	gtactataat	agaggctttg	cgtaactgct	169892897

FIG. 1.68

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ccttttagtc	ctcccagtaa	tactatgatg	ctgatattac	tcttcccatt	169892947
ttgtagataa	agaaactggg	agtcaggag	gtgaaatggc	tttcccaaag	169892997
tcttgcataa	aatgtatccg	gactgcaagg	atggggccct	ctggcccccct	169893047
caacacccta	tctgcctctc	atacccaggg	acctgcccac	aaggtcagcc	169893097
ccttggcaat	cttgccaacc	ttggggctca	aaattcagtt	tatggcttcc	169893147
caagatctac	tggatgcttt	ttctaagttt	ggagaattca	tgacattatg	169893197
aatccttttt	ccccagggtg	ggtattcaaa	ctcagagttc	cagccacgct	169893247
tgcattccagg	gctcagatag	cagagggacc	tgcttgaggc	ttgatttaga	169893297
aggggtccacc	tgaggatgtg	gatgaagcgt	gaattcattt	ctggcagggg	169893347
tggcagcaga	ggcagacagc	tctgtggagg	cagaggtggg	gaaattctgg	169893397
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caacgagggg	aattattatg	atgatgggcc	tttgaaacc	tctgccttct	169893797
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catttccaat	acccttctcc	acttaagttt	tgctgatgct	ggtagtctga	169893947
ggaccaccaa	tgaggtgggtg	aggttccagg	gacgcttaag	cctccagcaa	169893997
aacatcacac	aagacagaag	tgctacttcc	aattgcatga	gataatgaga	169894047
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taacatccta	agtcctaagg	tacotggagc	ttcaaattctc	ataattagca	169894147
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gagtgtgggtt	tgctatttgt	acctgtaact	cagcccaggg	agtgtcgaca	169894297
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cctgtcctaa	gccccaccct	tcccagcaaa	ggaaagtagg	cccctgaagc	169894397
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ctcttctctc	ttctctctct	cctcctctcc	cagtccaagg	aagttttatg	169895447
caaaggccag	aggaggggaat	aatgaggtgg	aggtctctct	gaccaagcat	169895497

FIG. 1.69

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gtagccttcc	ggatctgttg	tgctttccag	gagtccttca	aagctctaag	169895547
cttttggaa	tctgcaagct	caggaaattg	aaaacctttt	ctctcacaac	169895597
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gcggcattgt	tgttgcgcta	tcttgcaatc	ctacgtgcg	ggtagtgttt	169895947
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taaccactgg	gctgtaccac	ctcacaggag	ggcaggtggc	acagtgcctg	169896097
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gtgtgtcact	ggatcagtca	ctcaacaccg	ctaagcctca	ttttccacct	169896197
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attctcaggg	agtcacattc	cgtctccaaa	tgccatctc	ctgatccaca	169896397
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gcacatttaa	acttttataa	gtttatttga	acattcagcg	attcacaaac	169896647
ggtatagcac	agacagcaag	caactagcac	tctctagga	ggggccaaac	169896697
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aatgggttgg	aatggaaagt	tcttaattag	agggttcattg	gtggctcctg	169896797
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FIG. 1.70

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gagggcagga	aaggaggagg	gcaggatgga	agcatgcac	tcctgggcat	169899447
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agaaaaatta	ttactgaagg	agagattatg	ctccacaatc	tcaccagaat	169899547
gtggctttgc	aaagtgaac	gagggttcgt	tcctctgcca	gcacgaccaa	169899597
ctctcccggg	acaccccctc	aggctccgtc	ttgtgccaca	ggccacctca	169899647
cttcagggtg	gtggctcaga	gaggtgacag	ctcccatcta	aatgtggcct	169899697
ctagaacctt	ctcttctcct	gctgagaaag	gattgtgctg	agtagtagaa	169899747
gcagctggca	ctggagtcct	ctggcctggg	tcctacaatc	ccaactttga	169899797
caattgtgtg	acctcggaca	agtcacctta	cccatctaag	cacatgttgt	169899847
tttaactgta	aaatgaggaa	aatagcatto	aactcagggt	atgaatgagt	169899897
ggagccatgt	ggagcaacag	ttaagggcat	ggacttgga	gtcaggcagc	169899947
caaggtctgt	gattctaggg	aagtgatgtc	accactgagc	ctcagtttct	169899997
ccacctgtca	tacaggcagg	agtaaatgcc	tcctcacccc	ctttgttctc	169900047
tgtacaaacc	cttgccctgg	atgtttctgtt	tgtcctcagg	acccctctc	169900097
cactgttggc	tggggagggt	gacctgggag	gactctgtga	atgaggcccc	169900147
tgccttccga	cttcagctgt	tcatgacaca	ggcggagact	gcgggcagga	169900197
ggagagtgc	acgaggtgtc	aactcccagg	ctccctccct	gagggttata	169900247
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cagggaactg	ccctcttcgt	gtgctttccc	actctctccc	tacaccactg	169900397
tacacagtcc	ttttgttaca	cggccttcca	attccccaat	ctgaggggtgc	169900447
cattgtgtcc	agctgagacc	ctgaatgaag	caactgtccc	gtctggccac	169900497
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tgatgagtcc	agctcagtgc	taatccctct	acatgtgaaa	tctcagttct	169900597
tcagagagcc	ctgggaggaa	gctactacag	cctttcccat	tttaaagatg	169900647
agaaaactga	ggctctgaga	aggtttcaca	gccagagcta	agcctagagc	169900697

FIG. 1:71

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ccttaatgac	tatcctcatg	ccctctccag	tataggcagg	aggctactga	169900747
gtacacgtgc	ttgaacttcc	aaggcatggt	ctcaagtaga	agtgtcctcc	169900797
tcacaactgc	tctgaggcac	atgccatcgg	aaagctgggc	taataattaa	169900847
acaggggtga	ttttgtcagc	cccacatggc	ctgacaaagc	agaaacacaa	169900897
tggatggtaa	atattctatt	acgactgtta	ttcccaaccc	cctttccaat	169900947
gggggtggtga	gtaggaagcc	tccctatgac	cagtttcttc	cccacagtct	169900997
tgccagctcc	tgttcttctc	atcacaccag	gcttgtggcc	ttgattttgg	169901047
accctgttgg	aatgaggggtc	acaagaggggt	ctgtctgtcc	acacacacag	169901097
ttgttcctcc	tccttcttcc	ccacctccat	tcttaccat	tctcagtcct	169901147
tattccagac	tcctcccttg	caccagctgt	gtccttggcc	tggggatgca	169901197
taatgagacc	cagatgctgc	ccccaaaact	ctcagtttat	ggactgtcca	169901247
tcttgaagag	atgaccacag	gatgctcaat	gctccagcaa	agaggaatcc	169901297
tgtgggtcac	caaaggcaca	caggtctttg	gcacttagag	aaatcatttg	169901347
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ctagccttct	ttatgagatt	ttcctccact	gacactccct	gaactgctgc	169901497
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gatcatggcc	tcagaatct	gtctcatttc	gtccacatct	catcacctcc	169901647
tgttttctca	ctagcccaag	ccaaactcat	ctctagtcta	cactattgca	169901697
gacatttcag	gattgcctca	ttgccagcaa	atttgcctcc	tacaagtcac	169901747
tattaattca	tatgtcgggt	tgtcacttcc	tggtttact	tcaggtttta	169901797
ataagcctga	agggaaacac	ttgttttcat	tcccagcat	gaaactggga	169901847
catttcctct	ggtccttgga	gtgaaatcca	cactcccaac	cacagacttc	169901897
aaggccgcac	ctgctctgac	cctgctgacc	tcccatcttt	caccactggc	169901947
tgtggcttcc	ttgcactttt	gcaacaccaa	gctttttcct	gctttcaacc	169901997
cccagacctg	cccggtgggtt	gcaattttttg	ggcatccgga	tctcagcaaa	169902047
tgtgcctgct	cctcagaaag	gccttcctgg	ccgttctgoc	tgaagaagcc	169902097
cctgtccaca	tcaagggtct	tgcattctcat	cacctgtttt	tattttcccc	169902147
atagcgtca	tcccaaccta	aagtatcttg	tgaacgtgct	gctgggtctgt	169902197
tatccattgt	cctcgctaga	cttcaagccc	ccgaagagca	gggacctggc	169902247
ctgcctgttc	accattgtct	ctagcaccta	gaactcaggc	ctgggtacagg	169902297
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aagtgagggg	ctgaattggg	gggaataggt	tcttttggtta	tggcccaaaa	169902397
attgctagaa	gtttaaatgt	gtcttctaag	cccagctctc	tgtgttotca	169902447
aggtcgcaaa	tattaagaac	tcagggtaaa	taaaaatgta	tcctttccag	169902497
tgccctgcag	cccacactga	aatgagaaaa	gattttttta	ataataataa	169902547
taaaggaacg	atctttcaac	ctgcgtgcgg	gtctcagcgg	ctccacttgc	169902597
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tctgatgtaa	agtaaggctc	ccagataaag	ctgctttcct	tctagattcc	169902697
agggaaatca	tctcacaaaa	ctcaaagtgt	agacaaacaa	gatttcaggg	169902747
caaggaaaca	gactcaggag	ctttcctggg	ggcatggctc	cctcaaagcc	169902797
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cagccctgct	atgtggatct	tggggacaat	aatttatcca	caattacact	169903047
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tgtgatgaag	acctgccctt	ccctgaccac	aatgctatga	gtaatgactg	169903147
agaagattgg	gcagcccatc	ctcagtaatg	caggatgcac	tgtggcccat	169903197
gtctgaggca	tctgaaatat	cagaaactcc	agtgggctta	ccatgggtccc	169903247
actcctgcc	taatggttgc	cttacagtgg	ctttttcttc	caaaccaact	169903297

FIG. 1.72

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tgccttcaac	tgcagaaggt	gaggtcccca	aaacaccagt	aggccatagg	169903347
atagtgtgcg	gccggtagaa	taagaacctc	agacacttcc	cacttcccct	169903397
ggtagagaag	gtcttagtgg	ccacaccgaa	aggtaggtgg	aggctaacag	169903447
atctaaggct	gcccagtggt	ccatttctgc	actggatatg	aaatgtgccc	169903497
tctctgagcc	ctctctctgc	ctcagcgatc	tcattctatag	aatgggggta	169903547
tagagataga	caatctcata	tgtgatctta	ggcaagttca	gatctcacag	169903597
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gctgtgtgac	tttggaacaag	gcccttccac	tctctgagcc	ttggtttccc	169903697
atctataaaa	tgggccaatg	gtaggggtgg	gaaaaggatg	acctctgagg	169903747
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cacccaccca	ccttctgacc	tagtttggat	gctccaagcc	ataatgataa	169904247
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gttctcttcc	agttctccca	tcgtagtaat	atcatctaca	gagcaagatg	169904547
gggaaaaatgc	tcactgccag	atcccattct	aaagaggtat	ctccatctac	169904597
agatttattg	cacccgggct	cctagccata	cgccccaaaag	tcaaactgaa	169904647
caacagtaat	aattatttatt	cagccatgtc	acactgaact	gaggacctga	169904697
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gcaggccgcg	tcgtgacccc	ctggagagag	aaagatggat	tggaaagtgt	169904797
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gatatggatt	gagtcataaa	ctccccatgt	ggcactgggc	aggttcatca	169904897
cttgaactct	ctagacctca	gctttttaaat	ctaaaatgtc	ccatagagtt	169904947
gctacaaaaga	ttacatgaga	tatacactta	gcaaagtgcc	tggctcacag	169904997
taattgtcag	aaacagaaag	tgtcgagact	caaccctgca	tggaaaagaa	169905047
aataggacac	acatactatc	ttagtccatt	caggttgcta	taatagaata	169905097
ccttagattg	ggtaaagtag	tctcccctta	tccacagggg	atatattcca	169905147
agaccccccg	ttggcacctg	aaatcacaga	tagtgccaaa	ccctatatgt	169905197
actatgtttt	tcctatactt	atatacctat	gataaaggct	aattttataaa	169905247
ttaggcattg	taggagatta	acaacaataa	ctaataataa	aatagaacaa	169905297
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aagtccaagg	tcagtgcaca	agcaaattca	atgtctgggtg	agggccagtt	169905547
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gcctgcctt	cgtgacctaa	tcaccccgca	gatgtccac	ctctcaacac	169905697
cactgcaatg	agtattaagt	ttcaacatat	gaatactggg	ggacatgagc	169905747
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aagtagacac	ggacagtccct	catttttcta	agaataattg	gtaccagtac	169905847
aaataccact	taaagagaaa	cttcttaaaa	caaagtgtga	ctattttactg	169905897

FIG. 1.73

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tgatagtgaa	ggaaaaaggt	tggagtaggg	ccaaatcttg	aaaaaataaa	169905947
attgaaagca	caaaaataag	tcttttttat	tgtctagtaa	caaaatgtag	169905997
gttttagtgt	caaatgagtt	aattttttcc	attaaaaata	ggaattacca	169906047
agtgttgact	ttgggggagg	catggcacat	tttttagaca	aaatcctatc	169906097
ttagcacagt	ctaacagttt	tgattttgtt	tgactttcac	agcacaataa	169906147
ataaagaggg	tcatttgagg	caaataattc	caagctttat	ccattttccc	169906197
ataggcctct	tccaatcggt	agaagataac	atttttctcc	tttgaagcac	169906247
ctgacaactt	tgtcactttt	ctcttcttcg	gttgctaact	agtttaactc	169906297
tgocagtttc	tcatttgcct	gtagttaaatt	gtgaatggaa	aagttatcca	169906347
acaatacttt	tgctattttt	atgaaatcct	gaatctgttt	aaagatttgc	169906397
acttttcttc	ttcatcaatt	tcctttgaat	ttccattaca	tcacagaca	169906447
tttacaacaa	ccaacaagcc	gaaggaaacc	aatagatcta	ggttaaataa	169906497
gtaaggctag	aaaccagcgt	taatgggagg	taaaacttaa	gcgtgcataa	169906547
aacgtttaag	tgaccggctc	attcgtaagt	atttttgtgt	tatgaagatt	169906597
tttacttctc	tatcaaacct	tgtaacctca	gagaattgaa	taatgacact	169906647
tagttgtcaa	attcaagata	accgacaaga	gaccgggctg	ggtggctcac	169906697
acctgtaata	ccagcacttt	gggaggccga	ggccagcgaa	tcacctgagg	169906747
tcaggagttc	tagaccagcc	taaccatcat	ggcggaaacc	caatttctac	169906797
taaaaataat	aataataata	ataaaataac	tgacaagaat	ttctaaagta	169906847
gttcagaata	gaaagcttac	taagttgatt	catttaattg	ttacccttga	169906897
tattttaaca	tgtactatta	catgttaaca	tgtaccact	aaatgtctag	169906947
atctcattga	tacttcattt	aactcctgaa	caataatagc	ttttcagtgt	169906997
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actgttgggt	ttatttttag	caccttccta	tttgtttttc	tatttgtact	169907147
atctcttctt	tcttccttta	ttcttctcatt	cctgtctttt	caaaaattaa	169907197
gtaaatagtt	ttattattgt	atttttttcc	ttatattggc	ttcttgtttc	169907247
acattcctga	attttgtgca	gtggttaccc	tagaagtttt	aatatatata	169907297
tttagtttat	tatagtgtat	ttttaagtta	agacttttac	ttcttctctga	169907347
acaatgcaag	aactttacaa	cagttaaact	cctgtaccca	cttctttctt	169907397
tttgtgctgt	tgtaaacaat	tttacttctg	catagttata	aatctgataa	169907447
gacattattg	tcatttttaa	cagccaatat	tcctttatac	taaccctaat	169907497
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ccatcttttt	ctctattctc	tttaacagaa	taaccatagt	caaagtcctg	169908347
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ctttcttttt	ctctttgctt	tgtctctttt	ctttctctct	cttgcctttt	169908447
cacatgcctc	ataattttga	ccataagctg	gacattgtat	gtaaaagaac	169908497

FIG. 1.74

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tgtggagggtt	tcagctgata	cattccacca	gagcagcttc	cccccttcct	169908547
ctgttgaggaga	gtcaggggtga	aggctgatga	cctcagtccta	gtcagaaatt	169908597
taagaggatt	gcagtttgag	aaagactgaa	tcgaccacct	ctggcttttc	169908647
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gaaaaacagg	gatttatgtc	aggcccttcc	tctctctcat	ggaatgttgt	169908847
ctcctaagtc	ccgtgagttt	agcagaaatt	tcattccaac	cttccatcct	169908897
catttcccag	ccacctgagc	tgcatagagc	acttagcagt	gtcctatgcg	169908947
ttaaagccaa	cagtcacttg	gcttcttata	tttcaggctt	ctcttggttc	169908997
caatccatca	tgccagccct	gcacaactgc	caaaagtgtc	gcttgggttc	169909047
tgctttctcc	agtagacaac	ctctgcttgg	gccaatgcca	gtcctcaacc	169909097
cacgtccaga	atcagcagtt	gcccacaggg	aagaaaactg	tcaggagtta	169909147
tcagcctaca	gaggaccac	tttgtcctca	tttccacagc	tttctgatgt	169909197
cttcaaattt	tctatttttg	cggttttct	tttttttct	taatagtgt	169909247
tgtagtaggg	gagtcagcct	gccacaatct	actacatctt	acctggaagc	169909297
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taatataatac	agcaatatatt	agagtcactc	gcacataaat	attaatttag	169909397
agttaatcac	atatttgctt	tgtattcctt	tttgaatctc	tgactttcta	169909447
tctgtgctaa	ttttccttct	gactaagcca	catcttttag	aatttcctct	169909497
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tcttgaaatg	taatttccact	aagtattcat	ttacagttgg	tcaattgttt	169909597
cctcttgaca	catggaaaat	atcattcctc	tgccctctggc	tttcattggt	169909647
attggttgaga	agacagatgt	tagcctaatt	gctattttatt	tgtagatggt	169909697
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tggtactttc	atcttctgga	attgttcttc	cacatcttat	catcgtcttc	169909797
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gagtttacta	attgtctcct	tagttccttg	ctccatctat	atctgtccat	169909897
tgtgacttaa	aatttccttt	ttttaacttt	tattttaagt	ttaggggtac	169909947
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ctgctattgt	gaatagtgtc	acaatgaaca	tacgcgtgca	gctgtcttta	169910397
taatagaata	atttccattc	ttttaggtat	ataccagta	gtgggatttc	169910447
tgggtcgaat	agtattttctg	tctctaggtt	tttgagaaat	ctccacgctg	169910497
tcttcacaaa	tgtttgaaact	aatttacact	cccaccaaca	gtataacatc	169910547
gctccttttt	ctgcacaacc	tcgccagcat	ctgttatttt	ttgacttttt	169910597
aatagtagcc	attctaactg	gtgtgagatg	gtatctcatt	gtggttttga	169910647
tttgcatttc	tcacttaaaa	ttttgaacta	atgtattttt	catttctaga	169910697
tgctctatat	ggttattttt	caaactctgt	aagacatttt	tatagtgtct	169910747
tattacttgc	tgaaatgttc	aaacctcttt	tatttcatta	agcatataaa	169910797
ttttgccatc	tcattttctg	tgctaataaa	aattctaata	tcggaagctt	169910847
taataatcag	attctgctat	ctctttttcc	tgcaagcctt	atctcacagt	169910897
accttggttt	cttggtgtgt	ttacaattgt	tgacagtga	tattcttttag	169910947
aactttatcc	ttgataatta	ttagaggaat	gaattaaaaat	ttcacttctc	169910997
cggaaagtac	tgtgtttgca	ccttttaata	actcaagaga	ggtaacaacc	169911047
caagttcatt	ttcaattaaa	attttcattt	gaggtttttc	agaccacaaa	169911097

FIG. 1.75

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cccatgtgag	agctcacata	tggttacaaa	ttcttgaaga	aatgaggct	169911147
ccttccttcc	ccatccacct	tcttagtacc	aaagtcagga	cagacagggt	169911197
ttctgtgtta	gttcacttct	cattcacctt	tgtattaaag	gtctagctct	169911247
ttgaggttca	agttttatgt	tgggacctct	tcccacttgg	tagggcctgg	169911297
gttttaccta	ctgggtttct	aagcatattt	tgtggttaac	atcagaggcc	169911347
aggagactca	tcagtgtata	attaattctt	gtataactaa	ttattttaaag	169911397
gcagtggacc	tattcactag	cacctgctt	toggagtcac	tgaattcatg	169911447
tttgccctca	gctaaagcca	tcttgaacct	ctttagatgg	gagaaccctg	169911497
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actagggacc	tcacggtcac	tgtgagggat	gggggtctct	gcttggcttc	169911597
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ctgggatcct	ctcataagaa	gctatattta	ctctaatagaa	aaaaaatctc	169911697
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gttatatgga	agtattgcac	agtgatgaag	ccatggcttt	tagtgtaccc	169911947
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acccccctcc	tctgttttaa	ggaactggca	tttatgcaac	taattgataa	169912047
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aaccatttaa	cagtgtttct	gaaagtatgt	tccttgaaac	actagaccat	169912197
gaaaagtcct	ttatgttgaa	atatgcttaa	gaaatattat	atgcttgaaa	169912247
cttctcttgg	aaactcacga	agtataattag	acattaaagg	ctctaagaaa	169912297
tcttgcaata	aagaagccta	tttaatttta	tttgactcgg	tgttttcaaa	169912347
ttatgtgtga	ccacagaaat	agaagggaact	tggaggagta	ataattcatt	169912397
ttttgggtag	aattcactac	tgtcacagat	atttgatgc	tgtcaatgaa	169912447
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aaagatatag	ttctgtctca	tggagcttgg	aggagcattg	gactgtcgtg	169912597
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attgttggat	cacagccgtg	gaacaggccc	cagagctggg	aagttgactg	169912697
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FIG. 1.76

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ttagcaagac	atgtactcat	ccttcagggt	ccagctcaat	ggtgagagcc	169913747
tctctggggc	tttggctgat	ctcaccctgg	aatgcactgc	aatgttcctt	169913797
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cgtgctgcag	ggcagggaact	gtaggaggag	atagcgtggc	ccagaaaggc	169915397
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gtaagactca	cctcagagga	agggtgggcc	tttcattcct	agctgcaatt	169916247
ccttacaagt	aagaaggaga	gggcctcaaa	caggaaacct	ggggtgaaga	169916297

FIG. 1.77

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ggtgaacctc	agatgcctat	cttgtttaac	cttctgtctc	caggcttagc	169916347
acagtgcctg	gtacagagga	agtccctcagt	aacattgttg	agtgaacgga	169916397
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TTTaaaaatc	gtgtgtatcc	caaagaaaat	attatctaag	ggtgaaatcc	169916747
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cctggagcct	ccgagaggaa	ggtacatttt	gcatgccagc	ttatccggat	169916897
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taagtcttgt	ctaactttgc	agccaggtc	agccattctg	taggaggatt	169916997
aaaggatggg	actgtgtata	aaattggggc	aggatggcaa	gcgagggagc	169917047
agctcttgag	gccagaagag	tgggggaaga	tggcttgatg	acagacggaa	169917097
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ttatttttct	taagatagca	aatgtctttg	caggcatgct	tcccagttgg	169917247
gaaattcttt	ttatgtctca	tgtaatccgt	ctgccagagc	ctcctttgac	169917297
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ggctctatct	ccatatctta	TTTTgacaag	cactgtaatt	atccctcatt	169917597
gctggcaggg	ggagcagaat	cacgttcggt	cccagcccca	tcttctcaga	169917647
acaagagta	tcaggctcct	ggttgctcca	ccactaaaca	actgcctgtc	169917697
tcagttcccc	agcgagaccg	agactgagct	cagccattac	tcaggagatc	169917747
gcaggcgggg	gctcagccta	ctttttgaca	gcatcgtgga	ggtgatttca	169917797
gagcgcttgc	tgcatgcaca	tgggaaatag	cttccaagga	ggatcttttg	169917847
gggcagaagg	aatgaggtgg	gcacccatgcc	ctccaaaaag	acagaagtta	169917897
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ttgtcaaaat	cgtgtgtcta	gaaaaccacc	ctccttactg	gttgtgttcc	169918847
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FIG. 1.78

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gaggggtgata	gcaaggaaga	atgcatctga	gatgccagge	tcaggagatt	169918947
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gctgtgtgac	cttgaacagg	tcccttagcc	tccctcagca	gtggagtgga	169919597
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gaaaagcaca	aacagaaatc	cttaagagca	tcagccgtga	cacagaaatc	169921347
taatacaata	aaacaaagtg	cttataaacc	ccagagttgt	ttaaaaccca	169921397
gaaattgcc	attgacatat	gggactatat	cttcttagcc	cctagtaaac	169921447
tgagtggctt	caaacaagtc	cctatcacct	cccagggcct	cagtttcttc	169921497

FIG. 1.79

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acctgtgaaa	taagaggatc	aaaaaaagat	aatgtttctct	ctgtttctctt	169921547
ccaaccgagg	caggcatctc	aagtattttct	tagtcagttc	tactctaggc	169921597
tacacagtat	ctgtatctgg	cagctgtatg	aactactggt	gaaaatcctc	169921647
ttcccaatcc	cagtttcaac	atcactcctc	aaggcagcat	ccaccttcac	169921697
tctagactga	attaattcct	ctgtcttacc	acctaaactc	ctctagaaaa	169921747
cttgatagag	gtaaagataa	atgcattttt	tcaaaaattc	tacttttcta	169921797
gtcccaaggc	attgtgtata	tcattcttat	gtaagttatc	acaataaacc	169921847
cataattagt	tacttccatt	tatgtcaa	cgcctacaaa	gcagaaacat	169921897
gtattattca	tttttggcct	cctccccagt	atctagcata	cgaactgttt	169921947
gcaaacatgc	ccagttcttc	aaactttgta	acttcatgcc	ttttctatct	169921997
actacttggg	atgggcccac	cctccctttg	tcctctaagc	acactcctat	169922047
tcactcctca	aagtccagca	caaaaatccc	ctcctctggt	aaacttcaac	169922097
tgctccaggc	tgagtcttat	gtttgggtcc	ttcatacgta	cccctcttct	169922147
attgtttggg	gtattgtgtg	ctgtgggata	tgtttactct	cagttctccc	169922197
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tcctctgcat	tcttggccag	gctctgagag	ggcattggta	aatgttaact	169922297
gcctggcaat	ggtgatgctg	ttaacctgat	gtgtcagggg	tctgaataaa	169922347
gctgcctcaa	ggtaggcaga	tgcccacaac	caagcaagaa	ctcaaagctg	169922397
caggctcctc	agcctgaacc	ttagacagcg	tcttggtcac	catttcaaca	169922447
ccttgaccac	atttctcact	ctcccaaatt	tcctcctgct	tattcctcat	169922497
ccacatacat	aaggctgtgt	ctcccagggg	aaattcaact	acttggtaat	169922547
tatcctgctt	cttaagtttg	gggctagggg	attcatagat	gatgttcagt	169922597
attatgctgt	gcaatgtaga	tgtctcctaa	accttctcag	gagctaccac	169922647
tgagtggcac	ctggggacct	ctcaggaaga	gccagttttc	tggggcagtgt	169922697
ggggcgaggc	agagctcatt	aaaccagcct	accacctgtc	ttccagctcc	169922747
tcctctcagc	ctctgggctt	ccagcagaaa	gcacacgaga	gcattcttgt	169922797
tggttttctt	atgacttgag	ccagcgagac	gtacatgccc	agcacctgtt	169922847
acctgggctg	gctcttggtc	gagagcatac	atgcattggg	tcagggtttca	169922897
gatctgctgg	aggaacacag	ccagaatgtc	ttgacaggca	gccctggcaa	169922947
agccccagaa	aatataagat	ctgagtctta	tgatggactc	tgtgaccttg	169922997
agcctctcac	ctcgtgacct	tgggcactct	atgttctctc	cacagggtctc	169923047
ggttctggac	tccttcatgg	gagctgtcat	gccctgttca	cacagcagtg	169923097
ttgtgcccc	ggggatcagg	gaccaggatg	gtcctttctt	ggtggtgaag	169923147
ggggcatttt	gcatattcca	gagattcaag	tttccagacc	tatctagaaa	169923197
gaaacatttg	agtttacagg	ttggcgcttc	tcagcctctg	tctctcttcc	169923247
tctctgttca	tctccctctg	tccctcttat	gtatgtttgt	gtctctttct	169923297
gtctcctctg	cctttctttg	tcattgtctt	ctgcttctgt	cctatactgt	169923347
ctctcacctc	caccctgggt	ccccccgccc	cagatgctct	tctctctgtg	169923397
gggttttttc	ttccctctca	tttctctctc	ctctcccact	ccttctctcc	169923447
cagattctcc	ctcactacag	gcttctctct	aatctctctc	taactgocct	169923497
ttcttctcac	aagaaggagt	cccctctggg	gccagaggcc	caggcaaggc	169923547
attgtggaca	aggaggccat	ccgtgccatc	caacgggcag	gagcccagcc	169923597
tcctggctgg	tgctgtggctg	tgctgtgggt	ttgtttccac	ttaccaaagg	169923647
gcatctgtaa	ttaatgtggg	cagtgataaa	ggagctggag	atgtgtttat	169923697
gctccttcga	gggctgagat	gaaacaccca	taacatttaa	tgtggcgcac	169923747
tgacatttaa	atgtcaatta	gaaagtcccc	gctctgcttg	gctggcccct	169923797
gcatcctcag	atgagaccgc	cctcctccct	gccttgccag	cctgctggg	169923847
accaccagct	cacaaaagac	agtggccaca	cagcaaccgt	gactgaagag	169923897
tgtgcagggt	ccaaagaggc	taaagtggct	ttaagagcac	tccggagggg	169923947
gaggactctt	ggaacagaga	aaggaggagg	atggtgccag	gccaccacca	169923997
aaggcacgtg	gaagggggct	gggcaaatgg	tgaaggagca	tgtgggagac	169924047
aagtttagag	gtagcgttgg	cttctcctc	tcttccctca	gtacctacag	169924097

FIG. 1.80

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ggcagaatct	agagcttggt	tgtgccttgg	cccttagggc	ctatgtttct	169924147
gcctctgtgg	ttgatcacc	tccattagac	caagggttc	ttgagaccag	169924197
gttcccatct	cttcatcaca	caggacgcct	atgcacacac	ggtgcctggc	169924247
acacagtagg	tacacaaggt	agtctattca	gttcaataca	gtatatattc	169924297
gttgagttcc	cactgcgtgg	tgggcattat	cctaggaact	gaggctacaa	169924347
caatgattgg	gactgagacc	tgccccaca	gagtgtacag	atgctcttca	169924397
aattaccatg	gggctacctc	ctgagaaacc	cattgtaaat	caaaaataca	169924447
gaaatcaaaa	acgcattttag	tacccccagt	taatccatca	taaagtcaat	169924497
aaattgtaaa	ttgaaccatt	ctaagtccag	atgctcctta	acatacaatg	169924547
aggttatgtc	tcaataaacc	catcataaag	tcaaaaaatc	tgaagtcaga	169924597
ccgtcgtaag	tcagggatca	tctgcgttac	attttttaag	acagacagaa	169924647
aaatagatat	gtggcaaagt	tttagatgga	agcaaagaaa	agaggcagcc	169924697
ggccccacct	ggatgacaag	aaagcttctt	ggaggaagtc	aaatagagct	169924747
gagacccaaa	gaataaatgt	gcatttgcaa	gacagagagg	cagaggggaat	169924797
actggacaga	gggcccagca	caagtgtgga	gccaggaggg	agcctaggag	169924847
tgcacagggg	ttggtggcaa	tgggcacagc	agcttccttg	tgaaatctga	169924897
gctcagagac	cacatgactg	catgggggtc	tgcaaccagc	acgtgagctc	169924947
tgtgagggca	agggcctcat	ctgtcttgtc	cactgctgtg	ttcccagagt	169924997
tggggaaagt	gcttgatgtg	tagcaggcac	tcgacaaaca	tttattggat	169925047
gagtaaata	atgctgtctt	cactggcctc	tctcctcttg	tccagttccc	169925097
aaagctcagt	gggtccccgc	aaatgcattt	attttgcaaa	agcctttccc	169925147
aaagcctggc	atccaatggg	tgcctcattt	cctcatcccc	tgcacgccgt	169925197
ctctcagtc	ctgagctgct	gtgcccacga	catgctccat	tttctcataa	169925247
aagcccttcc	aacaaggggc	acatttgcat	ttcaagtttc	ctggaattgg	169925297
agtacagaga	aatctgactt	ccagagccca	gggctctaag	ctgcagctgg	169925347
agaactgaaa	cacagcaagc	aggacacctg	cccagaataa	ggttcaggcc	169925397
ctggaatata	acatgggacc	catgctcctg	tagctgtctg	cagtctcgag	169925447
ccccaaggea	gtagaacagg	tgttcatctt	ctcctgcact	ctggaaatgg	169925497
agtcaggggc	ctgagctact	gagttttag	actgcaactt	tggttagcaag	169925547
aggcatttct	cctcctcacc	tccaccaca	cacagatcta	gttcccctcg	169925597
tacgtgccc	tttcagtctt	ggacactgca	gaagacctgc	taggagagcc	169925647
taagaaaccc	aaagccttcc	cacctgccat	ccaccaacta	tcattttactc	169925697
acccccactc	ctccagagtg	cagatgacta	tttcaacttac	tgattttggca	169925747
ggcgtgctg	ctcctcacct	tgggtggagt	agagtttacc	ctgcccagcc	169925797
ctgcaggccc	agtggtaaa	ggaaggaggc	tagtgattat	tccgactttg	169925847
gatcaatcag	ttgctcagtt	tattggaatt	acatcccagt	ggctgctatt	169925897
gatggaactg	ctggactcgg	gccacaatc	ctcatgccag	ttttataaca	169925947
ctgacatcac	ctgctcacac	acagggttc	ctctcccatc	ctgtcccat	169925997
acctcactct	gtagcctgag	atttctaagg	tgggggatct	gcactgggtg	169926047
tttggcataa	atgatgtaag	agatttctct	tgtattgtct	tcagctacat	169926097
cttacctttg	tgtaagaatg	caaagtcata	agcacagttt	acaattgcaa	169926147
tgggaggtat	gtgctagttt	taaggtgttt	tgtttttttt	tttgtttgtt	169926197
tgtttgtttg	agacagtttc	actcttggtg	cccaggctgg	agtgcaatgg	169926247
cacaatcttg	gctcactaca	acctctgcct	cccagggttc	aacgattctc	169926297
ctgcctcagc	ctoccaaagta	gcttggatta	caggcatgtg	ccccacacc	169926347
tggctaattt	tgtattttta	gtagagacag	ggtttctcca	tgttggtcag	169926397
gctggtttcc	aactcctgac	cttgtgatca	gcccgcctga	gcctcccaaa	169926447
gtgctgggat	tacaagcgtg	agccactgca	tcaggcgttt	taagtttcta	169926497
ccatttgggg	catattcagg	aagattccta	tcccaacaca	ccccttcctt	169926547
ctgcttttat	aaacacacag	agtccccaac	cacctacgt	cctctttcct	169926597
ccataaccac	gtcacagtgc	actgtaaaca	cattacgaac	cagctatgca	169926647
ataacaatct	gctgaatctc	agagatgcag	aaagaaatca	ctgggccttc	169926697

FIG. 1.81

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tattgataca	ttcttatggt	atcatttttta	attttotataa	ttatgtttttt	169926747
aaggtacatt	gtgtatcagc	acagcagcag	atgctaataa	tatattaaaa	169926797
actgtactcg	tgttctggga	gtgttcacaa	attatagctt	cacactattc	169926847
tcatcttctc	ccgcctctgc	tcagatgtcc	ttgaaacatc	tctaaggatc	169926897
ctggaaggca	aactgactac	aacactttatt	tgcacagcac	agcatctttc	169926947
ctatgacacg	tcttttggtt	tttccaatca	tcaaaagcaa	gaggtagcag	169926997
gagaccgagc	tgtaggcac	tgaccgtggc	attgcctcca	gggtgaattg	169927047
cgggggcaca	ggaaaaacag	ctcagattcc	tagcttttcc	ccaccttcc	169927097
gatctactga	accacacttt	ctccagggat	gtggcccggtg	atctatatatt	169927147
taagaaaaca	cctcaaataa	cttcccagcc	aggtgtgtgc	accacagtgc	169927197
tgggacgtgg	tattgttctt	gccatgggag	gtgggagatt	cttgtccatc	169927247
cttcacccag	aagcctgcat	gtgggttgtc	aatttttttt	tattttatga	169927297
aacttttttt	ctgtttacac	tcttgacagaa	caaacagaca	aattatatag	169927347
ctgatgtcac	atcccttttg	aaaatctatc	aggtttcatc	cattcattca	169927397
acaattgttt	ttaccagtta	cacttttttt	ttcattttgcc	atatacagaa	169927447
actgaggctc	agtgagactg	agagatttgt	ttctgactta	gcttgtaaga	169927497
aagagattca	ggaactcaac	ctagggtacc	tggccccaag	tcctgtgccc	169927547
ttttaatttt	acttccgtac	attttaatga	aatggctgcg	agaccagagc	169927597
tctgtgtgtg	aacaagttgt	gcctttcaac	cttcctttat	ctccccctt	169927647
ctttcccccac	caccaagagc	aggctgatga	gaaaattaac	attcaggaca	169927697
cgttctgctc	ccttctgatt	cccacagaga	gaacacagcc	tctgcctgcc	169927747
aattagtgtg	gttcagatct	ctattagaga	tggggacagc	tagttccagt	169927797
tatgcaaattg	cccttgtctg	agagtagcca	tgggccagca	gcatgccagt	169927847
ctcacctctc	cccatggagt	caccatggat	gtgacttgca	cctcccgtgt	169927897
tgttttaacc	aataatcaaa	tcagtatcta	tttatataag	cactggccaa	169927947
ggtactgcag	gaagctcagg	gacagatttt	atttcagcct	aaaggaactt	169927997
acatgagta	gagagtgtgg	ccagggaag	ggcagatctt	tcaaagacac	169928047
tctgttcttc	tctaaacact	cacagtttct	atttattacc	caaaaaata	169928097
cataaggaaa	aatacctaac	atttgtttaag	tacctactat	gtgccaggca	169928147
ctgttagaca	ctttatacac	attatctcat	tcaagtccat	taattttata	169928197
taagaagcaa	tatgctattt	ggttcaaggc	atgtgtttta	agtaggaaaa	169928247
actaggattt	ttaaaactag	gatttttaatc	ctgccacttt	ctccatgtgg	169928297
gactttctga	cctcagttat	tcatctgcga	aatggaagga	aacaatgtct	169928347
gtttgccagg	aatatatttca	gaagcaatta	gataagggtat	ttaaatccaa	169928397
gcacctcatc	ttcatatgac	acagcatagt	gttaagatgc	ctaatatgta	169928447
gggaaatgac	aaaaatggac	aaatgcagga	tattattagc	aacaatgcaa	169928497
aaatatctgt	atatggatga	agagtgggaag	aggacaatta	tgggggaaac	169928547
ttgttgtctt	ttaatttctg	aactatctgt	attattatta	ttatttttaga	169928597
tggagtctca	ctctgtctcc	taggctggag	tgcaatgggt	caatctcagc	169928647
tactgcaac	ctctgcctcc	cgggttcaag	cgattctccc	gcctcagcct	169928697
cccggttca	agcgattctc	ccgcctcagc	ctcccagta	gctgggatta	169928747
caggcacctg	ccatcatgca	tgactaattt	ttgggttttt	gtctgtttgg	169928797
ttgtttgttt	gtgtgtttgt	tttgtagaga	cagggtttca	ttgtgtttggc	169928847
taggctggtc	ttgagctcct	gatctcaggt	gatccaccgc	cctcagcctc	169928897
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gtattattat	gtattttcat	ttaagctttt	aaaggaaaat	ggaaacactg	169928997
cattaaactg	agcctcagag	aaattcagtg	acttgtccaa	ggtcatacaa	169929047
ggactggagg	gaccaaggca	ggatctatcc	attttcaatg	cccatgcttt	169929097
ccccacaca	ccatgccacc	acatgtccct	caggaaacag	gtctgcaatg	169929147
attcaggaga	cctcgtagtc	tacattgata	gatgtaaaca	gcattgggtt	169929197
ctgtcttaga	gagtgggcca	gtgaggaagg	catggatcaa	agcaaaaaga	169929247
aaagccaagg	agggggagga	tggagattaa	acaggtcctt	ggttgtcagg	169929297

FIG. 1.82

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ggcaaaactg	ttaatgacgg	tggagcacca	tgaaattaat	gacccaccca	169929347
aagcacctga	gaaattgaac	tggttattaa	aatgcaaata	ataaaccagg	169929397
aaaaggagga	aaacaagcac	gaggaattag	gaagaaggaa	gatatggcat	169929447
ggagtaccac	gaacagaaag	tctgtggcca	gcacctggat	attcagagaa	169929497
agagtgtgat	ttaggcttca	gaagggcagg	ggtctgtagc	ttagggactg	169929547
ggcagagctg	ttacctagaa	aagctagaaa	cagaaatgca	taaatcccag	169929597
ttgtccctga	cagtgggata	cagtcagggc	ctgaagtgca	ggggaaggcc	169929647
atcttaggtc	agaggcagtg	gttcttggca	tacagtgggt	ttccccctaa	169929697
gaatgttagg	caatatttgg	tgacatgttt	aatgagcaca	accagggttaa	169929747
gtatctactc	actgctaata	tctgggtgagc	agggagacca	ggggtgctgc	169929797
taagcatcct	acaaggcctg	gggacctccc	caccaactac	agttatccag	169929847
tccaaaatgc	catagtgtcg	ctggggagaa	accctgatct	aaggatgagt	169929897
gagaaggtgg	atacaggagg	tgaggagggtc	agaagtcaga	ccaacatca	169929947
gatgggaagc	taggaggaaa	agagggtcaga	aaaggagtta	tgaaccaaag	169929997
gacaaaagga	agttaagtag	tcagtcagga	gatgaggatc	atagaggaga	169930047
tcaggcaaag	agaagtccag	aggtggaaaa	aagcttcaga	gctcagacgg	169930097
gctgggctct	aacaatcatc	acagaagcag	caaagatcaa	gaagcaatgg	169930147
ggaaggacag	ttgaggctag	cgccaggggg	aagggccatt	ggtgaggagc	169930197
ctttctgata	agaagttgga	tggagaacac	catggtggat	gtggatggag	169930247
gtcaaagtga	tgatgttctg	gaaagcagtt	taaacaaaac	aaggggcctg	169930297
cgtgctttac	taccagaggc	catctgttaa	tggatgatgg	gaaatgccac	169930347
tcttggcccc	cacagtcagg	agcaggtcac	cttcaactgg	gcacagcaac	169930397
acgtcccact	gcaggcaggc	acaaaagcag	aggctcatta	aagagctgcc	169930447
ctgggcccag	gctacatcct	tggcaaagga	tgagatttgc	acccaaggtc	169930497
aggatggctc	gggtgtgtgg	agcacgggct	acggagccag	gtcaatggag	169930547
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actgcctctc	tctgaagctc	agtttctcca	cctataaaaa	tgggatcgat	169930647
aacagagggt	acatctgtgt	ggatcaccta	aactgtagag	gattttgcaa	169930697
atgtgttgtt	gtgggttgcca	ttcttattgc	tggaaacata	ttccctcatt	169930747
agtatttctg	agtgtctctg	tgcatatctg	ctgcagcaga	atccttcatg	169930797
catccagcaa	acatttcctg	ggcatgtagt	atgtcccaga	cactgtgctg	169930847
acactaaga	ttacatggag	gaatagagat	taatttctgt	tctttgttta	169930897
ctaagctcct	aggggctgaa	aggcatctta	aagtcataaa	acttctcctc	169930947
gatgcttaag	taccctccac	aacatcccac	ttatgtgtcc	tgggcttgca	169930997
cacttctggt	gctgatgagc	tcaccgcctc	ctgagacagg	tgattccttc	169931047
tacagaccac	tcagactatg	agaaagttca	tgccgggtgc	agtggctcac	169931097
acctgtaatc	ccagcacttt	gggaggccga	ggcgggtgga	tcacctgagg	169931147
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aaaaaaaaaa	aaaaaaaaaa	aaattagcca	agcatggtgg	cgggcacctg	169931247
taatcccagc	tacttgggag	gctgaggcag	gagaatcact	tggacctgag	169931297
aggtggagggt	tgcatgagc	caagatcaca	ccactgcact	cccgcctggt	169931347
tgacagaatg	cgactccatc	tcaaaaaaga	aaagacaaaa	gaaagttaat	169931397
atatacctgt	attgagctga	aattctgggt	ctggcccttt	ctctgcggtc	169931447
acccaggctt	gtgttttcat	ctccacatt	acctcctatt	agggacttta	169931497
atggatgaca	tattgtcacc	cagcctcctc	tgctggatcg	ggatagcttt	169931547
ccatccagac	aaagaatttt	catgactgag	tgaccatccc	caggatgggc	169931597
tttgggtgtc	ctcttccctc	agaaagtggg	aagctccaag	tgctgcccc	169931647
tgaaaccctt	ttccagtaac	catggcctcc	aggggtcctg	gggtgatctc	169931697
agaaaggtag	acagacctct	ttagcagtaa	cctggaatat	tttgctacct	169931747
tcctgaaatc	tagagaacag	agcaactttg	caagcttctt	caaaggagcc	169931797
cgttctgacc	caggtcgatg	gagctcccaa	aatctgcacc	cccaccccc	169931847
gctgctgtgt	gcaacaggag	aggggctttc	ccggaccagc	ttttccagaa	169931897

FIG. 1.83

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acatgaattc	tttttgacac	ttggcaaaca	tttggggacc	ctctcagacc	169931947
tcactctggg	caggcccgaa	ctgtcttttc	catgccagag	ggcagtcacg	169931997
gttcctatca	gagttatttg	aataatcttc	ccaacacctc	tgagctgcag	169932047
tttcttcatg	tgtcaaatac	agataacaat	agtacttcac	tcataggatt	169932097
ggtggacaaa	gtcagtgagg	taccaggtgg	aaaaagaggt	agaacaagct	169932147
gggctttgcg	gcatgccacc	gtagtccctag	ctactcggga	ggctgaggta	169932197
ggaggattgc	ttgagcctgg	aagttcaagg	ctgcaggag	ctatgatcac	169932247
accaatgccc	tccagcctgg	gagacagaac	gaagccctgt	ctctaatttt	169932297
ttttttttaa	agaggttgaa	aggtgtctgg	cacttagtaa	gccttcaccc	169932347
tagttagctt	tgctaggatt	atgatttcca	tccagacaaa	gaagttgccc	169932397
tcagtgaagt	tctagcagag	tcatacaaat	tgggttaaaa	ggaagcaatt	169932447
tagcatggag	cgagcctaaa	aatgcaccaa	agtaatgaaa	agagcaaagc	169932497
atctagacat	ttgatattctg	gctgtttttc	cctaggacca	ttgtcatgga	169932547
tggggatagg	agagccatct	aaggtccctg	cccattctgca	acactctcct	169932597
gtttctgctc	cgatgctcta	cgatgtcgta	cgtggcagag	ccagcccagc	169932647
gtggacttca	gctctcccag	taactggctg	agtgatatta	gaaaagtcac	169932697
tgagcctcta	ttttctataa	aattaagaaa	aatcacactc	ccttataaaa	169932747
tccttaggga	aattaaagat	ccttgggaaa	atagatctct	tacaggcata	169932797
tcttgataac	ctgatcaatg	atagctgcta	tagtcttctt	ctgatcatgc	169932847
ttttcataat	aatcatctta	atcattactg	gcattcaaag	ccatgaagca	169932897
cctgggagaa	ggagaagctg	atctgtccat	gcctgtctcc	tttggaaaat	169932947
gcacgctgtt	acacttcccc	acatgttcaa	attcatactc	tctcccccac	169932997
cccctttttt	gagtgcctcc	aataggcact	tgagaaggct	gaagctggga	169933047
ttgtaaactg	ccagatctcc	tgcttctgctc	tcaccctctg	ttccaaatct	169933097
tatcaaatat	taaaagctgt	gaaatagagg	caggttttaa	atcattttta	169933147
tcacagcatt	cctcagcctg	ctcaaaaggg	ctcaaaggaa	tcgattcaga	169933197
agtggtaatt	atgactgtgg	cccctgtcca	ggcgggcggt	cagcatttga	169933247
gcaccagcga	cagacggccg	gcactgactg	gggagggtct	ctcccagggtg	169933297
gggacaccga	acaggagatg	cctcctggga	ggaaataaag	ctaagtcac	169933347
ccaggctggg	tatcaggttt	taaaattcat	aaccaagtca	actgaaaatc	169933397
agcttacctt	tattaagtcc	cccactaagt	gccagatgct	tttagcctca	169933447
tttaaccctc	agataactcc	tggagggtatg	tgctattatc	ctgattttata	169933497
agtgaggaaa	ctgaggctaa	aaaatgataa	gtagtgtccc	aaagccaatc	169933547
aaaaagtagc	tcaactagat	ctatccagct	tggagcctg	caatttggtc	169933597
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aggagggtgt	accacaggtt	ccctgtgtgt	ccttctccag	cctccaccat	169933697
ctgcccggtc	ctcactcact	ttcctccctc	ttccccaca	ttgtcttttg	169933747
gactctgggt	gactcttgct	gtcctctggc	tactgggatt	catccatgca	169933797
cattagaacc	cagttagggtc	actaaccttc	tgaccatcac	agcccagctg	169933847
tcataatcct	ccctagactc	atctcttccc	tggccctttc	acctccatgc	169933897
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ctcctgcctt	cctgacctgtg	cgcaggcttt	tccccactg	gagcaacttg	169933997
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aattgttggg	attcctttta	ctggccagac	tggaggagga	cagagagcac	169934197
gtccatctga	ctcaccacag	tccagggtta	agcagggttg	ccggtacatg	169934247
gcaggcactc	agtagacaat	ggctgagtga	gttatgtcaa	taatgggacc	169934297
gtgcttaaat	gtggacattt	ctgggggctc	agggaatagg	tcatttctgtg	169934347
ggccagacaa	agcatgcaag	tgagcagagc	tggcccttcg	cctacaaaat	169934397
accgaagaat	attottcaat	atcacaagaa	agtatctttt	ccatcatttt	169934447
tcttgaaaaa	tgcattccctc	ctgatctatc	tttcattttc	tcacatttaa	169934497

FIG. 1.84

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tagagatgtg	aatacagaga	actatatctc	tactataaga	caaatagcac	169934547
cctacgcaca	gtaatgacag	cccaagtagt	ctacttgtag	gaacaatgaa	169934597
aggaagtgat	gggggctggg	gtgaatggag	gtgcaccgag	cctgtctaaa	169934647
gaggctgctg	cttctcaacc	tcagcctggt	attgccccag	gaaatgtgaa	169934697
ccagtgcagc	cagatttcct	gacttcaaga	ggagctggaa	atcgactgta	169934747
tgcgtaatgt	cccaattttt	aagagctgcc	tcaattgaac	acgcacaggc	169934797
acaaacaaaa	acaaaataaa	caagccaaat	gcaacatctg	ctgagagggt	169934847
ttggttcttg	gattgcaacc	tctgcacaca	ttttccact	aaataaagaa	169934897
aagctccttg	cagatggacc	ccggtgggac	ctccaatacc	cggaatgcac	169934947
cgaatggctg	ggatttgtgt	ggccccaaaa	ccctcccttc	ttgcgctcac	169934997
agtgccttct	tgaagcttca	gcaaaccoca	gcgccaaagg	aaaaatattt	169935047
ataacctgac	taggcagcgc	ttaaaagatc	aaggcatacg	tgggtgtgcag	169935097
aaatcactcg	cacattgttc	ctgtttcctc	tctgccatag	gatcaaatgc	169935147
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atgttattga	ctgaaacaga	aatattcatt	tcaggactct	gctgctggaa	169935247
caaacacaag	ctctggggcg	gggctgatga	tgaactgatgg	cacaggttgc	169935297
tgcacatggt	tctgtgctat	cggattcaaa	ccaccctga	gactgctctc	169935347
tttacagatg	ggactcaggg	aagctcaaac	aactatccaa	caacaatcat	169935397
ttagtgtgac	tttattaatg	gccactatcc	atggaatggt	tactctattc	169935447
cggatacggg	gccaggaaca	ttacctatac	catctcattt	aagcctcata	169935497
acaccactg	ttatatattg	gaaggagcct	tggcagtaac	attttatact	169935547
tgaataaact	gaggcagaga	agcccaaggc	tgctaagcag	cagagcagag	169935597
gggccagtcc	ccagcccaga	gtccccacct	cggctctggc	attgctctcc	169935647
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ccctctgaaa	ttcgagcact	cttgaatctc	ttgcctgggg	cccaattgag	169935897
catggttgct	ctccaggaat	gtcccagggc	agtgcctctc	taactcaaat	169935947
cctgggagat	attctccagc	gtctatgaat	tctccaggta	acctctttac	169935997
aaaattttaa	atttttcatc	aaataataat	catgtaacaa	tcaatttact	169936047
atttttaggt	gtctgtttta	atcaccttat	aaccatctat	gttgggggtc	169936097
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aaatttcagt	gtccataaat	aaagttgtat	tgagacagca	gttctcattc	169936297
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tttgtgcttc	cagctgagtt	gggtactctg	tctgttgtgg	ttttgttcaa	169936497
gttcttggat	tgcaacctct	gcataaattt	tctgtctaaa	tagagaaaaa	169936547
ctccttgcag	agggacccaa	gtgggacccc	cgatacccag	aatgcaccaa	169936597
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aagtcctcac	attattgtct	acaggttctt	tgatattgca	actttattaa	169936747
gtgaaaagac	atataaagaa	accaatttga	ccagaagcta	attgaaagaa	169936797
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tgagctatac	atgcatttaa	gaaagattaa	gcaaaacaag	tcagataatt	169936947
atttacccaa	gtttggtgaa	ttagcgagtg	ccagcagtc	tagtggtggt	169936997
ctgttggatc	aaggaataaa	tgtttgaaag	caaaagttgt	caggagcacc	169937047
tcctcctacc	acacagttca	aaaacaatta	cagatatggc	aggctcgcca	169937097

FIG. 1.85

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agcacttoca	taccacatgg	tttattgcct	tgcattttgta	cgattatctt	169937147
ctgctttaca	aattttttatt	ttacaattac	ttttattcat	tgactgattc	169937197
atttttccaat	ccacttattc	cagttcaggg	tcacaggtgg	ttggagccca	169937247
tcccagcagc	tcaggggtgcc	aggaaggaac	ccaccctggc	caggacgcca	169937297
tcccatggca	gggcacactc	acacacacct	acatactcac	actgggacca	169937347
caccagttca	cttcacatgc	acagctctgg	gacgtgggag	gaaactggag	169937397
tccttgagga	acaccctgtc	agacatgggg	gaaacgtgcc	gattccacac	169937447
agacagtggc	tctgccaggg	tttggtgttt	gtttgtttgt	ttttcatcaa	169937497
tgttatatga	agcaacagta	ttcgaagacc	tgctgtacag	ctttccagca	169937547
gttccaggaa	aaaagagccc	tgggagactt	aagccatcac	agtacaaggc	169937597
agtagaggca	gggtgaaata	gaatggaaaa	aaaaaatgtg	aaccacact	169937647
gcagtcatac	tgggaagcagc	aatcccat	caaccaaaca	acctcacatt	169937697
aaactaatgt	tgttaatttg	aagtttattg	gttttgcagt	cgtattttgtg	169937747
tttaatttg	aaatttg	cagttttata	gctgaataag	agctaaaaag	169937797
cataaggatt	ttatacctaa	gttttatgtc	tgtacatatt	aagtaacatt	169937847
atggtaaagt	caacacttac	tgaatatgtc	ccctttaata	gggcataatgt	169937897
tacttaagtt	taagcaggaa	aatgggttt	aagaaatacc	aattgtatta	169937947
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gttaaataag	aattctaagc	ttaagttgga	gacaggttct	tgggttgggg	169938097
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cctttagaag	caaaattctg	gcttgacttt	ccaatgtggg	agtgggagag	169938347
gactgctaaa	aataattggg	ctttcttctt	agcaattcac	cttattacaa	169938397
ctgttaggtg	gaaaactttt	ttttcggttt	actgaaaagt	ttaaccagg	169938447
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taaagacttc	aggagtaagt	attccaggaa	gcaagatata	agctatgtgg	169938897
ccttctaaga	cctagcctca	gaggtcacat	agtgtaacct	ctatcacacc	169938947
ctattggtag	atattgtaac	agaagccac	ccagtttcac	agatggggac	169938997
atagactcca	tttcttaata	ggtaactggc	cagagttgta	aaagagcatg	169939047
tgggatggaa	gatattgttg	caagcatctt	tagcaaatat	aactggacat	169939097
acccaatgca	agcacaggat	tgatcctcca	ctctgcccc	atacccatg	169939147
atttattagc	cactcggaca	agtgacttca	actctccaag	cctctgtctc	169939197
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gtcaccatat	gtctttccca	agaggggtgac	tgacttctctg	ctttggtccc	169939647
agtttccctg	agattttcct	gaaagccctt	ccggctagcc	cagttgggag	169939697

FIG. 1.86

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tgtagtaca	tcagatocca	tgctttggtg	aaaaatgtaa	acacagacct	169939747
gatttttcat	tttaaataaa	gccaagcata	ttgctcccag	cagatgccga	169939797
gtgactcaat	ctgtcctctc	ggttctgaag	ggaactgaag	aacaacatgg	169939847
taaaataaaag	caaacagcac	atattattggt	tgataaaatg	ctgttttagt	169939897
ctaccctggc	attatatggt	gattgctatg	tgccgaacat	ctgttattaa	169939947
atccagactt	ctgttgccctg	gatacattga	gtcaaaagct	ggagcggatg	169939997
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gcctttgtct	tcattctaac	tgaatctttt	aatatggacc	gtctcacttg	169940097
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agaatacaaa	gaaacagtgt	tttctcaggt	gctctaagta	attctgttaa	169940197
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gagttcatat	tatgaacca	ataattcaga	tcctagggcc	ttatcctaag	169940297
gacataatag	aaatgagcac	atattataaga	acaaagatgt	tcaatgaagt	169940347
gttacttaca	acagcaaaaa	aacttgaaag	tcacctaaat	gtttgttaagt	169940397
caagagcttc	attgatattg	actgcaaagt	ccatgttatt	ccatgtgacg	169940447
aatttttttaa	tcaatcacct	cttgatggat	tttaaatttt	ttacaatttt	169940497
ttgctatcct	aaaaaaaaatg	tgtcaatgaa	caactttgaa	ctaccctgac	169940547
taccacttta	ggatagattg	ctagacgtgg	aattactagg	acaaagccta	169940597
tggtataata	ttcactcagt	caacaaacat	gtcttgagtg	cccactatgt	169940647
ggtaggcagg	ctttgctcta	aacctcagag	gccccgtggc	agatgaaagg	169940697
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aggaatctag	tagacagtag	cagatgctga	ggagactgag	aacagtggaa	169940797
aggctacaca	cagggatctc	tgagtgccat	ggttcagaga	tcattgaatg	169940847
aggtgagatt	caaagagtct	gagaaagtgc	ctgatagaag	aggatggttg	169940897
gctctggagg	gacagaagtg	gaggggtggga	gtggggggaac	tggccttgcc	169940947
tgagtgtatc	caaagagcaa	atctttctca	ctgggctgac	tgacctcgag	169940997
aacaggccta	tggcccttgt	gtttcttcac	tgccatcaga	aagactgtgc	169941047
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tgagatccgt	ggagaatcac	cgcagagctg	gcagcgttta	tctaagaatg	169941147
tggcattggg	aaaagtgggtg	caggctacat	tccaggcgat	aaggaccaag	169941197
caatgaaata	acaaataagt	catcttaaa	ttaaaggaga	tggacaatag	169941247
acaaacaaat	atgtttcaaa	acatgataaa	tgctatggaa	gaaataaaga	169941297
gggttggaga	gaggggttcta	cttagatagc	ctgatcaggg	agaatctctc	169941347
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gaaagagaca	gtcatgaaga	gagattggga	gcgtaagatt	ccaggcagaa	169941447
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accttctctat	gtacaatcca	ctttctctta	aagtcacagc	agcctcagaa	169941747
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agagaatcag	tgatggaaaa	ttcaccaaga	acagccacag	gcaggccaga	169941997
agaatggccc	tgcccctcta	cttttaggat	taagcagaag	ctggccctag	169942047
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atgcatctcc	ccatgtaaca	aacctcccct	aggactctgg	tccacaccta	169942197
tctctgctag	attctctggc	attgcaagaa	attcttcaga	ctgccccaa	169942247
agattcgttc	caatctaggg	gctccttatc	cccagctcag	agctggattt	169942297

FIG. 1.87

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ggctcttgct	tggaggcggg	aagccctgct	gggccagggc	ttagaggggc	169942347
tcacaagaaa	tcaaagcaag	cattctccgc	ctctctccta	cagccctgca	169942397
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gttctaaatt	tgattttctg	agtctttaag	gaaaaatggc	tactggtecc	169942647
ctggacgctg	attgcttcag	catctgaatc	tgctccatca	cttctacctc	169942697
caccactggg	tccacgtcca	gtgggtagag	gtaaagggga	tggagatata	169942747
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tctaggaaga	caaggtggta	ataactaaca	tcaaatagag	agttcctatg	169942897
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aagtcttttg	tgcaagggtca	tgcaaggttg	aggcccccac	gtcggtagac	169943047
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ctgagcagac	catacccgga	tggtcatggt	cagggttggt	atcaatgcag	169943147
accacgctgg	gcatattcag	gggacggata	ctcagaacta	tataacataa	169943197
ggaatagagg	aaggactgga	ggatgtatta	acatgaagaa	aaggtagact	169943247
catggcagga	gatgagcagg	gtaaagaggt	gcaagacata	aaaagccaat	169943297
ttcatataca	tgaagattta	tcaagagcca	gaaggccctc	tatgggtcca	169943347
agagttacaa	ggcctaata	ggtgaattaa	tgccagcata	taaggaaaag	169943397
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agtatctcaa	gtacagatac	agatgaccca	aataaccact	gaggcacttc	169943547
tgaccccaag	tataagagat	tctattgtaa	cgcacaggag	tccatctcaa	169943597
gcagcacact	gagccatctc	cttgataaac	ctaaaggtag	gtattattcc	169943647
tcccagatgc	tgtcttctta	gcctgggatg	caaaagccat	aggatcactt	169943697
cacgtccaac	ccccatcagg	tgatctgtca	tgaatcacia	gttattggag	169943747
ccagatggaa	ctacagagct	aaaagataca	tgaagacacc	gaggcctgca	169943797
gacagggact	aactttccaa	ggtcacagag	ctaacaagt	tcagagtcag	169943847
gctagaccca	ggactcacia	gttgagctca	caattagttc	cacttcctac	169943897
accacctgga	tcatgagtgt	caagaatgaa	ggacotttgg	cagtcttctc	169943947
atccagcagt	gacaaacagg	atgcacttca	tgtgccagct	tttaattcat	169943997
tggtcatggt	ttcctgaagt	gctgttgtcc	agaaatatte	tgaggccata	169944047
tctggatcca	gtggacatga	gtgaatcatt	tatgatgtct	gctttggaca	169944097
cagggtggga	agtgacaacc	tgtgtaccaa	gggtttggca	gcottgagct	169944147
aatccatctt	aatgactttc	tgacatgct	gcctggaagt	gatattaata	169944197
ttgcaaaaga	gattataatg	tgtgataacg	ttgtagtacc	tcacttatta	169944247
aaataattca	aggatccatc	tttgatgggt	aaaccactg	tctatgtctg	169944297
tttgtgttcc	tacaaaggag	aaccacaagg	tgagtaattt	gtaaagaaga	169944347
ggtttatttg	gctcacagtt	ctacagagct	tcaagaagca	tggatccagt	169944397
gtctgcatct	ggtgtggacc	tcaggctgct	tccattcatg	gcagaaagt	169944447
aagaggagct	ggatgtgcag	agatcacatg	gcaagaaagg	aagcaaggga	169944497
gagggggaga	tgccaggctc	ttttaaaaca	ccagctcttg	ggggaactct	169944547
cttaggacta	atagagttag	aactcacttc	ttacctggac	aatggcacca	169944597
aaccatttat	ggagaatcca	ccctgtgac	ccaaacacct	cccatgaggc	169944647
cccaccccc	acactgagga	tcaaatttca	acagatgaga	tgaggaggat	169944697
caaatatcca	aactatagca	cccacctaac	gaatgcaaaa	gatgtgcagt	169944747
gaccttaagc	cccaacaata	tagagcagat	gacagttgat	atgtagatag	169944797
tttgaatgac	agtttaagg	agcaggttgg	cagggtggctc	caccatatac	169944847
ttgttgagta	gtcctgagca	ggtgtttctc	tgagatcctt	tggctgggtc	169944897

FIG. 1.88

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gtaaaatgag	agataatgac	tctctcacaa	ggttgccatg	agaaatagag	169944947
aaaataccaa	gtactcagca	tagcctaaca	tttagcagtt	gctcaataaa	169944997
tgataggaag	tattggcttt	ataatattgc	atctaccccc	ttctctctat	169945047
gttagaacct	ttccaggcat	ttaaaagggtg	agcagcaaag	gccacccata	169945097
aatgtgctgc	tagagagcac	atagggtcacc	aatctcagac	tattgggtctg	169945147
aggcagattt	ttggagtctc	ttattcccga	agagatccag	ggacctgctt	169945197
tgcaggtgac	tgagaagacc	aaggccagga	gggaaggcca	aaaagctcca	169945247
agcagatcac	ttatctgtat	aacacttttc	accttccagt	ccttcttcat	169945297
ggagtttccc	aaagtacaca	cccacagtcc	tacaaattgg	ggaagagcca	169945347
gaggcaataa	atgtgtggga	gcagtcagct	gagaactgga	tggtgaagga	169945397
ttgtacattt	tcttgaatta	catgggagca	aactgcctcc	tgagcctgct	169945447
gtacccaaat	ttatcaaagc	acaaagcatt	tttaaagacc	atttaataaa	169945497
ctgattaaat	gtatttgaca	acggagctag	aaagccagtc	aattcatgtc	169945547
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ggcatgctgg	gaggccgtcc	cagcccatct	tcctgacatc	gctgcttttc	169945697
ctgtactgtg	ctaagtgcag	agaagggtcca	gcgccttgc	tgtttttcac	169945747
ttgcattctt	gtctccagac	tttctttctc	tccccacct	tctcatgacc	169945797
actagcatct	aagtttatcg	cttctctctc	gttacctctg	tatcctccaa	169945847
gtacatgata	tacctctaca	gctcatctgc	caatgctgca	aagtttactt	169945897
atttataacc	ttcccagtg	cttggtgata	ttagatgcag	gagtaagatg	169945947
ttgtgatcga	gatcgtgggtg	gtgatgatga	tgatggggag	ggagaggaag	169945997
aggaggggga	gaagattagg	caagaatgta	aaagccctca	tgggtcttgg	169946047
aaatcacagc	atctaagttc	tctccttcct	ctccccctct	tccccctggt	169946097
tagagatgct	ttagctagcc	taagggcaga	atagcctgcc	tcttcatttg	169946147
ttcttcaaaa	tccattgttt	ggggcacaaa	atgatcttca	gagtttaggc	169946197
tcttgaggct	caataaactt	aaaatctttt	ctcagctttc	ctgtagatc	169946247
accacccccc	gaggcaatga	atgctgctga	gctgatggaa	aaagggcggt	169946297
gagaaactcc	agaaatat	tccggcagtg	tttcttcttt	atctctgtcc	169946347
cccagtagct	cagtgaagga	aagataatca	tcagttttta	attttttatg	169946397
ttattattgt	ggctgcataa	cagttgtaca	tatttatggg	gttcatgtga	169946447
tactttgata	ccagcatgta	atgtgtaatg	atcacatcag	gtcgttattt	169946497
taacactgag	gatatggatg	ctcagaatgg	acattggcct	cactgaggtga	169946547
atgcaggggt	aaatggaggc	actggatggg	gctggaaacc	ccatctgtct	169946597
gactcaacta	cctgaagatg	gaatatgggt	tgtgctaact	aaattaatga	169946647
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gaacttggtg	agaaaagaag	tgctgtgac	tattagtaat	gtctgccatg	169946747
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ccgtgcttct	tagaaattct	gattgttgtt	tggtcaatag	ataaatgaat	169946847
gcagaaactg	cttctttaat	gtaggcttag	agaaggggat	tggagttagga	169946897
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aaaagcttac	aatgccaaac	taggaagcct	gagggtcgtg	aaagggttgg	169947047
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gggacacgta	gagtcaagga	gacagaaaga	ccagcttgga	gagtgggtga	169947147
gtctgcacga	ggcgtggagg	ggtgcccagc	ccccggcaga	ggcaggtcac	169947197
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ggcagagggg	actcttttcc	ccagtgactc	atatgctcct	ttttttctag	169947297
ctgaatttca	gtttttattt	cagctccaat	cagtggcaat	agaggaatcc	169947347
gtgtgcttta	tttctctctg	tccacattcc	tccccacagt	ctcccagagg	169947397
ctaacattct	cccctcctcc	aaagagaaga	aatccacagc	ccagagcaga	169947447
gcaggcctgg	tggttctcatg	acagtcacga	gtgtggcccc	atctactagt	169947497

FIG. 1.89

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gctctccaag	tccagcaatg	tgtaaacct	ttacaggcat	tatcccatgt	169947547
aaccctaac	agccctagga	agtagacact	actagtacct	ataattcaca	169947597
ggtaagaaaa	ctgagggtca	gaaaggcaaa	gtaactgggt	gagggtcaca	169947647
cagctaagaa	gtcgcaaagc	cagagtcgaa	aatattcaaa	accaaaaaga	169947697
aaaaaaagaa	aaaaaaatct	gagttgaaag	cttgctctct	taacgatata	169947747
gctctggccc	aattaagcta	taaaatgtca	caggtagcag	tgtccttaga	169947797
gaacacctaa	gctgagaact	cctcattttt	tcagaggggg	ggatctgagg	169947847
gtcagtgagg	agatctgttt	tgtccagggt	catcagtgag	ttaggggatg	169947897
agccgggact	tgaaccttac	agtggaagaa	atgtgagcca	cagaacttac	169947947
catgttgctt	gttgacttcc	tctggcacat	tccactgtat	tttccccgaa	169947997
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cctctcacc	cccgccccgg	aaatgggtct	gttggtaccg	gaccaatcag	169948197
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cggggccatt	cgctgagtg	cacatgacag	atgttcacat	ggaacccagt	169948347
cgcagggcc	ccttctactc	tttcaccagc	acggctgtct	cccagccctg	169948397
gccgtgcttt	agagcactct	gcacccccaa	ccctggccct	ccaagccctg	169948447
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tgtatctgct	tccaagtccc	aaccttctgc	ctcactgctg	ggcaggcccg	169948597
gcaacatgcc	tgaatctcag	tgcccccatc	tgtaaaatgg	ggataattaa	169948647
taccaccccc	acagtgggtca	tgtgaattca	atgtgattat	gagtgtaaag	169948697
agtttgtccc	catgcctggg	atacagcagg	tgttcaataa	acgatggcta	169948747
ttatgatcat	cgattgctct	ctgtcacctg	tgtatcctcc	aaatgcatga	169948797
ctggcctctg	caattcatct	gcctcaaagt	ttacttcttt	gtaaccttcc	169948847
cagtaccttg	catatattag	gtgcaggatt	aagggtgttg	gattgagatg	169948897
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aagattaggc	aagaatgtaa	aagccctcat	gggtcttaga	aatcacaaga	169948997
gggcaatttg	ttgcagcaga	aattgaatta	cctttggagt	tatacagatg	169949047
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atgccacatt	gttctgtgtg	gctggggaaa	gttacctcat	ctctctgagt	169949147
ctgggtctca	gtccctcatc	ttctccagg	ctgttgtag	gagtgaatga	169949197
agccatgctc	acaaagtgtc	tagcacagta	cctggcctag	tgggtgttcg	169949247
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ccccaaactta	cagatcacca	ctccocttga	gagcagagtt	gtacacttca	169949347
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tcacagccca	gtggggaaga	cagatatata	ggcaacaagt	ttttaattgc	169949547
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atataaatgt	attatcttgc	agttctggag	gtcagaagtc	caaaatgagt	169950047
cttatgggac	tcaaatcaag	gtgtttagt	gctgtgttcc	ttccgggggc	169950097

FIG. 1.90

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tccaggggaa	agtgtttcct	tgcoctgttac	agcttctgga	ggccactcac	169950147
attccttgte	tcacggcccc	ttcctccatg	tcctaagcac	atccctccaa	169950197
tctctgcttc	tgatcatcaca	tgcccttcct	ctgaccctga	gcctctgcct	169950247
ccttctgaga	aagacccttg	tgattacatc	aggttcacct	ggataaattca	169950297
ggataaatctc	ttcatctcaa	aatccttaag	ttgatcacat	ctgcaaaaatc	169950347
tctctttacca	tgtaaggtaa	catattcaca	gcttctgggg	attaggacat	169950397
gcatccctag	ggaacccatga	ttcaacctag	catgggggaa	cccactacag	169950447
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catggatatt	cattcagaga	gagcatgcac	tgaggcaagc	ctgacctcaa	169950547
gatcaagaca	ggaaattggc	tttcatgggt	taaggacctg	ttactttgct	169950597
catcaatgta	tccttaataca	tcagagggtca	gatctgctgg	agagtgcatt	169950647
ctttcagttt	ccaaaagtaa	gactggatgc	cttagaactt	aaagtccagg	169950697
aggtagccaa	gaaagcaatc	atagactgag	tcctccatgca	gtgcactttc	169950747
tcggatggac	aatttctctg	ttctgacagt	cactgttgac	tccattttctc	169950797
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cagtccaggaa	gtggaaatcc	atggaaaactc	atcatcagct	gcctcgcatc	169950897
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gtagtattgc	aagatttgaa	cagaagcgag	cagcagcttg	tagttgtgtg	169951047
tgtcactcac	tcctgcctgt	ggggatgcca	cgtgattgtt	taaaggggtg	169951097
gaatcaggag	aaaggcaggc	tcagagcagg	accaagagag	agcccacccc	169951147
tcgcctcccc	aaatccttca	gcttcctgaa	gtgtggctgc	tgggtagcag	169951197
ctccccagg	gaagaaaata	taagatatct	ccaagggacc	ctggaagctt	169951247
tatcccaagg	cttcacatgt	gtaggctgtt	tcctgtgatt	cggctctggc	169951297
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atgtagtgc	ggggttcagc	atccaggcct	aggacttaga	ctgaggctct	169951397
ttacctcct	ctgtttcttg	ctgatggcct	taggcaagtc	gcttcccctc	169951447
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atgttagcca	gtatggtctc	gatctcctga	cctcttgatc	caccgcctc	169951797
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cgagctcata	ctttcatgtt	agcattagca	tagttcctga	caataagaac	169951897
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atggggatgg	ctcagaactc	ccagcgggag	ttaggaggaa	taatgtatag	169952597
gaagtatgag	cagagtgcct	ggcctggagc	atagcgcag	gccgatcata	169952647
ggttaagtgt	ggtgttgatt	ttattggaca	caagtttggga	aactcagagc	169952697

FIG. 1.91

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ctgcagggat	ggccttgaag	gtaaagaaga	ggtagttggg	agttttacac	169952747
ttcccaggac	ctaccctcag	agagacaggg	gtcattccag	agtatctgga	169952797
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ggagaagtga	gtctggaggt	ggaaatgaga	tctccaagga	ggggatggct	169952997
gactgaggct	gacacgtttc	tatccaaccg	gtagaggatt	tgcagttgga	169953047
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gaggggtgatg	ggaggggtga	gggagggttc	agtctcacgc	taggctgcct	169953147
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aactctgacc	attcctggga	ctgtctccat	ttcaaacat	cagatccct	169953247
gccagactgt	attagtcaga	gcagtgcaaa	tgctgtaaca	aacagcccca	169953297
agtgtctgtg	gctgaaacca	tgacagttta	cttctcgttg	ccatggcagc	169953347
cagtgcagct	cagagtggat	gggcatgtct	gcactctgcat	gcatgcaggc	169953397
tccttccatc	ctgaagctcc	ccatcctcgc	ccttacactg	ctggctggga	169953447
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ccacacagac	ttcccttgga	aggagaagag	aacaaggaca	ctgtgcacct	169953597
ttgtcaagcc	aaccaccatg	cccatggagc	atctactatg	tgagagatg	169953647
tcagctcctc	cagacaatgt	tctctgtcat	tttccatctg	ttcaagctga	169953697
gtcagagggtg	tgtacatgtg	caaatgcgaa	caatccaggc	tcacttcctg	169953747
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cacttgctga	gatctcccag	ttcgtttttt	aaaaattgtg	gtaaaatata	169953997
tgtaacagaa	aattttaccat	cttaaccatt	ttggagtgcg	cagttcagta	169954047
ccaccaagta	ccttcacggt	gttggacaaa	cttcaccacc	atctgtctct	169954097
agaatgttct	tcatcttgca	aaaccaaacc	tctgtaccca	ttaaacgact	169954147
ccccattccc	tcttccccca	gctcctagca	actaccattc	tattttctat	169954197
ctctacaaat	ttgactactc	taggtacctc	gtataattgg	aatcaacagt	169954247
atttgtaccc	tggcttattt	catttagcat	aatgtcctca	gactttattc	169954297
atgttggtgc	atgtgtcaga	atttccttcc	tttgtaaagc	tgaataattt	169954347
ttcattataa	gtatatacca	cactttgttt	atccattcac	ttgtcgatgg	169954397
aaatttgggg	tgcatccacc	tttttttgct	attgtgcata	atgctgctat	169954447
acacatggct	gtgcaaatat	ctaattattag	tccctgcttt	cagttccttt	169954497
ggatatgtat	ccagaagcag	aattcttgga	tcatatggta	atcctatttt	169954547
taattccttt	aggaactgcc	atattgtttt	ccacagcagc	tgacgcattt	169954597
tacattccta	ccagcagtg	acaagagttc	caatttctcc	atatcctcac	169954647
caacacttgt	tattttctgt	tgctgctggt	tgttttttta	ttaatagtca	169954697
tcctaattggg	tgtgaagtgt	tttctcattg	tggtttgctt	tgaggtttt	169954747
gatttgtaga	ttttcctgat	gattagtgat	gggtgcactc	tttcatgttc	169954797
ttactgacct	tttatatata	tttcttgagg	aaatgtctgt	taactctact	169954847
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gatattagta	tgttcgtggt	acagtaaagc	caactaaacc	ttagaaagac	169954947
taggttaatt	atccaaggtc	acacagctag	aaaatgacac	agcttgatt	169954997
gaaacatcag	tttttctctt	tccaaacctc	acgcacattt	catgaaacct	169955047
acattattgc	accataacat	catgttgatt	tacttatctg	ctctcctgcc	169955097
tgtcccatct	actacataaa	ttgagtgtgg	tttgaaatca	gagactactt	169955147
ctcatctttg	gcacagtggc	agccatggat	cagaatctct	tacatgctgg	169955197
ataagtggat	gcaagctcaa	ggccacacct	aaagtcccca	ggtgacttga	169955247
tcacttgagt	tagctgctgg	aaacctgggc	ttcctcttct	gcaaaatggg	169955297

FIG. 1.92

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gagagaaaat	aaattctcag	tggattgttt	agaagatttg	agcaaagacc	169955347
tctgcaaagt	gctaagcatg	tggctagcat	gtggcaggtg	ctgcctaaat	169955397
agtagaaatt	aacactgcc	tgcttataag	ctccggacaa	acacaagaag	169955447
cccgaaacat	aatctgtgcc	ttctgcttgc	attcctccta	gttgggggatg	169955497
taaaatagcc	cagctacaat	caaagaagaa	aatcaaagtc	agcacagact	169955547
atggatatgc	ttctatatgt	gtagattatt	tccagactca	ttcggaagaa	169955597
tctggacata	ctggttgcc	cagaggtcaa	gaaaattggc	tcattttactt	169955647
ctgtaactta	atttcgactc	tctatgcttt	tacatagttg	gaatttgcca	169955697
tgcacatata	ctacatttaa	aagagcgtgt	acgcgagaat	aatgtggtca	169955747
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accccatctg	gcttctacct	gccaacccca	tgtattctgg	agactctcca	169955847
cacctcctgg	catgaagcag	aatccctctc	aggggggtcac	ctcacctcct	169955897
tccagaaatg	tttaacagaa	agaacctacc	attggctttc	tccatcccca	169955947
gcacctata	gagatatcac	ggagagggga	gcatttgtaa	tttactttgg	169955997
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gcccccttcc	acctatgaat	agcttcttgc	tataattgtt	cacattctgc	169956147
tgaattagaa	gtattcaagg	gagaatttaa	gaggtattta	ggcaacaaag	169956197
ataaatcggg	tgtgttttcc	accctcccac	aatccctcat	taagcgagac	169956247
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tcagtcactc	tctccctgag	tggagggagc	cggaggggtt	gccacagcag	169956347
cgtggacctc	aggaaggggc	tggagtgttg	ggatacatgt	ttgggggcct	169956397
tcccttccca	gctattactg	tagaaaaaga	agaggatgcc	tgaggtggtg	169956447
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tttatggacc	tctgttgtat	aacagaatac	aagatataat	tcttcattca	169956547
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gacattgagg	gtccccctc	ccatgttatg	ggaactcaagt	cttccaaagg	169956647
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gaatattcaa	caatacccag	taggggtatga	agcaccgtag	gagttccgtg	169956747
actattccca	tcttccctca	tttttgttgg	tacctcttcc	ttcctgataa	169956797
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tccaccccac	tctgcctccc	aaagtgtctg	gattacaggc	atgagccact	169957347
gcaccagcc	taactacagt	ttctttatct	gtaaattgga	aataacaata	169957397
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tgtggcaggt	ataagagtca	aggcccactt	caaggccacc	aaagtccaag	169957647
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ggtgggggtt	aaaaatggag	ggcagcggta	ccagtgaagg	ggaagcagtg	169957797
ataaaaacca	tttgagtctt	tgctctgaag	cagagtccat	taggatgacg	169957847
gctccttgga	ccaggggagct	gcgtctgagg	ggctgtgccc	agttccatca	169957897

FIG. 1.93

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gtggtgggat	tgggagtggt	ccatgaaaat	aactcacatg	catgtgtggc	169957947
tggctgaaga	agcagagaag	cctgcatggg	cagccaatcc	ccatgctgag	169957997
cgctttgott	ggaatggctc	tgataaagaa	gcccattgatg	ctggaaggaa	169958047
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accctccaga	atatggtcta	ggatggcctt	gagtgcgtag	gtttcagaat	169958147
gtgggaagaa	ggggcaagga	gaaaaaaaca	agcacctatt	gatcacctgt	169958197
gttagctcat	tcaatctttc	taacatctct	gcaggttaaa	tattctatcc	169958247
cattttacag	agggcaagct	aaaactgaga	gatctaagat	gattttgcca	169958297
aggttacact	gctagcaaat	ggttagattt	gaacccaaga	ctctaactcc	169958347
aaagagccaa	gctctttaca	gtggatcagt	ccatcatctc	tttacatttt	169958397
acaagtttgt	gtcatgggtt	tagacaatat	gtttgacatg	caagacgctc	169958447
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gtattcaaga	aagagccaat	aattcaaaca	actaattcta	gaagaataga	169958747
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cagctgctc	ttggaccagg	agctaaggga	gaaactcctt	ccttagagac	169958947
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gttctggaga	tctgcgagca	ggactgtatc	catgaatcag	gactctgtct	169959047
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catgagtagt	gtgagctcac	gctgagttag	caactggctgt	gcaccagtat	169959497
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tggttcaatc	cagtttaaag	gccaggagca	ggacagtgc	ttgcagctgc	169959797
agcaatccta	tgactcaaac	caaagcagct	gtgacaaata	aagggaactga	169959847
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atatatatat	atatatatat	atatatatat	gaaagaaaga	aagaaaagag	169960397
agagagagaa	agacacaaag	gggaagcttt	catgccaaagt	ggaaacaaga	169960447
caaaataaat	gcacogaatc	cgatttcaaa	agctgtttga	aaactctgtc	169960497

FIG. 1.94

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cggaattgct	ggaaagggcc	ccagcatcca	caggaaatgt	atccctgcc	169960547
agccctgtgc	tactgaactc	tgtggccccc	actcctgcct	cccgggtgact	169960597
tgtttagaac	tacttcagat	cggaacaaat	cacagccaac	tgcagtcgct	169960647
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agagaaggca	ctgaaaaggg	tcattctgagt	ccatgtttgg	tgaatgcca	169960947
ccttgagctg	gacacctggc	tgtggtccct	ggagttggat	agcctgggtt	169960997
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gacaagggtac	ctaccctgtg	agtatagaag	caaaccccca	gaaaaaagca	169961097
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gctcaggaaa	cttttatcca	aagacacaga	ggagctgggt	gcagaggaga	169961197
gcttaaaactc	acacagagag	gggaggcctg	ggaggtgtca	acaagttatc	169961247
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aagggaccag	tggacagaag	tcagcagagg	ccatgtaggg	gcaggagctt	169961347
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gcgcgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtttgggtggg	169961497
gtgggagggg	aggcagaaga	ggaagagagg	gcagagagcc	aaagactgag	169961547
gccccggccc	ataagtaagg	cagtttgca	atctcaatat	cctgtgcaga	169961597
cccacaggct	gccgtggggg	tgagggtctg	tggtgtctta	accagaggca	169961647
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gaagactcct	cactccccga	ggaatcgct	gcaatgtcat	gatggcatct	169961947
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agtggagctc	agaggtgccc	tcccaccccc	agattccatg	atgctcagga	169962147
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ctggtagcac	caggtagcac	cccatcctct	gtgtgcccac	gcctacctcc	169963097

FIG. 1.95

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tctctacctc	acccacccctg	gacagaccct	cacaccacac	ttctcacatt	169963147
acattgaaac	tgatgactgc	cttgtcatct	tctccctgga	gcatgtcatt	169963197
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gtttgcgcgc	taaggctgta	gactgggctg	cagtgccttt	taaatacacc	169963747
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agacatcaca	ggagaaggag	gcagaagctg	gaacatcatc	cgggagctgg	169963947
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tgactcatt	tcgcccttca	acaattatac	taaacacctg	ctctgggcca	169964247
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gtgataactt	tctcttgtgg	aactgtgaaa	gtgtaagacc	agctcctgta	169964697
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cttataaatg	gggtcctggg	ccgtggcact	gatctgggtc	tcccaccttg	169964797
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ctcactcact	cagtgtctga	cacagtgggc	ctgacaagac	agtgtgtgtg	169965197
cttccatgaa	cctaggacag	ggatagactc	aaggactaag	aacaaaccag	169965247
gaagaagcat	caccacaggc	tccttgccag	tcacctcatc	tcacctcct	169965297
ggccctggcg	gatgggtctc	catatttaca	ggggccagat	gaaaaaacca	169965347
gaggagccag	gaaaaggagc	ttccccttcc	caagggcgca	aggtgaggtg	169965397
ccagtcatga	gatgcaagcc	ctgagctttc	tgattccact	gcatgtgggc	169965447
ccaaggttcg	gcgccgcac	acacagttag	tgagcacact	ctcctcccct	169965497
ggccccaggt	gagccagctg	gatggcagat	cagaaagaga	agtcccgggt	169965547
gcccccaaca	tggctagctc	cttccaggac	caggggctag	gccccagcta	169965597
aggctggtgc	acacagcagg	gcagggggcg	aaggagtggt	atcccaccca	169965647
gggatccac	ccaccccaaa	cctgctttcg	gacatctttc	caatgcataa	169965697

FIG. 1.96

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tgtgcagatg	aggccctttg	ataaggacca	aatccctttc	cgttgcttgg	169965747
caacctggct	cacaagtcac	agcaggggaag	taattttacag	gaattcaaag	169965797
tgtcgctgga	ggttctgctg	agctgaattg	ctgcaaagag	gaacctcaat	169965847
ggtccaaatc	acacctctgg	cggggaggag	gggctgaagg	aaaagcttcc	169965897
acttccgtca	cttgagagta	cagagccctg	agctcagact	cagcgatcgt	169965947
tttccattaa	cggattttact	ggttccatgt	tgagctcctg	ctgtgtggca	169965997
ggccctgtgc	tgggagccag	ggacacagtg	acaaacgaga	cagatgcca	169966047
ccccggatgc	acagagctca	aagagacaga	ggagtaaaca	gggctacaca	169966097
tgtgacaaga	taggctgtgc	acaggggtct	gagcaggacc	cttggggcag	169966147
gaggaggcag	tggagggatg	ggagggtagg	gacgcagtgg	tgaccagcta	169966197
gccagataga	gaacagaggg	tgtcccagca	cagggccaca	caagcaaagg	169966247
cagaggtggg	gagagaagag	cctgccacac	tctcagatca	ccatgtgggt	169966297
gggccagggc	cccagctgag	gctgaggaca	catggagccc	agatccggca	169966347
gggccttgaa	tgccaagtca	gaaagcatct	gaaatttagt	ctacagatga	169966397
tgtgggttat	tgacagccag	gacaggggaat	gacatttgtg	tttcaggaaa	169966447
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tgtgaaactg	gagaagaaaa	ctgttgaggc	aagagttgac	aaaacttgaa	169966597
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ggtgggaacc	aggggaagagg	aggggctttg	caggtgtctg	acttgcccaa	169966697
caggtggcgc	catttaccac	gatgggaagg	gccggggaga	agggaggggt	169966747
ccattctagg	gaaatctcag	gtcctcgtca	ttaggattct	ttcggttgcc	169966797
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gatgccagag	cccatgggga	cagcgggtga	tgttggacac	agtagtcctt	169966947
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gaggctgagc	agaacattta	ggatccttgg	ccccatctca	ttgtgccctt	169967047
tgctgtggct	catctcacac	ttgcagggag	aagccaatgg	atctctgtga	169967097
atggcgaggc	tttgtatgca	taaatgtggg	ccattttgtc	cccaagaatc	169967147
cctgggggtg	aggaagccac	agaaaattga	ggtcctattc	cctgctcact	169967197
cctgggtatgt	agtggaagct	ggagagcctt	tgtccaggca	ctgacagcag	169967247
gaggtttcat	gcagagctgc	tcagggcatt	tcccagatct	gtcccacccc	169967297
tgggaactgg	ctcagtggcc	ttgccccacc	agaagactgg	gaactgcacc	169967347
caagacaggt	tcagcccccc	caggagagga	cctgctgggt	tgcgtgtcca	169967397
cacacagcac	agaagcaagg	aagatctggc	aaacaacctt	caacaaaaaa	169967447
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gatgagaatc	tgccatgccc	ctgcccacca	gccacctgcc	caccctccct	169967747
tatcatgtgc	cccgacctcc	catgggtgct	gctcatctga	gtccctctgt	169967797
cctcactatg	acggctggtc	tgggaacccc	tctggcccta	ctctgcttca	169967847
agaccattta	gcctctgctc	ctgcttccct	attttcttgc	tatttcccag	169967897
ctgcaatttc	tttgcaagac	agggaaagga	ttggatatac	tcagcccatc	169967947
ttaatttttt	tactgtggga	aaatacacat	aacataaaat	gtactatttt	169967997
aaccattttta	aaggatgcaa	ttcagtggca	ttaattacat	tcacaacggc	169968047
atgcagccat	caccactatc	tggttccaga	actttctcat	cacctcagat	169968097
ggaagccccg	tattcactaa	gaagccactc	cccattccca	cctcccccaa	169968147
ctcctggcaa	ccaccaatct	gctttctgtt	tctgtggatt	tgcctattct	169968197
ggatattttca	tttaaaggca	tcgtgcaata	tgtggccctt	tgtgacctggc	169968247
ttctttctct	cagcaccatg	ttttagggtc	tatctacgtt	gtagcatggg	169968297

FIG. 1.97

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tcagtacttc	aaccctgttc	tttttttttt	tttttttttt	ttgagatgga	169968347
gtatccctct	gttgctcagg	ctgaagtgca	gtggcacgac	ctcagctccc	169968397
tgtaacctct	gccccctggg	ttcaagtcac	tctcctgcct	cagcctccca	169968447
tgtagctggg	attacaggca	cgtaccacca	cacctggcta	agttttgtat	169968497
tttttagtagc	gacgggggtt	tgccatgttg	gccaggctgg	ttttgaactc	169968547
ctgacctcag	gtgatctgcc	cacctcggcc	tctcaaagtg	gtgggattac	169968597
aggcgtgagc	caccacgcct	ggccacttca	tcccttttta	tggctgagta	169968647
acattccatt	gtgtggatat	accacacggt	tttgtttatt	catcagttga	169968697
tgaacctttg	gattgtctca	cattttgacc	attgtgaatc	atgctgctat	169968747
aaatattcat	gtacaagttt	ttatttgaa	acttgtctct	aattctttgg	169968797
ggtatatacc	caggagtggg	atcggtggct	catatggtaa	ctctgtgttt	169968847
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acgatccctc	aagcaagggtg	caagggtatc	agtttcccca	catcctcatc	169968947
aatgttcttg	tttttatggg	ccttcacagt	gggtgtgaggc	tctttttact	169968997
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actgatagcc	tttgtgatca	atcagactgg	ctggagaaca	ggaagatgag	169969097
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catcttccag	ggctgtggac	tggggcagttt	gggacccggg	aggggcaggc	169969197
cgtgagacct	gtctagtgc	catgtgcgac	ctcatccgat	cctcatagta	169969247
acacttacta	aaattcttaa	ccattacccc	accagtctat	gtccacacgg	169969297
ccacgctcac	agccgtccct	gcagtgtccc	aggccactc	tcacttggtc	169969347
tttgcagaac	ctcatgatga	atgcagcatc	cactgtttcc	ttcttctgct	169969397
gctctgggtc	ccctccaccg	aagcactact	ttgtccaaga	aactgctcct	169969447
tcccaccagg	cagcgcccta	ggctggggcc	aaactagcca	gtatcaacca	169969497
caggcttctg	tcccctggcc	tgagatcaga	ttcttagctg	cacagctgcc	169969547
cctgagagtt	cctttcccca	ggatgtgttc	tcaagcgggc	aatgcctcaa	169969597
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cagactagac	aggacggctc	cgtctgtcgc	gcttctgttg	gtctctcatg	169969697
cccaagggtg	tggctctggg	atcagcctgc	cctgggttcgg	atctacttaa	169969747
ttgtcactgt	cacttttcagc	togttattta	gcctccagtg	cttccatttt	169969797
ctcaggggtg	tagtgggatg	atgaaaacaa	ttcccgtttc	gtagagtagt	169969847
gatgaagagt	aaatgagcta	atcccagtaa	aaagctttta	ctcctgagcc	169969897
acagtaagt	ctcagtttat	ctaagcatca	ttatcaaaca	taaacaatca	169969947
tttacagagt	gatgaccacc	gtatgctcca	aaccacgggc	tgggggcctt	169969997
tctacttct	acagtgacct	ttagagggtga	gcagtctagc	ccccacttta	169970047
gggataatgt	gacgaggtgc	tgagagggtca	tgatctccca	gcagtgagtg	169970097
acagagcctg	aggtgaaccc	caaactctgtc	tgactctaaa	gttcatgctc	169970147
attccaatca	tggcaaagaa	aatgcagtg	cttctcacga	agggttcac	169970197
cctgcctcct	cagtggctgt	ttcaaggagg	gccctttggg	ttgcccagat	169970247
agactattca	cactgaaagt	gacaatggag	aaactggcca	ggacactcca	169970297
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atgtgtgacg	agaaagtttt	ccctcttctc	ccctcacagc	ccgcaacaaa	169970447
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aacaatagac	atattattctc	tactgccct	gaaggctaga	aggtccagat	169970597
caaggagtga	ggacagaaga	aggtaggcac	tagaacttga	cccagaagcc	169970647
tgtgacacac	acacacccca	catccttctc	cagcccccca	ttatctgtct	169970697
cctaggaaca	aggacaccac	tacattcatt	ccagaaaaga	ccccttttgt	169970747
ctgccagcca	tcctcagagc	cgaaaagcaa	acctttgctg	ctgagagctg	169970797
ctgatagaag	agcaggaagc	acagttaaag	gggaacaggc	tcccaactct	169970847
ggggcagcag	atcttttggg	cttcatgtca	tagtattgta	aagacaattg	169970897

FIG. 1.98

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ccaaagtcag	acaagatcag	ttgtgtgac	ttggcaattc	actttgtttc	169970947
tctgagcctc	agtttactca	cccataaaat	ggggagaacc	acgtctacct	169970997
gactgactcg	tgatgaagat	gaaattaaca	caaagacaag	gctgggcgca	169971047
gtggctcacg	ccagtaatcc	cagcactttg	ggaggccgag	gcatgtggat	169971097
catctgaggt	caggagtttg	agaccagcct	ggccaacatg	gtaaaacccc	169971147
gtctctacta	aaaatacaaa	aattggccag	gtgtgggtgat	gggcaccagt	169971197
aatcccagcg	actcgggagg	ctgaggtagg	agaatcgctt	gaaccgggga	169971247
ggcagagggt	gcagtgagct	gagatgcact	ccagcctggg	cgacagggtg	169971297
aaactgtctc	aaaaaaaaaa	aaaaattaat	gcaaagacaa	aattagtgtg	169971347
ggaaaaccct	ttgctcagag	aaatgatggc	cacaaagtca	tattactccc	169971397
cccttactct	gtaaaatctc	ctttgctaga	ggaagagtta	aaagtccaag	169971447
tgggaagcac	agtcccgggc	ggaggcaggg	aaggctatcc	tggctctgag	169971497
tcgggctctg	tctacctgga	ttttgtgcct	ccacgttccc	tttcatcact	169971547
ctccaacagg	gagatgtctg	tctccctca	gtgtgatagt	aatataatgg	169971597
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aattctcctg	cagaatgtac	acagcaaaga	ctggaacga	gaaaactgtc	169971697
ttcccagggg	tggcttccta	acaaatataa	tgagaaggcg	cttcctctct	169971747
tcctttcagt	cacatgggga	ggtcaacaga	gagcaatgac	tgtcctgagg	169971797
ctatttattt	attttttgcc	tgataataat	tataataatc	acttgcattt	169971847
attgagttgt	ctgtgtcagg	caccgggcta	ggcacttcac	tgcattgagt	169971897
atcgcaagca	atctttccaa	agggattagg	aagcaggagt	tattttacag	169971947
atgaggaaac	tcatgcatag	agagggtgag	tgtgacgctc	atgttagcct	169971997
aacatgagga	tccaagagct	tatccattta	ctcagacttt	ttgattattt	169972047
tttgtgcaat	ttcacagact	tttgggtgat	cataaaaattt	tttttagagta	169972097
ctagtgttggg	cctggcatgg	cagctcactc	ctgtaatctc	agcacttttg	169972147
gaggctaaag	cagcagaatc	acttgaggcc	aggagttcaa	gaccagcctg	169972197
ggcaacatag	cgagacctca	ctaaaaataa	aacaaaaaat	aaaaataata	169972247
caaaaaatta	gccaaagcatg	gtggcacact	cctgtagtcc	caactacttg	169972297
ggagactgag	gcaggaagat	gtcttaagcc	cagaaattcg	aggttgaggt	169972347
gagctataat	cacaccactg	cactccagcc	tgtagtacag	aacaagatcc	169972397
tgtctctaaa	aacaaacaaa	caaataaaca	aataactactt	tgctcattca	169972447
tttaagtcag	taaattgtga	caaattgaaa	aatgcaagaa	aaaaaaggaa	169972497
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gatctgttag	gtaaatctct	atagcagtgg	ttcccaagac	atggtctcct	169972647
gaccagcagt	atcagcacta	cctgggaacc	tgtagatttg	tcctctcca	169972697
ccctcgaatc	tgggagtcag	gccagggcat	ctggtttaac	gagcccccta	169972747
ggtgatgatg	atacatgctg	aggagtacga	accacttatg	ttagaataaa	169972797
tacacaccag	cttctaaccat	tgatatcgca	gagaaatttc	tgcattgacac	169972847
agtgagctat	tatattgacc	aaatcccat	tataaacacc	atcatgtact	169972897
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ctcaaggcac	agcttaatatga	aattagttcc	agaggcacca	agctatgtca	169972997
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ctggagccag	gctgacccaa	atttgaatct	taggtgcacc	tttcattaac	169973147
tgagtgcct	tggccaattc	ccttaattcc	ctccctctgc	ctcagtttct	169973197
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ctaattgagtc	cttataaatg	ttcccacgat	tatgaactgc	tagagtgtgt	169973347
ttcctgtagg	taaacctcca	agccatcaaa	cctatgtcca	tgtctcctgc	169973397
caccatctgt	cctggatgat	tattgttcag	atgcatatcc	caaacttact	169973447
gagtacctag	tatgtgcggg	gttctttcac	ttatatcatt	tgcctttaaa	169973497

FIG. 1.99

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cagctctgca	ctgtagttat	tattacccat	tttctgcac	aggaaactga	169973547
gttcccccca	aaatgaactg	acttttcaaa	agtcacacag	gtattaagtg	169973597
ccaaagccag	gatttgattc	caggccttct	ggcttgacag	tggcactcaa	169973647
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aagcccctag	tttatagctg	tgagagtcca	ggctacaaga	gggacttggc	169973847
ttgccctgga	cccaaagagc	taagcagaac	aaatactcac	atgttggtgct	169973897
gctcatttct	ctcccctggg	ccccacagca	tcttcgaaag	gtgaggtcaa	169973947
ttcccatgaa	aagtaccaca	ctacgaagtg	cagccaaggt	ccagaggggt	169973997
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tgtggaatca	tccacatagc	cotttgcaagg	aggtatcaca	tacatccact	169974097
cagggtcgaa	gacacagaca	gcatgtgtct	ctctagcctt	ccctctctcc	169974147
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caacacctcc	caagcccact	ccaccttctt	caaagggtaa	cctcttccctg	169974247
acctaactcg	tttcagagga	aagagcagga	actttggagt	caggcctggg	169974297
ttcctaataca	tcatattggg	caaagcaagt	cacacagcca	agcccacagg	169974347
cagtggggct	gggaaggaca	gagagagaag	ggagaatcgc	tactgaatga	169974397
cagtctacca	cacctattgt	gcaaagtgtc	ggaaggagg	atgtgttcat	169974447
tcattctgtt	aatatatatt	aactgaacac	gagccaggca	ctggcctagg	169974497
tgctgaatat	gcagcagtga	atgaaataga	cagaagtact	tttcctcctg	169974547
gagttcatgt	tcaagtgaat	aatggcccca	cacctcgatt	aatccacaag	169974597
cacttaactg	tctaccctgt	caggtttcca	tatgtgccag	acacatcatg	169974647
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agacagacag	acacccaatg	acaacattga	aggcttgca	gcacgagggg	169974747
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gtaagaggca	cttgctctcc	tggcggtccc	ctttcggaga	ctaattggga	169974997
tgactagaga	ggaggatcca	gagcctatgg	ctgaaacctc	atcaacagct	169975047
tgggagagtg	acagccagcc	agtcttctgc	ccgcaggctg	aagaggcagt	169975097
gcttcccagg	gtgagccaga	ggtcaggaat	cagaaggcct	ccccagagct	169975147
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gtggagtccc	gttgtcatgg	tggcaggagg	agaacagacg	gatcgccctg	169975247
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ccgtgtgtcc	tgccttcccc	ccaagtgggg	caggctagaa	acctctagtg	169975397
gactcctcac	cccctcccaa	gacccagtca	atctataggg	cccgtggtt	169975447
ccttccccca	ggtctctcct	ctctccctgg	attgtggcaa	tagcctcctg	169975497
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atacacacac	ccagcatagc	acatttttct	agaactcaca	cctgaacgtg	169975597
cctctcctct	ggtgaagaca	tccccagaag	ctgatccctt	tgttcccaat	169975647
gcccctccac	cctgtctcca	cctggcatat	gcctgtgttt	ccctgaaatt	169975697
ccagcttaaa	tctctctcca	tgtttggcct	tctctgcctc	ttgctggatt	169975747
cctcatctcg	cctccacccg	gtttttgcatg	gatccctgcc	actacctgtg	169975797
tgtgtccatc	gctccatcca	ttgagcctgt	gaggggaaag	cctattttaat	169975847
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acaaaacatt	aattgagtgc	ttatttttatg	tcaagtgtga	tttgaggact	169975947
ttatatgcac	taattttattt	agcttcccaa	aactccatta	ataggtacta	169975997
ttaatgcccc	ctacttgaaa	gattaagcaa	cagaggcatg	aaaataataa	169976047
agtgatatgt	ccaaaactac	acagctaata	agtgagagag	ccaagatttg	169976097

FIG. 1.100

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aacctgaagg	agatgggagg	gagagaaata	gttggggaga	ccacagggaa	169976147
aggaggaaga	agagaaggga	agaaaaggag	gcggggagg	ccgggagctg	169976197
gaaatgtacc	tttgtatfff	aagtcattga	gatttggggg	ttgttactgt	169976247
cacagatcct	agcctgttct	tactaataaa	ataaataact	aaattttataa	169976297
agaagtgtca	gaaaaaaagg	tcatattaga	ccacgaagga	tgacaaagag	169976347
cttcttaaaa	aggggaactca	aggcccaaac	atgggtattg	ttgtgtcatg	169976397
tgaatccttc	acagggggcca	cttgggtgtct	gtgtggctgg	ctctttgtgg	169976447
ccctggagag	ggaacaagca	tgaatgcatc	agtggcttcc	agcctgaaca	169976497
gaataagttc	aacaagagat	ggccccagct	ccgggtgtcta	ctggggagggt	169976547
gatgaagtga	agtgttcaat	tccctgcatag	ccaccaacaa	gtccctggaa	169976597
acacaattgt	tgaggatgtg	tccctcgggg	aggcatgggt	catctggctg	169976647
tgtcacaaag	cagatgggaa	cagctggcga	ggaaggactg	cctgtcctgg	169976697
gaattgccct	aatcatcttc	ctaaatattg	ccgcagccag	gaggaaagcc	169976747
tgattccctg	cagatggggc	cattgacagg	atgctactgg	tccgggttgg	169976797
gagaaaagga	atgctgtaaa	cacagtcagc	ccattcggca	ggcagtggaa	169976847
gctgtctgag	gcttcagggc	cccctcctca	ctaggggcta	taattcatgc	169976897
agtttcttat	ctgccagatg	gccaggagga	cacatgcatt	ccagtgggtg	169976947
catcttctaa	gtgttggcag	cttgccagtg	atctcaactt	cattttcatc	169976997
attgcctfff	gagactffff	gttcttaaat	accccaacca	accatgaaat	169977047
tttaatacca	gaaatatatt	ctctgtttac	atactttatg	caaaatctgt	169977097
tttttaaacg	taaaaaagggg	attttttcac	acgtgcattc	ccacaagaac	169977147
caattctctc	ccccgttgag	aatgcctgtt	gtacactaaa	ccttcagata	169977197
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accaggaaac	aaatgctctt	tgcattgttt	tgtctcttcc	cagaagcctc	169977297
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gcttcacaga	tggttaaagc	aaaacagaac	atggggccggg	tgcagtgact	169977497
cactcctgtt	gtctcagcac	tttgggaggc	caaggcgggt	gaatcacctg	169977547
aggtcaggag	ttcaaggcca	acctggccaa	atggcgaaac	cccatcttta	169977597
ctaaaaatac	aaaaaatagc	tgggcgttgt	ggtaggcgcc	tgtaatocca	169977647
gctactcggg	aggctgaggc	aggagaatca	cttgaacccg	ggaggtggag	169977697
tttgcagtgc	gccaagatcg	cgccactgca	ctccagcctg	ggcgacagag	169977747
tgggattcca	tctcaaaaat	caaaaaacaa	aaaaaggaaa	aaacagaaca	169977797
tgaagccac	tttcccacag	cctgggcacg	tagctactgt	ggtgaatcac	169977847
ctttcctggc	agagcacact	caggaaccgt	cagctccaaa	agcaccaaac	169977897
agtttcatta	agaccgtggc	tccttcgcag	aagcacacgg	aacgcagact	169977947
gacaagcctg	tgataacatt	ttaatggcct	gagttcagtt	cccaataaaa	169977997
tacttaagtt	tctgcaatca	tggagctggc	attttctatta	atactcctga	169978047
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cattcagacc	tcaccactca	tacactggga	cctggaacta	cttaaattgc	169978297
ctcagtttct	ttatgtgtca	aatggcgttt	gacacataaa	gcactaatac	169978347
taatagtact	tacataataa	ggttgttgta	aggattaatt	gagttgggtac	169978397
aagtaatgtc	ctggcacgca	tctggcacat	agtgagtgtc	tcctataata	169978447
aacagtagct	gggtttgttg	ttgttttact	attatffffc	ctccagaaag	169978497
gcgagagtgt	catcagcctt	ggaagaggca	ggactgagat	gtttgggaac	169978547
aagaccactt	tcacaggggg	cagccttttg	agaaatgtca	tgtctacttg	169978597
atagggcttt	aaatatggag	tagtgggaat	ctgcacattt	ggattcaaata	169978647
cctggctttt	ccaatggctg	atgatggaac	ccttataggc	tcaaatacact	169978697

FIG. 1.101

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cacttctctg	agcctcccca	aaaattgaga	ataacagttt	ttattccata	169978747
gggtagtttt	gagaattggt	aagatgatca	taaatgtaga	agggcctggt	169978797
actcataact	gttttcttca	tttattttatt	tagtcaacaa	tgttttctga	169978847
gcacctaccc	tgggccaggc	acactgaggt	gggccttggg	attcatcagg	169978897
gatcaaaggg	aaaaggcatc	ccatctccgt	ggagcttcac	atcatcgtag	169978947
ttaagggtgga	taatgactgt	ctcgacagat	aggacagtgg	ccaggacaca	169978997
ggccttcagt	ctggagcatg	cttctcattt	tgaaataatt	tcttggtcag	169979047
agtcagggtt	gaaggaaggc	cttgcagggg	ctgggtaagg	atggcggtcat	169979097
ctctgcgttc	acgtctgtgt	gctcaccatg	agagcccacc	tctctctggc	169979147
ccaagtttcc	ttctgtaatg	tgaaagaggt	ggggttccat	gctctcctct	169979197
tcagcatcct	ccttagatac	tcaatctggc	actcatcagt	ttcggaccct	169979247
ccatgctgcc	ccaaaggaag	ccacactgca	ccttcatcca	gtttcttaaa	169979297
cctgcatgtt	ctctcttgcc	tctagacctt	cgcccaggct	attccatctg	169979347
cctggaacat	gcttccatac	acctgccttc	acttggtctaa	ctcctacttc	169979397
tgcttctgtc	cactgcttgg	attgaatgtc	ctctggaatt	cagccttcct	169979447
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attttccctg	ttcatcacco	cagttatgac	actgagttgt	aactgggatt	169979547
tctaactctgt	cgctccacc	aagcagcaca	ctctttctgg	ccagggtcca	169979597
tgtcttattt	gtcttggtat	ctctagggcc	cagaatctgg	tacctagtga	169979647
atgtgtaaca	aatattttct	ctgagctaaa	ataggaacac	agggctccctg	169979697
caatgaagac	cccagggtctg	gaggggaaga	caaggtagca	ttacaagata	169979747
acaggccttc	cctgcaaagc	gtcagcactc	agactggggc	attgtggaca	169979797
agaaggggtg	agaggagaga	aggcatgaag	gcatcccaga	tagggacaca	169979847
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aggttaagat	gggtagtgga	aagctggacc	actgtcaggt	tttgaccctt	169979947
ccagacaatg	caccgtgac	ttctggcttc	catatgtccc	tggctgctgc	169979997
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agccaccagc	cttacaaatt	acagcagaca	gaggggggtcc	aggcccttct	169980097
agagatagt	ttcacagcac	tttcccaaag	ctgggtctgc	tcaattccct	169980147
aaaagatctc	ctgcaatggg	gcctccaggg	tcctaaaagc	accatctgct	169980197
cttaaagagt	ctcactgctc	attagcatat	caaaggctct	gaaatgtcct	169980247
gcaggaaaaa	actctgggct	aacttttgta	gccctgttcc	ccaaactaaa	169980297
ttgaatgaag	gattcttttt	ttatgaccca	cctacagttc	tgagagatc	169980347
ctccagggaa	tgagatcta	acctattctc	tgtgcagtga	atggcagaga	169980397
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tgagagagta	aataagatgc	aggagagaat	tacaaccgga	gatataaaac	169980497
agttgtctta	cagggaatag	tctgtttgct	caggaggagg	gttttcagaa	169980547
tacaaagtac	catttcttct	ccacgacatc	cccaggggag	aaaggaaagt	169980597
gaaagaagcc	ctccaaccga	ccactggaga	tgggagcatt	tctgctgggt	169980647
tcattttacat	aagtgtcctt	ggcaatttgt	cccaatttgt	ctcattataa	169980697
atgatgtaaa	catccggggc	taatcacaga	caaaatggga	tggttttaaa	169980747
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tccacataga	gocctagcaag	aatgcatcat	cttctctata	tctcttataa	169980947
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aaggaaagaa	gaaaagaaag	gaaagaagga	aggaagggaag	ggaggggagg	169981047
aggaaaggag	gaaggaagg	agggaggagg	ggaggaaagg	agggaggagg	169981097
gagggaggga	gggaggggag	gagctaactg	acattttccc	ctttgccatc	169981147
tgattggcat	gaagggcaat	gtaactgagg	agtctgggga	ccaaagtga	169981197
tcctagtaat	gtcactcact	taatatgtgt	gatttttttag	accaatcaca	169981247
tcatttgccc	aagcctcagt	ttcctagtct	gtcaaatggg	aatgatgatt	169981297

FIG. 1.102

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tgacatctgg	tgtgtctctc	actactggtg	agacattata	taatgagagc	169981347
atagcccttt	ataaagacag	ggtttctgtc	ctctttctta	cttcattctt	169981397
tccttctctt	ctttccttct	aatagaaggt	atagagaaga	cagcacattc	169981447
ctactgagct	ctatatggag	agctgcagtc	atgggggaca	ctgtctagat	169981497
ctggggaccc	tcccaagctc	tcagagcttt	ggaaggaagg	tccttgcagg	169981547
gaaactgtgt	gtgtttcttc	aacagtgtat	cctcagtgcc	tagcacatgg	169981597
taagtgttcc	ataaacagct	gttgaagaga	cggatggata	actgaatgaa	169981647
tggatgcttc	catgggcaat	gacacactaa	tctgaaaagc	cctgtatcaa	169981697
tgaaagaatc	acttaatagt	ttaacttttc	cctcatcctt	cagaacacag	169981747
atggcatgcc	atcttccctt	caaactctct	cccagtgccc	cacacagaag	169981797
aggcacactt	ggacactggg	gtctgatgga	cccaagttca	cagcctgtct	169981847
ctgggtcatca	ggtatcatga	ccttgggcaa	gaagcttaac	tctctgagcc	169981897
tcagtttccc	cttctgtccc	ccagggaaaa	tgagtccctgc	ccctcctaag	169981947
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ttcaggtagg	aggcaggtaa	ggaggtctgc	tagattggaa	tgagtttctg	169982047
gaaggcccca	aggagctcaa	aatcagacct	ggggtgaagg	tgtcttgacc	169982097
aaaatgagac	ccatcaaaga	agcctggatg	aagggtgcca	cagcatccat	169982147
cagtgcctaaa	aacagaaaaca	cttttagcca	ggatacaagg	aacatttttaa	169982197
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ttcttggccc	ataattagtt	gttatgggac	cttaataaac	ttcttgccct	169982297
cttggtacct	ttgccaaaca	atctgatgag	gagaatattg	agtcatggtg	169982347
ccagggaaaa	ttagcatatt	ctgcaaattc	ctggcactgt	taacactgga	169982397
ttctgtccac	ctttagaaat	cctcagatca	ctatgtcagc	atcccccaat	169982447
cacagctctc	caacttcaag	gaggggtgag	gggtctgaag	aaggagagag	169982497
aggcaacaga	gccagaaaacc	cttcagaaga	tgccaagagc	aaggtttgga	169982547
cccatagtc	accacttact	aacttcaaga	gtgttatgag	ctacaaactt	169982597
ctcagtcctc	gttgactcat	ctcaaaaatg	gaagtaaaat	tattttaccat	169982647
gcaatatggt	gtcaaaaatgc	attgggttta	gttcatagca	ggtgctcaaa	169982697
gaatatcagt	tccacttccc	ttgtccctag	agagccttgt	agtggatggt	169982747
gatgtgtctt	ccaacacatg	caccaacctt	tccctgtcct	gtagcagttg	169982797
agatggaatc	atcccactcc	cagctccagg	aataggctct	gatgggcttg	169982847
aaccacagcag	cttaattcca	ttggttctct	aggccttcat	cattagtaca	169982897
ggaaaggcac	ttgacctaaa	ttagtctgat	aagattttaag	ctcagaaaatc	169982947
tggtttggtg	gatggagaaa	gagatgcttt	ctttctctct	ggaaggagtt	169982997
tattgcaaaa	gtaagggtctg	gggctgctac	agccattgtg	ctaccatgag	169983047
ggaactagcc	atgataacaa	aacttgctctg	gggaggggct	acgcatacaca	169983097
gaaaatgatg	ccaaagtcc	gctcaaaactg	tgcttgatgc	ctgcctgatc	169983147
tatggacttc	ttagtcccat	gtaatggatt	ctctctatct	ttaaagccgt	169983197
atcaggttga	atttttggag	aaataaaaaca	aaaagcatct	tgactaatct	169983247
aaaaaatctt	ctttgggtat	tcaaccctcc	taaactcacc	cccaaatcca	169983297
ctggggagcat	gtcaagattt	ttgtgagccg	atttaggaga	tgcaaatcca	169983347
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agattccaag	acattaggca	tagaaacagt	ctggcctaga	ccctgtaggc	169983797
cagtaggcat	ttgatcaatg	gcagctgtgg	ttgagatttt	tatcatcatt	169983847
atggctgccc	ttcctgcttt	ccagggctag	tgtagatcta	agattatagg	169983897

FIG. 1.103

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ggctgcaacg	ttcctcagtg	gagcagatgc	agcaaggtag	taagagaggg	169983947
cattctcact	tgtccccaca	gagtgtgggtg	tgggggagat	ctgtgagcac	169983997
cccagcagcc	atgaggggtca	gcacttgaat	ctctgcaggt	cagtcatact	169984047
cctcttttatt	atTTTTtattt	ttattttatgt	attgatttat	tgctctgtca	169984097
cccaggtctgg	agtgcactgg	caccatcata	gctcactgca	gccttaaact	169984147
cctgggtctca	agtgactccc	acttcagcct	cccaagtagc	tagagccaca	169984197
ggcacatgcc	accacgccta	gctaattttt	caattttttg	tagagacagg	169984247
gtctcactgt	gttgcccagg	ctggtttcaa	attcctaggg	ttgagtgate	169984297
ctcccgcctt	ggactcccaa	agtgtctggga	ttacaactgt	gagccactgc	169984347
acctggcctt	attcccttct	ttttatcagt	tttcaaagcc	atcagtatgc	169984397
agagcactag	gcccagaaat	gagaggagaa	gagagatgga	acgacgaaga	169984447
ccaaaacctc	tgtcctcaag	ctgctcataa	gccagtatag	agacgtgtgg	169984497
agtctgtctg	cctgagttcc	agtcccagtt	ccccttgcaa	gcagccgtgt	169984547
gacttgcagc	aagtcataga	atccctttga	gcctcacttt	ccttgtctag	169984597
aaaacaacaa	aaactggaaat	aatactgctt	cccttccagt	ttgtcaagga	169984647
tgaaggtgct	ttgcacggtc	cctggagcaa	aatgtgttct	caatcaagat	169984697
tccgtctgtg	gtgggtggag	ccgcgtcctt	cccaaattca	tattcactca	169984747
gaaccttcaa	atgtgacctt	tttcagaaat	agcatctttg	caagtttaat	169984797
tcagttatgg	gtctcaagat	gaaatcatct	tggatttggg	gtctatccga	169984847
aatccagtga	ctgatgtcct	tataaaaaga	agggatacag	gccggggcca	169984897
gtagctcacg	cctgtaatcc	cagcactttg	ggaggctgag	gcaggcagat	169984947
cacttgaggt	taggagttca	agaccagcct	ggccaacatg	gtgaaacccc	169984997
gtctctacta	aaaatacaaa	aattagctgg	gtgtgggtgg	gagcaccat	169985047
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gacaagcgtg	agactctgtc	tcaaaaaaaa	aaaaaaaaag	agtggataca	169985197
gagaggcagt	gaagaaggct	gtgtgcaaag	acaggcagag	gttagtgagg	169985247
tgcagcgcga	ggctaaggag	tgtctggggc	caccagaagc	cagggaagcc	169985297
taggaagggg	tttcttagag	ccttttgagg	gagcacagcc	ctgctgacac	169985347
cctgacttca	gactcccagc	ctccagagct	gggaagggat	aagtagctgt	169985397
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gttcagtggg	agacaatttt	tccacggaca	gggtgtgtgg	ggtgggagat	169985497
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gcaatagggt	tcatgtcctt	atgagaacct	aatgocggcg	ctgatctgac	169985647
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actcaggaaa	aggttctcat	ttggacactg	ggaggtctta	cattgggggg	169986397
cctgagcctc	cagcccttcc	aaatctattc	tcagcaggag	ctcagccaca	169986447
cctgtgtccc	agaactgagg	ccaggcccag	ccttcactcc	acgcccagcc	169986497

FIG. 1.104

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agccccaagg	aaccgactcc	ctgaggctct	atgctccctg	cctccagtgg	169986547
ccccgtgtct	gggaaatagt	ggccctggcc	tgatgccctg	acctgggcaa	169986597
tccatccccct	ggtcctctca	gctcccgggc	ccagggttttc	tgggctactt	169986647
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ttgactgacg	aaggggtaca	aacaacaaac	accttccttt	ctccaaactc	169986997
tatctttaac	tgtattctct	cgttttcctt	cctctccatt	ttacaatcat	169987047
tttacaacat	ctctggctat	tctcctatat	ttctgatcac	ttcgggtctc	169987097
atcacaataa	taatttcagt	tttcaagcat	tggaaagtcc	catccaatta	169987147
aatgtcaat	ctcacacgca	gtttaaacgt	ttcgccctgcc	cgtgagctca	169987197
gacctgtctt	ggtgcctcag	ttcttggtgtg	gaggggagga	gaggagaggg	169987247
gaggggagga	gaggaaagga	gaccggggag	gtgggggggg	agaggggagg	169987297
ggaggagagg	ggaggggagt	gggggagaa	gggagaaaag	cgcagctggc	169987347
ttcctcactc	tcctttcctt	cctcaccatc	cttaccctgg	cccagggcag	169987397
gaggaggatt	ggcagagtag	aggcagggtc	ttctgtctta	gctgggcctg	169987447
ttggtgactt	tctgttgggc	aacatgggct	gactggaatg	ttctccagca	169987497
tggcacatgg	tcacccagat	gcaggctctt	ccctggggca	ctatagcaga	169987547
gagggtcttc	ttccagtcta	ttgcagatgg	atgccctcgt	gagctgagtt	169987597
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tctggtcctc	tgggtcccagc	agcagccctc	tgggtactga	ggggagggca	169987697
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cgcaggaaag	tcacaaaacc	ttgtgctccc	acagggcaca	cgtgtgcaca	169987797
cgtgtgcagc	taccttctct	ctagttggta	cctgaggctg	cctcctggat	169987847
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ggaccocctg	ctgcggcgta	agctaccagc	atccccttct	catgggcacc	169987997
ctcatctccg	gctccccatc	gctgggctgt	gacctgcggg	ggcgccctc	169988047
tatggaaggg	aaggagaaaa	attcacagtg	ctatctactc	ctctgaatgc	169988097
actcccacca	atttccttgg	aaatttctag	ctttcactga	catatctggg	169988147
atggggcggt	ggtcacaaaa	tcaatcccac	tttcctcctg	ctagtcttac	169988197
aagcacccaa	cagctctatt	cagaatacag	ggctgccag	ctacttccca	169988247
ttcattatcc	ccagggttgca	agcttttagtc	aaaaccaga	ggcagcaggg	169988297
tgtctggttc	cacctgctgt	taggatgatt	tcaggagtgc	aaagtgttag	169988347
aaacgcggta	aaacatgatg	cttagagatt	aagtgggatg	gggactgggc	169988397
agatgatgct	gctttggacc	cagcgagtga	ggtgagactg	cgacaagaca	169988447
gagccactga	gcagtgcact	gggggatggg	cattgcaggc	aaggcagaac	169988497
cccaagtggg	aacaacctca	ctgggcttag	caaaactaaa	gaggcccaa	169988547
gtatactgag	cgatgagggtg	agtggcgtgg	gataagggtg	gagaggaggc	169988597
tggaaaccaga	ccctgcaggg	ccttgccagg	gatgggaagg	agtttggaag	169988647
gtgctggaag	gtttgaagca	gaggagggat	atgatcatgc	ctgtagctgc	169988697
tatgtagaac	aactgtatgc	atgccaggcc	tgtgccacgc	atgctcta	169988747
cattactggc	tttaaccctt	gcactaacgt	tgtcatgcag	gtaggagcat	169988797
ctgcacccag	caaattgaaa	ctgaagctca	ggaatattca	gtcacttgtc	169988847
caaggctccc	cagctgttag	gtgctaaggc	tggattcaat	ccaggacttg	169988897
cagactccag	tatcttggct	tttctaacga	gagtgtgcta	gctttcta	169988947
gggggtgggg	aaggcagctc	gccccctcc	catggcaccg	tgagcaggtg	169988997
tcactgctcc	agccagtacg	cctggacacc	gactaggaag	gagtatgtgc	169989047
tactaggagg	gatggtctgg	gctgactctt	tgaagttgac	aaggagttgc	169989097

FIG. 1.105

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ataatcccag	ctaataatta	tgctggacca	ggggcagaga	cattactcca	169989147
aggggtgacca	ggtgtggaga	agaggctgct	gactccgggg	ccccaggacc	169989197
tggcccccag	gtctcattgc	ccgagtgtctg	ccccagaagg	agtagaagct	169989247
ggagctgtcc	gggccacagc	cgaggctggg	tgaatgctgc	agtgaggctg	169989297
ccgcacaagt	tgcgtgttgt	gacatttgtc	ttctggaggg	gattgggatg	169989347
ggctacttca	gcatttataaa	accctacta	ggtctgagaa	atcccctcag	169989397
cttatgagcc	tgggtgggca	gcaggccttc	tcaagaagcc	cagaaggcca	169989447
gatgctcact	tcccaggctc	tcttgaggct	gagctgagag	caggcacctg	169989497
aggcctggca	agtgtgacag	ctggtgacac	agacagacag	ggacagggag	169989547
atgggactgt	gcctgcagcg	gtagccctgg	ccggtgttca	gtggggccag	169989597
catccgtgtc	tttccctggg	gccagtggg	gccgtggctc	tgacgatgca	169989647
tccctccccc	acgttttttc	tcttctgtc	ttggactttg	cagggagcac	169989697
tctgcttttg	ggaacaggag	ctgggtctct	ggccattctc	cgcagccctc	169989747
caccattcac	tcagtggctc	tcaaaaaata	gaacctgggg	caaagctgtt	169989797
cttggcccca	aacaacatga	ggaaaaataa	ataaataatg	tacctggtaa	169989847
ctgagagagt	tccctctgca	tcttgggctc	tttcaatgag	atgtcctctg	169989897
cctgcagcaa	gccccaaagg	cttccctcac	caggaccage	accctgggtt	169989947
gectgacccc	acacctgcca	atgccggggc	aagaatgtcc	caggctgccc	169989997
tggttcccag	agctgatgct	tcccacagtg	cccagctgtg	ctggcatgga	169990047
gctaaggaca	gggccagtcc	caagaaaaca	acaaggctcc	agggccaccg	169990097
gccactgctc	aggaccctgg	ctgacccccc	agatgcggag	tgccctgagat	169990147
ggctcatggg	tgacccccag	gcatctggca	aaggtcacaa	tggctgtttg	169990197
gcttgaagac	agcccttgca	agatctgttt	tgagccaacc	tgtggcattt	169990247
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tgggagtccc	catctacccc	caccctctca	gcccaccagg	gcccagactg	169990347
gggaactgct	cctgcttcga	gggacagggc	tgaagaggag	aggggcttgg	169990397
ggctccccc	gatcccaaag	ctccagggac	cccaaagaaa	cgtatcagca	169990447
gcatgagaat	atcgggtgac	ctctctctct	agtaaatgtc	aaaactttta	169990497
acaaaaatgc	cttcatcccc	cagcgccagg	cctgagctaa	tctcataggt	169990547
gtcaggactg	ggagcctgga	ccctctctcc	ttctgctcct	gctttgcaga	169990597
gaagtgagtg	gggaattccc	gcctctggga	attcagagac	gaagtgacag	169990647
agacagcatt	ggaagataag	aatgcagcca	aagaggctct	cagggtagcg	169990697
tgtggcctgg	gcgctgagac	tattgggctc	agcaacttct	caagcagtct	169990747
attaaccaca	gocggtagcc	agcttttccc	cgcccttctc	ccaggcacac	169990797
acagccacct	ccatcaccaa	aggtcaggcg	aaccacctcc	catggctacc	169990847
cccagcctga	cttgctttat	agaaatcatg	gcatctcatc	ctcacaacag	169990897
cccacactca	cagtgaatct	tggccattat	gacaactggg	gacactgagg	169990947
ctcggagtgg	tggaaattct	cagaatcaca	taacaataag	tgttaaagtc	169990997
agaatttcaa	cttcatctct	ctaactccaa	agggcgtgtg	tgtgtgtgtg	169991047
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gctaggaaca	ctggttttgg	gaaaaaatgt	aataaaatat	gtgatccaga	169991147
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gttgtcctgc	gaagacaccc	gtcaatacat	gaatattgac	acacaacgct	169991297
gcagtgcacg	gccttctggc	aggggagctg	ctgactcga	gggcagctca	169991347
aggtaatttt	gcagggttca	tgtttggagt	ttctgagcaa	gtgttgacg	169991397
tttggccccc	agcccccctga	ggggagctct	ggccgtgcat	gagggtcaga	169991447
cagaaaatct	cctttcctcc	atccaggcct	gcagtctgca	gcactgaggt	169991497
cagcgtggc	cacaagccca	ccctgtgcct	cgtcagcccc	actgagcctc	169991547
tccatctatc	atgccacagg	ctgacctga	aatgcaaaat	cattctgtcc	169991597
tccgcctc	cactcccacc	tcgcacatct	atggatttgc	tgttcagaaa	169991647
acatctgttc	cctccttcgc	ccctgacata	cgcacgcac	tcacgtctagc	169991697

FIG. 1.106

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ccagctgcct	aagctcacca	ctctgggaga	cagactctca	gtcctcatca	169991747
gacagagatg	tagggggctg	taagggacgg	ggtgcaggta	gggcctgagg	169991797
attccgacaa	ggtgagccat	gggcaggggc	attgttcattg	cagggacctc	169991847
ctggccaagg	tcctacgtca	aggttagaag	gaaagagtaa	atgatcggat	169991897
aggctaagac	agcaactcag	caggccaagg	gactcctccc	ccaggacctg	169991947
ctccaccctt	agaggggtcc	cggacagcca	agccctgatg	gagttgggtca	169991997
gcaaccaacc	agccctgggg	ccaaggcctg	cagaagcaga	gaggaggggt	169992047
ctcaggcagg	ccagaggtgc	tagctgggat	gcctgggtcc	cccacccccc	169992097
cccagcacac	tgtcctttct	ccaggtgctc	agttagattg	agctgggtcc	169992147
catcttgggc	ctttgctggt	ccctccctag	aaagtctgcc	ccctccccct	169992197
gcagggtggc	atcagcattc	aggcctggcc	ctgacgccct	cctctctggg	169992247
ccaccttcac	ctccacaacc	ccggcaccag	cacccatccc	caccacatcc	169992297
ccagcacgca	gcattctagta	agggcaccaa	atgcatgccc	agacatatga	169992347
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tctctagaaa	caatgtgaat	tgtgcagaag	gaaattaacc	ctactccatc	169992447
cagcccatcc	taaggcaggg	acttggaact	gttcctcttg	atggggctgg	169992497
ggctgaggcg	ggcaaggcag	gcaagtgtctg	aacagttggc	aacattgccc	169992547
atcccgtctc	cctgcaccag	gctgggcctg	gggtgagggg	gtgggggccc	169992597
gggtagctgg	gctcctccag	caaagagcag	gactgagtcc	ctggtgacta	169992647
ttaggtaaaa	ggtccctgac	aattttgagg	ggccagatgc	caactcgagg	169992697
gatacagaga	agatctaggc	acagtctttc	cccaccatgt	cagacaaaaa	169992747
ggttagatac	aggacctgat	atgttataaa	actcaatcaa	tatttactta	169992797
gtgaataaat	ggacggatgg	atggatggat	gcattaggca	gccaagtggg	169992847
cagcacccgat	gacttaattgt	actgagtgtc	ccgactccag	caacatgcat	169992897
tcattgttcc	tactgtgtgc	cagtgaacaa	gagcaatgaa	ctcaatgact	169992947
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atltgggctg	ggacgtacag	atgagtaggg	ggtcgagtgt	gtcgttatgt	169993047
cgctggagcc	cagaggcgctc	catcaggact	tgggggaggg	cagatgaaag	169993097
ggccttactg	cctaacttgg	agccactgta	tgtttcaaaa	caaaggagag	169993147
agaggatcct	gggaaagaga	aagggtactc	taggcagagg	atgtgaatgg	169993197
gcacagcaca	ggtgagaaca	tcaagaccag	gggtcaggga	atctactggt	169993247
aaacaattgt	accccaaggg	agcaatcaca	gcctctccat	ccacaggga	169993297
atgcctgggtg	gggaggaatg	ggaggaaaga	aacagattgc	atgactgtgt	169993347
cttgaaggtc	taattccaga	gtacagcatc	acccctatct	tccaggtcca	169993397
gaaactgagg	ctcagaggga	gactttctga	tgagtgcagc	gtgcagataa	169993447
gagcatctcc	aaagctacct	ccttccccag	tcacaccagg	gcataagcaa	169993497
ctgataacag	ctgtcagcac	gggacagtgg	agggaaact	aggttaggaa	169993547
taagggtacg	aggcttgagt	acagattgtc	aatgactcag	tgtgtgaact	169993597
tggtcagggtg	actccaacca	gatgacttcc	ttctctgagc	ttctgttccc	169993647
tcctctatga	atggggacaa	tcactcagct	tcacaaaaca	atggctgcga	169993697
aattgcctgg	tacaagagag	agaacttcca	gtgtgtaggg	gctgttgtcc	169993747
taactgccc	gccccctaga	taggtagtta	tgtcatctgt	gaaatgggtg	169993797
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gtgtgagagc	ccaagcacca	tgcctggcac	atagtaggtg	ctcaggaaag	169993897
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attctccatt	tcaaacgctt	tttgaaagca	gctccagacc	caagcaggag	169994047
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cacacagaat	tgtctcctgc	acagaaggga	agctgtcttc	cacagcacag	169994147
agccaccagg	ccccagactg	ctggcttatg	tatttgtcat	tgctcatcat	169994197
gaatggatgc	caggaaagtc	tctttgtgat	gggggcacaa	ccctcaaat	169994247
ctcctcccct	ccagatgcc	tccactggag	ctgagactcc	caggtcccct	169994297

FIG. 1.107

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agggcttctc	tcccaggggc	ctctgggctc	cccaaggcca	cgtgctgccc	169994347
ccactagaga	cctgggcccag	tcctgaccag	gggaaagagt	agcgccgaca	169994397
acagccccag	atgggtatgtg	cactgggcaca	tactggcagc	tgcccttcag	169994447
acagcaagcc	ataggtccaa	atccccgccc	ttcacaggga	cattcccaac	169994497
tggtcagggg	tggaacctccc	cttcccggct	gtctttgggtg	tccaggacga	169994547
tttgccacag	acaggggggag	ctaaaggggc	ccacgcttga	ggccgctcag	169994597
ctctgagtc	tcgccggcca	cagaggacct	tcgtgcctgt	cctctgtcct	169994647
cctgcccagt	ccccaggcca	ggctcagctg	gagttgggga	gcagaaaaac	169994697
acgcatctga	atcaaggctc	tcggagcctt	tgcttctgcc	tccaagaggc	169994747
gagggaaaat	gaatacccag	gcgagcgagc	aagagagacc	ctcagaaaaac	169994797
cccagatgcc	cctggaatca	agccctgtcc	caccaacgcc	acgtggattg	169994847
acaggctatt	agtcttcctg	taattaggat	tctcgctca	aatcttgtat	169994897
ctttttcccc	cagaagattc	tcctccagcc	ttcaccactg	ccccctggcg	169994947
cttccctgca	aggcttttga	agaatcctt	gcagagaagc	agcctccttt	169994997
ggcaggggct	gcagagcact	ctgcctccct	aggccagggc	gaaccaacag	169995047
aggcgggaga	tgaggaggag	cagcgcggt	ctgctgcgtg	gccctgggca	169995097
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gggcggtaaa	tgaaagagac	cagcacaac	cagtgtcagc	tccttctctc	169995197
gattcctaaa	atgtgatgcc	caaagatggg	ccagcctcct	gctgtgcctt	169995247
ctctgggggg	acatttaata	agtggaagag	ccctggctct	gagtcaggct	169995297
agaatcccag	ttctgcactt	aaccagctgt	gtgacctcag	gcaagcaacc	169995347
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tgtgctgagg	gttccatggg	acaaccatgt	aaaagcacc	agcacgcacc	169995447
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ggcttgagca	cgggttgaac	ctggaagagg	ccatttccct	cccttctccc	169995547
cgaggaataa	ttgtgaattc	ctgggtctca	gaggaaacat	ccgctttggg	169995597
ggtcagaaa	gacatcctcc	tttgagcagg	gggagagcag	agggaagggg	169995647
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ggagcaaatt	ttaaaaatta	agtgactgag	gtagtccagg	ggcctcactg	169995947
agaagtggct	tggagtaaga	cctgaagtgt	gggactggat	atgcagatgt	169995997
ctgggaggag	agcttttcag	gaagaagaat	cagccagtgc	agaggcctat	169996047
ggcagaccca	agcaggaggc	aaaagaaaac	cagaggcttt	ccaggatgga	169996097
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gaaatatcgg	gaacttatgt	tcggacttgt	taagtttgag	atggctggga	169996797
gatatactaag	tggagagggc	aaggaataaa	atgcttccta	aactccagca	169996847
tccattcagt	cccctggaga	gcttggttaa	ccggatggat	gggtgccacg	169996897

FIG. 1.108

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ccccccctg	cacccttgag	ttgcaatagg	cccaaaatga	ttcaataggc	169996947
ccaacatggg	gcccaagggt	ctacatttcc	aacagcttcc	caagtgatgc	169996997
caatgctgcc	agactgagaa	ccacacttcg	agtagcacca	aagtaggcaa	169997047
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gggagtgtgt	gtgtgtaaag	aggggaagaaa	agagcattga	gtcccagagcc	169997197
ccaggctctt	caatggtaag	agggttggcag	attaggaagg	accagcaaag	169997247
actgggatgg	gaaaccactg	aagcaagagg	aaggccaggc	agatgtgtcc	169997297
tgaaagccaa	aaagagaaaag	gtcatcatta	atatgatata	ttttgcaatt	169997347
tgtttatatg	taagaggaga	ttaatagctc	atagcattcc	caggcattgc	169997397
tgtaggaat	tgcagctcca	ggctggcaac	ccttaaatca	caaactagat	169997447
tgtcaagagg	actgcctgga	attccagctc	tgtaagtaat	atgctgtgtg	169997497
gcctcagcca	ggtcacttca	cctctctggg	cttctcttgc	ttccatatat	169997547
aaatgtaata	agaaaatcct	ttattttatta	tttattttatt	tattttttgag	169997597
acagagactc	gctttgtcac	ccaggctgga	gggcagtggg	gcgatctcca	169997647
ctcaccgcaa	tctccgcctt	ccgggctaag	gcaattcttg	tgcccaacc	169997697
tcctgactag	ctgaaattac	aggcacccac	caccacaccc	agctaatttt	169997747
tgtattttta	gtagagacgg	ggtttcatct	tggtggccag	gcttgtctca	169997797
aacacctgac	ctcaagtgat	ctgcctgcct	cggcctccca	aagtgttgag	169997847
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tgttctaaga	gtctctttca	gttctgaatc	tctttgttat	cttacctgtt	169997947
acccctcag	agatgccttc	cctcactccc	ctgtccaagg	tagctctcca	169997997
cccaagtcag	cagtcatcac	agaaccatca	caacctgaag	ccctgtgcat	169998047
gttgctgttt	atttctgttt	tacatcacaa	cctgaagccc	tgtgcatgta	169998097
gctgtatact	aacctatagag	ttagtatagc	ttagttaaag	tttcatttat	169998147
tgctaaagggt	ttatcactgc	tgtctctatc	agcctccctg	cactgtaagg	169998197
gacaaggggg	caggctccagt	ttctgtcttg	tttcagggtt	tgtctccagc	169998247
caagataagt	atctttgcaa	ggctctgttt	ttattctgaa	aggaaattag	169998297
gagctattgg	agggtatgga	gtggaagggg	acagtcttct	gccttggtatg	169998347
tataaaagggt	atgctggggc	acgctgatgg	gctagaccat	ggcaggcaga	169998397
gaaaacaggc	aggaggccag	gcaggggctg	ccagtgccca	gacacaggcc	169998447
gggagggtgca	ggtggcagtg	gcaggcagtg	gccaggccct	gggtatatatt	169998497
tgaagggtcaa	gccaacagga	cttgccagtg	ggctgggtat	gggcatgaga	169998547
caggcaagtt	ctcccagatg	tgactccgat	gtgacatttt	ggagactccc	169998597
tcaacaccca	cctggggaag	acagaccagt	tgggaggaaa	tatctggagt	169998647
ctcattttat	taattctgag	agtttgttgt	attagacagt	gaagcggaaa	169998697
tgtcaggaag	tcagctggaa	ataggagtct	ggagtgtggg	ggaaagccta	169998747
gccagagaca	ggaattgtgg	cgtcattggc	gtagagacag	cgttttaaagc	169998797
tgtgacgcta	gatgggttca	ccagggggaat	gagagtcgaa	agagaagagc	169998847
agagcagagc	tgagccctga	gggggggcaga	aaggcacaca	gggacagtgg	169998897
aggcaggagg	cagaaggcag	agggttggcg	gccaacagct	ctgaagggtca	169998947
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gaggcactat	cccaggcctg	ccttctcatg	ccagcagcag	tgatctatcc	169999047
tcaaggagaa	tattgattga	gcacctactg	catgcagaga	cctcatcaat	169999097
ggctcaatca	atatgacacg	gccacgcttc	ctgatccgag	ccctctgagc	169999147
aggatatttt	catcctggac	ttatccctgt	ttctcaggag	agggatggac	169999197
ccaagagaca	aatagttccc	ccaagatcgc	acagcaagcc	agtgtaaaac	169999247
aagcatagaa	accagctttt	aggggggctca	agggtggggg	cagaaaatga	169999297
ggtgagagca	agcatttact	gagcacctcc	tgtaaataatc	tcctacatac	169999347
gaagtgtctc	acccacatta	ctgaccaccc	aataaaggca	ggtcctgtaa	169999397
ttcccaattt	gcagatggat	aagcagaggc	ttaggggtgt	gaaacaacct	169999447
cctcaagggtc	atggcttcta	agtgggtggag	ccaggcctgc	aaaccaggct	169999497

FIG. 1.109

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gtctgaatcc	aaaatccacc	tccaagtcca	cagtgggttg	gccccacccc	169999547
caaccatcc	ccatcaccaa	caggacggtg	gtcagagtcc	actgaatgaa	169999597
agcatgcgtg	cattcaaaat	agacagccaa	tcagcagcct	tccatcagaa	169999647
atgtcatctt	tatgacaaca	gcatcgattc	caggcgtacc	ctgcatatgt	169999697
gaaccaaggg	ggatgggtgga	ttgtcctttc	caagcacttc	ccagccccct	169999747
agagtccac	aggcccagaa	ccacggccct	tgacaccctc	taccaccccc	169999797
tgtccccct	tctcctcaga	ccccgagtgt	ctggccaggc	tttctcactg	169999847
ggaagtggcc	actccatcca	aatgaccacc	gcacccctcc	tcaccagctt	169999897
cctgtctct	gccctggccc	ccactctttg	agtccattct	tcaaccagca	169999947
gacaaagggg	tgctgtacac	gcctctgcac	agaacccctc	caatgccttc	169999997
tgtctcaact	cagagcaaaag	ggcagcagct	agcacactcc	aaacactccc	170000047
acccacacct	cagctcctcc	ctctgtccct	ctgctctatt	ccctcagatc	170000097
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ttgtccagge	tgctccact	gcctggagca	ctcttcctgc	agacaccac	170000197
gaggctcatt	tctctttagt	gaggtcttcc	tgccgcctc	ttccagataa	170000247
caactctcct	ctccttccct	gccctcctgc	tctcctgtt	cgcgctacat	170000297
aacagactct	gtggggcctt	ggtttatgta	tttcttctc	tcccctactg	170000347
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caggggaaag	atttgtcatt	ctccaccctc	ccagttcagc	ttaaagcaga	170000547
gaagtgagag	gtgcccacaa	aggggtgtgt	ctgggggggtg	gggggtgggg	170000597
atgttccaag	atctccaagg	cctggatttt	aagcaagggt	tgagatgcc	170000647
gcaagagggc	ctggcattgc	cagattgata	gtctgcattt	cagagaagga	170000697
caacccacc	tctgacctta	gcccagcct	caacagcctg	ctcaaggaga	170000747
tccaccctta	gtaggaggag	gcagccaggc	caggttccag	tccctgccac	170000797
cgcttgccag	gtgtgtcttg	ggcagcaggt	gcctttgtctc	ggtggtcttc	170000847
agctttgccc	cctgccaggc	acgtgctggc	ctcctgctg	catcgtagct	170000897
catggagtcc	tctcagtcac	ctctgtatgc	cctgcagcat	ccccagttct	170000947
cagtgagaag	agtgtgctct	gaaagttaag	taacttacc	aaggtcacac	170000997
aaggtctgag	tctcaaattgc	atacaatttg	accccatagt	ctaaggtctt	170001047
gaccgcaatg	gaataagaaa	ttattttacc	attctgagtg	gcagtctctg	170001097
aagactacag	caataattga	tgctctcag	ggggataggt	gtgtcactta	170001147
caggtgatag	tgaggttgct	ctcagcctcc	ctgctcttcg	ttagacctcc	170001197
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ctcctaacaa	gtcatgtggc	cattgcccac	actacaacga	cagaggaagc	170001347
ctcaggggaa	ccctcctcct	ctcccgaatc	tccgggcttc	ctgcatccct	170001397
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gcctggggaa	gaccagagg	cccaggccta	ggggagaggc	cggtgtctcc	170001497
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gccttgctct	atttcttcac	aagcttcccc	atgacactga	cccaaggctg	170001647
tctggccact	acagctgctg	atgatgatta	gcaataataa	taataataaa	170001697
cgaaatgcct	tctgcttaga	tcatctttaa	tttccctcc	agaatgacat	170001747
tcgactctgc	ttagagttac	aggcagccca	gcaattactg	agcgcaaata	170001797
ccgtgttcac	ccgcctcacc	tcatccacgc	ccccacaaca	cccagccctg	170001847
agactggctc	cacgatcacc	tccactttat	aaaataagat	atcaaactct	170001897
gaacagaacg	gacgtctcaa	aaaatgggca	tattacattt	aaacctcaa	170001947
tctgttgggt	atttgagtga	aatggacata	cctccaggga	gtcggtggcg	170001997
agggccggct	ctgaggactt	cctgggttgg	gatcctggct	ctgcaggact	170002047
gcgtgacctt	ggtgagttac	ttcatccctc	caaacgcgct	gttctccttc	170002097

FIG. 1.110

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atagaatgga	gatgaccaca	gggccagatt	cataagggttg	ttccttgtaa	170002147
tacaggtgaa	tatccatacc	cagcaactgc	tggaccacct	gtggtttcaa	170002197
ggataatttc	cctcccacgt	ccccgtggcc	cttggaaacct	tcctctcctc	170002247
ctgtctcccc	ctgcccccat	cactttgtaa	ttgaaaagtc	atgattgctc	170002297
tcccaggtgt	agcactgctc	acagggtcaga	ttgcctgctc	tgacgtagt	170002347
actcagttgg	atgcggttca	gctgtgtatg	atcaactccc	tccccctgac	170002397
aaaaacatta	ttttgcatca	cagagaagtt	gatttctttc	acacataaaa	170002447
gaaggcaaaa	agtgggtgct	aaagggctgg	tacagcagct	tcaagaaatc	170002497
aggaagaacc	tgggctcctt	ctgccttctt	gttctgccaa	tatcacccca	170002547
tggctgccac	ttcatggccc	aagtggaaacc	atggagcacc	acccttcaga	170002597
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agacttagga	agtagaatca	acaggacttg	gtgacagatt	tgccacagag	170002697
ctggggaaca	gggaggtcca	acgggtgactc	ccaaggagct	gatgtgagaa	170002747
ccagagctgc	tgtgaatatt	gttcccaact	cctgagacag	ggacagtggg	170002797
cccgtggcta	ggaagtggta	ggcagtagag	agtcaaatg	cacattagta	170002847
tatcaacatt	gtgagtaggg	cacgcaggga	agaaacctgt	tcaaccagc	170002897
cccgtgctag	aaagacatca	gcagggcctg	caaaagccct	gattaaatct	170002947
cacaagtttg	cacctggagc	cgccatcttg	aattgcaggt	gaatatcagc	170002997
ctttggtttg	ggctgtgtgc	cccagatgat	ggtgggtccca	aattacatag	170003047
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aatgaaattt	gtttaaccgg	tacttcaggg	ttttgagcac	agaacagcgt	170003147
ccatccctcc	aaacacacac	tgaggatata	cacttagcca	ggagggaaca	170003197
taaggagggg	tggacaagcc	atgtttacta	aaatctctca	gtgtgtgcc	170003247
ggcatgttca	tgtatattca	ggaagaagt	tcagtattta	agatcctcgg	170003297
cccttgcccc	agtcaccaac	acgccttctt	gtctggagaa	ctgtaaatct	170003347
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ctcatcacat	ttctcccagg	ctattgactt	gttcaagggt	aaggatgaa	170003847
gagagtcatg	cagcagccct	acctggctct	gctctgctgg	gggaagcctt	170003897
ttcagagcct	gcctcttctt	cagcatgagg	ggctgctcgg	gcccagtcct	170003947
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cccgggacct	cgctagtctt	gcctggatgc	tcagaaggcc	ctcgtcctcg	170004447
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ttacctgtgc	gtgtgggagg	ttggattgtg	acatctttgg	agggccgggc	170004647
ttctgaagcg	acatttgatt	tctgggtactg	aaatgtcaaa	gggtcctgag	170004697

FIG. 1.111

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gcacccgcta	gggcagcacg	cggagcatcc	acctgcgtgc	gcatcctggg	170004747
ctctctctgg	gccacttggt	gctggggaca	tgccgggagc	tggtggtcag	170004797
ccctcctcct	gcctcctcag	tgtgcatct	tcaccttctg	cagctgccta	170004847
ccagaagcag	ggggacctgg	aaggcaaaagg	agagggagtt	ggcatgtagt	170004897
gagcaccgac	tgtgcacaca	gtgccagcaa	ggagcttcac	actcatctcc	170004947
agcgtcacag	ctgcccagtg	gctgtggaag	ccgatggact	gggccctctc	170004997
ccagtacaca	atcattagag	ggtctcagtt	cactgagtaa	ctgtgggagc	170005047
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agccgggagt	aaaggacaga	tgccggggaat	ctggaaggag	attcacttca	170005197
agcaccatcc	cactctattt	gttaaacttg	tgctcctgtg	aaaactgctt	170005247
gtgtctgcat	caaaccacgc	tagggagggc	tgagggctaa	gggtaaacct	170005297
gggagagttg	aattccagtg	ctgtgattaa	aaccaatatt	ccacataatg	170005347
caatgtaact	tgctcacatc	gtcccatgta	atctttaaaag	ccacagccct	170005397
tttgcaattg	ggattattat	ctccatttta	cactggagga	aactgaggct	170005447
ctaagaggtg	aaatgattca	cccagttagg	aagtgatgag	tccagatgtg	170005497
gtagactgaa	taatggccct	cacaatggaa	cctgtgagtg	ttcccttaga	170005547
tgacaaaggg	cctttgcaga	tgtgattaaa	ttcaggatcc	tgagattggg	170005597
agacattatc	ctagattatc	caggtgggtt	ctaaatgtca	tcagaagtgt	170005647
cttcataaga	ggaagacaga	gatttttgcta	cagaagaggg	ggaaacatga	170005697
tgatgagtca	gaggctggag	tgacacctgg	aagggggccat	gagccaaggc	170005747
gtccaggtgg	ctggaagcca	gaaaaaggcc	aggaaatggg	ttttctctgt	170005797
gagcttcccc	aggaaaccag	cctggccaac	accttgactt	tagcccagtg	170005847
caactgactc	cacattttctg	gctccagaac	tgtaagagaa	tacattttgtg	170005897
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tgctctgcag	tgtgctggag	ctcacagggc	tctgctgctg	ggagttagta	170006047
tctagtccaa	cactttaccc	actcaccccc	caagctaagg	gactcctgaa	170006097
atcagggacc	agatgcataa	taggtgcccc	ggaagtgaga	ctcgccttcc	170006147
ccagattaag	aataaagaag	acaaactatc	cacggctgct	gtgagcctct	170006197
catcagacct	cagcttctag	ggcagggtcc	ctgcctgtct	ccagtatgtg	170006247
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caggaaggga	ggggatctgc	aggcagccat	cagggctcta	attgcagctg	170006347
gctgggggac	catgggtcag	ggctgccacc	ccctggctct	gtgccttcac	170006397
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tggggacaag	ggaggggagag	aagaactcaa	aatgactgag	gtttccagct	170007197
accagaaaaa	tggaaggacc	ttgaaacaaa	tggggccatca	gcaggggaca	170007247
ctggctggaa	gccagagtc	cagtcagctc	tgtaaggccc	ccagaatagg	170007297

FIG. 1.112

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catttgactt	caagtcacag	gcatttcagc	aaaagcctct	ttgctacagt	170007347
gattatggtg	aagcagatgc	ccacagctga	gatgggcaac	tctcaggcct	170007397
ccagtgggga	cagagaatcc	ctgggcccc	acatagcttg	gcctgaagat	170007447
ctgagtcagg	catccaacct	cttctgctca	gctctttcag	gaagatgtgt	170007497
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actctgtagt	tatgttagaa	ataaatctta	tgattaccag	gattagtctc	170007747
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agaaccaaaa	gaaagtgaga	gtagctacat	tgatttcaga	cagagcagac	170007897
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gtcaatactc	caagaaaaca	taacaatcct	taatgtgtgt	gcacctaa	170007997
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caacaagagc	agatatcgta	tttttctcaa	accacatgg	gacgttcacc	170008247
aagataggcc	acattctgag	tcattaaaca	tacttaacaa	aagcaaaata	170008297
ataaaaaatca	tacaatgtct	gctctcaaag	cacaatggaa	tcaaactaaa	170008347
aatcaataaac	aaggagatag	caagaaaaatc	ccaaaatact	tggagattaa	170008397
aaaacactcc	taaataacat	aggtaaaaa	agaaatcttg	agaaattaaa	170008447
aaaaaatact	ctgaatcaac	tacagatcac	acaaacatca	aaacaataat	170008497
aaaggaatat	tatgaacacc	tctatgccc	caaatttgac	aacttacatg	170008547
aaatgaacca	attcttttaa	gtaaataatc	tgccaaaatt	cgcacaagaa	170008597
gaaatagata	atcttaatat	ccctatgtct	attacagaaa	ttgaatcaat	170008647
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attctaacaa	atattttaag	aagaaaatgt	atcaattctc	tacaatctct	170008747
tctagaagat	aggaacaaa	gaaatatttc	ctaactcatt	ctatgaggcc	170008797
aatattacc	taataccaaa	accagacaaa	gacatcagaa	aagaaaacta	170008847
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ttgcaaattg	agtccaacaa	cgtataaaaa	gaattataag	ccatgaccaa	170008947
gtgagattta	tcccagttat	gcaaggctgg	tccaacattt	gaaaatcagt	170008997
taatgtaac	catcacatca	acaggctaaa	gaagaaaaat	catataatca	170009047
tataaacaga	tgtggaaaaa	gcatttgaca	aaatctaacc	cccagttgtg	170009097
attaaaactc	tcaaaaaaca	aggaatagag	gggaattttc	tcaccttgat	170009147
aaagaacatc	tacaaaaatc	ctccagctaa	catcatactt	aatgggtgaga	170009197
aactagaagc	tttctacta	aggtacaagg	caaggatgtc	ccctctcact	170009247
cctccttttc	aacatcatat	tggaaagtcct	aggtaatgca	atgagacaac	170009297
aaaaggaaat	aaaagggtata	cacataggga	agggaaaaat	aaagctgttt	170009347
ttgtttccag	atgacatgat	tatctgtata	gaaaattgaa	aagaatcaac	170009397
aacaaaaaca	aaaacctcat	gtaactaata	agctattata	ctgaggttgc	170009447
aggataagggt	taatatacaa	aagtcgatca	ctttcctata	taccagcaat	170009497
gaacaagtag	aatatgaaat	ttaaaacaca	ctaccattta	cattggtaag	170009547
gtatatccca	aaatgaaata	cttataatct	aaataagtat	aatcaaaata	170009597
acatatgtac	aagatctata	tgaagaaaac	tacaaaactc	tgatgaaaga	170009647
aatcgaagaa	gagccaaata	aatgaagagt	attccatgtt	tgtggatagg	170009697
aaaccttggt	attgtcaggt	tatcagttct	ttccaacttc	atctatagat	170009747
taaatgcaat	cccagccaaa	attattgggt	attagcaact	attaacaaat	170009797
tatttttatgg	atatcaacaa	agtgatttta	aagtttacag	agagaggcaa	170009847
agactcagaa	tagtcaattt	aatactgaag	aagaagaaaa	aagttggagg	170009897

FIG. 1.113

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attgacacaa	cctgattcaa	gactaactct	aaagccatga	taataaagac	170009947
actgtggtat	gggtgaaaaa	tagacaagta	gatcaatgga	acagaacaga	170009997
aagcccgagaa	atagaccac	atgaatagag	ttgactgac	tttgacaaag	170010047
gaacagaggc	aatacagagg	agcaaagaca	gttttttcaa	caaacagtgc	170010097
tagaacaact	ggccatccac	attaaaaaaa	aaaaagagtc	cacacacaaa	170010147
ccttgacccc	ttcacataaa	ttaactaaaa	atgggtaata	gatctaaata	170010197
taagacacaa	aactataaaa	ctcctagaat	ataacatgga	atcatatcta	170010247
gaagatcctg	agtatggcag	tgactttcta	gatataacac	caaaggcaca	170010297
atctgtgaaa	gaaataattg	agaagttgga	attcattaaa	attttaaact	170010347
ctgcccgtga	aaaggcaatg	ttaagagaat	gagaaaataa	gccacagact	170010397
gggaaaaaat	atttgaaaaa	atatatatct	gataaaggac	tgttattcaa	170010447
agcatacaaa	gaactcttaa	aatcaataa	ttagaaaatt	aaaaatctga	170010497
ttcaaaaata	agcagaagac	ccgaacagac	atttcaccaa	ggaagatata	170010547
cagatggcaa	gtaagcatgt	gaaaaaatgc	tccacatatg	tcattaggga	170010597
attgctaatt	aaaacaatga	tgagatgcca	ctacagaact	catagaatgg	170010647
ccaatatcca	aaacacttaa	caacacaaaa	tgtaggtgag	aatgtggaga	170010697
aacaggaact	ctcatcagtg	cttcgtggga	ctgtgcaaaa	cagtacagct	170010747
gctttggaag	acagtttggc	agtttcttac	aaaactaaac	agacccttac	170010797
cataagattc	atcagtcagtg	ccctttggta	ttcaccocaag	tgaacccaaa	170010847
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cataattgac	aaaacttgta	ggccaccaag	atgtccttca	gtgagcgaat	170010947
ggttaaataa	atgatgggtgc	atcctggcag	tagaatatta	ctcaagacta	170010997
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cacattacta	agtgaaaaaa	gccaatcatg	cttccaacca	tgtaacatta	170011097
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gttgtgggga	ggaagggatg	attaggtgga	gcacaaagga	tttttagggc	170011197
attgaaacag	ttctgtatgc	tactacaatg	gtagacatat	gtcgtaatte	170011247
atttgtcaaa	acacagagaa	tgtaccagga	gtgaacccta	atgtaaaacta	170011297
tggactctgg	gtgatagtga	tgtgtcattg	tagattcctc	agttattaca	170011347
aatgcatcat	cctgggtgtgg	gatgttgatg	gtgggggaag	ctgtgcatgt	170011397
gcggggagtag	ggagtatatg	ggaactcttc	tacttcccac	ttaattttgc	170011447
agtgagccta	aaactactct	aaaaaataaa	gtttattaat	caacaaagaa	170011497
cacagtgage	tgcaacttca	taaccagtag	attgacaaga	attaagaaat	170011547
ttaataaaga	attgattaga	atatggagca	acaggaaactc	ttacacatta	170011597
ctgatggaaa	agaaaattgg	tatacctact	ttgtaaatag	tttggaatg	170011647
cctagaaaag	ttgaatatga	ccccaaaatg	acctaataat	gccactatta	170011697
agtattgacc	ctaaaaaatt	attgttgaac	gcatttttta	agagataaat	170011747
gcaaaaacat	ttgttgagtg	atcatttcaa	cagcaaaaac	tggaatcaat	170011797
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caagccatgc	atttggtgct	aggctctgtc	tctaccocaga	gagaggaggc	170012097
atcttttact	tcagatatgt	atgtcatcta	ttccccaat	ccagtgtcta	170012147
caagtctgga	tctgccctgt	gggaagtatt	tttcaaattc	atctactcag	170012197
cctgagcatc	attttctaac	tcacacaaag	gcatttttta	gattagtagg	170012247
agcactgacc	tgttcaccac	ccagcctatc	catcctggta	caatcctggt	170012297
gtaaccaagc	aggtacccag	gcctttttta	tgcagcagag	aaataggaag	170012347
tgaggcagga	gggaggcaag	gtgatgtctt	gtcttttctt	tgtcatgaaa	170012397
aggtcaggaa	agggacagat	agagtgaag	aagattggaa	aataagccag	170012447
agaggctcgg	ttgttcttca	taacaaaaag	aagttggggg	taagtaagag	170012497

FIG. 1.114

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aaagagccag	gaaagagagc	cagaaaagtc	ccaaaggagg	ggtgccctgg	170012547
ggagccctct	tgtgctttat	agcatgagtg	gctcctgtgc	agttggggaga	170012597
aggaagaaca	tcagagggga	gagaaaaggg	aatttttaaga	aatattgcta	170012647
agcgttatag	attagatacc	ctttaatgta	aatattcaaa	ttccttttta	170012697
taaaaaaga	tatattgaaa	tataattgaa	atacaaaaaa	attgtacata	170012747
ttaaacaat	ctgattttat	tagtctggac	atatagccag	acctatgaaa	170012797
tcaccacaat	caagatatga	atataactat	cacccoccaa	agtttcttca	170012847
tgtccttttt	aatcccacct	tccatccctc	ccaccctgcc	atccccacc	170012897
tcaggtaaca	ctgatctgct	tcccgtcagt	agagagtagt	ttgcattttc	170012947
tacagtttta	tctaaatcag	ccacgcagta	tgcattcttg	tctggcttct	170012997
tttattctgc	attattctgg	gactcattca	cgttgtgtaa	ctgaatactt	170013047
cattcctttt	tattgctaag	tagtattgta	gtatttcttt	gtatggatat	170013097
accacagtag	gcttattcat	tcatctattt	atagacaatt	ccaacttttg	170013147
actattacaa	ataaagctac	tatgccattc	acatacaaat	ctttacgtgg	170013197
aaatgctttc	attcctcttg	ggcaaatacc	taggggtgga	attgctggat	170013247
cacatgatgg	atgaaacctt	aactttttta	gaaattgcga	atttaggatt	170013297
ttccaaagta	gatgtagcat	tttataccca	ccagctctcc	attaataaat	170013347
tggatttcat	caaaaattta	aacttctgct	ccaaaagaca	ctcttaacaa	170013397
agggaaaaag	caagccacaa	tatgagagga	aatatttgca	aagcatctga	170013447
taaaacatgt	ggatctaaaa	tatgcaagga	gaataacaac	tctattttcc	170013497
actaaggaat	gaatgactgt	acaaggacca	cattctaatt	aggagcttct	170013547
gaacccaaag	gaatttcaga	taaggggaaa	tttaggccca	aagccaggag	170013597
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caactctgga	ctccattgga	agaaccttct	aacagtcagg	gctccagag	170013747
ataaactaga	caagtcacca	agagaggcag	tgggtacccc	tcacaggagg	170013797
ggtgcaaatc	aaagccaagg	cttggagtg	accatttaa	atccatttct	170013847
tatcctgtga	ttcttagagt	cctatctgta	tcaggggaag	gcaggtgggt	170013897
tctagaactt	tctaaatgtg	tccctgtgga	tttttcttcc	tccagctaca	170013947
cacaaacttg	ggcctaataa	gaagtctatg	gcattaaccc	agcaggaatg	170013997
cttaatgctt	atatctgacc	tcaaaccaag	actgtctcca	cagtgaacaa	170014047
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ttacttttaa	atatttgctt	ccgtaaaaaa	acaaatgaat	gcctcggaca	170014247
gattttataaa	gaacattcct	ggagaggcgg	gtggattaat	tattcagcat	170014297
cctctccctt	tgtactatt	tattgtctca	tatgcattta	tatggtacct	170014347
atcactgcag	atctcgctcc	atgctggaga	cataatttcc	agtgactgac	170014397
tacttgtcta	agatatatat	cgtattgcaa	tactatttta	tttctgactg	170014447
taagggcacg	tgccactggt	gggtaattgt	gttcatgttt	ttaaatgtga	170014497
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attaaccac	caggaagtta	ctcggcaaat	aaataggcgt	ttgtggctgt	170014597
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gttgtgttgg	gggaaaggag	cttctaattg	ccaagaatag	aagacctgaa	170014747
gttggctagt	gcgtggctag	tgcctgtaat	cccagcactg	tgggaggcca	170014797
aggtggatga	ttcgtcttag	cccaggagtt	caagactagc	ctgggcaaca	170014847
tggaaaaacc	ccgtctctac	taaaaataca	aaaagttagc	caagtgtgat	170014897
gacacatgct	tatagtttca	gctactcggg	aggctgaggt	gggaggatag	170014947
cttgagccca	ggaggcagag	gttgcaagtga	gccagattg	aaccactgca	170014997
ctccagcctg	ggcaacagat	tgagacccta	ttaaaaaaaa	aaaaaaaaaa	170015047
ggaaggaagg	aaggaaggag	aaaagaaaaa	agaaaagaaa	agaaaagaaa	170015097

FIG. 1.115

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agaaaaatga	cctgaagtca	ctggatttcc	ttcgaggtag	ccagaaacag	170015147
aggaaagggg	gcattgcccc	cttagggtaa	aaagtagagc	accgaattgt	170015197
ggaaggctgc	aggttttcat	gtgtgcttgc	ccaagtgatg	ttccatgtca	170015247
ggctctaggg	tccctgcagg	gacagagagg	gactaacatt	tacttacatg	170015297
cctatagtat	gtcaggcata	tacttgtgcc	tttatatata	tcagctctgt	170015347
ttttgtcatt	aaaacatccc	tgtagaaaga	taggcactgc	tgtcccattt	170015397
tacagatggg	gaaacccaag	ctctgagtgg	ttcagcaaac	cctgggtgca	170015447
tacccccacc	ttgcccctgc	aaaaccaaca	aaaaaacgaa	ggccctgcct	170015497
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cccagctatg	aacccccattc	ctttcagtat	gagccaagag	ggatggcatc	170015747
tgtcagagtt	gctggatttg	ggattttgca	tcttgccaag	tgtccatgag	170015797
gaattgggga	aactctcccc	ctggctggac	tgaggcttca	gcaagcattg	170015847
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ggtatcacga	acatatcttc	tcctttgctt	ccttctcctc	actcttcac	170015947
atcatcatca	tcacatcat	caaatatgga	tctgtgaggc	tacctctggg	170015997
gttgaaactt	ggttttgggc	aaaatttggt	atgttctctc	tgcccaatcc	170016047
agcctcaggc	tacaaatgaa	tgtaaaaatc	tctaatttag	tgccaagtaa	170016097
cagaaaacag	ctctacttat	cttaagccaa	aaagagggac	ttctcagagg	170016147
catactaattg	gaggatggca	agagggcctc	acgtggaacc	agggcctgga	170016197
gcggcacagc	attcaggaag	ctcagtcctc	ttctctctct	ctctctcatc	170016247
tctgcttggt	tccttttacc	tgtagacatg	ctatcatttt	tccaatatcc	170016297
atggcagaat	gtggccacca	gtaactccag	gtgtataaca	gaagcctggc	170016347
ctcccaggag	aggggtgactt	gatgccctta	gctccagcct	tccactccca	170016397
ccctggggcca	agcaactgggt	ggccaggagg	agctcatatt	gcaggaatat	170016447
tgaaattttc	actaaaatca	tttgaatcga	ggagacatt	tcctagaaaa	170016497
aagggtgcta	gtctgacaag	cccacagtgg	tccccttcat	ctggcaattc	170016547
atcttctgca	aaggtcacac	catccttttc	gctttccaac	ctctgcacca	170016597
gtgcccaggt	ctgtcactcc	ctcctctcat	tctgaaacat	cctctgcact	170016647
ccattcacca	gtgccaagcc	ttgcccctct	tcagggttca	actttgtccc	170016697
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gttttccaca	tattgagcat	tgtctgagcac	ctattctgtg	ccaggcactg	170016847
tgcttcaggg	ccattggggga	tgtctcaagc	ggtaaaatgc	aaccaaagcc	170016897
ccgaaggagc	tcacattcta	gtcatgtcca	caaagaggta	ataaatccat	170016947
aaattgtatg	tactattcta	gtcacaataa	aattgtgtcg	tactgtaatg	170016997
ctgggtatcc	atttttaaac	ggggggcctc	ggctgaatct	gggtcattac	170017047
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gttagccatt	tggtggcaaa	aattacagtg	ttaactaatt	tccagggtat	170017297
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ccacttataa	aaataaggat	ctgtaagtgt	gctggataaa	atatattaca	170017597
aaataatgac	ttaagtggct	ctggagccag	cacaaaagat	aaaaattggg	170017647
tataactcaa	attaccttca	aaatatctta	agtcattctt	aaaatacatg	170017697

FIG. 1.116

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taaatatgcc	aactcaaaat	acatccaaca	aaactaatat	ttttcccaat	170017747
ttgttggaag	aaattttctct	ttcttttagtt	gtgcattaga	tgaggaagtc	170017797
agagtgcatt	aattattcggg	gccctgttgt	ataaaaatga	cagattttca	170017847
atgtatgcta	atatgcaggt	cacactcggc	ccagtgagat	gcttgccctag	170017897
aggaggcacg	tggaagccaa	ggccaaggaa	ggcataattc	actctggaga	170017947
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cccgccaccg	ttggccaata	gcaattttcta	ggccccacct	caccaaggca	170018097
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gtgtgtcaga	gtagaggaga	aatgactttc	agtgtctggga	ccataaccct	170018247
gtttccactc	cacttctgac	ttgcaactgtg	ggctgagaat	tgacattctg	170018297
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caaaacaggc	tgggtactga	ccttcctcgt	actccatggc	tcagaactct	170018597
gacctcttgc	caacctgcct	tccgcaagca	gcgagagtag	cacggctctg	170018647
aggggcatgg	ccagggagga	tgtgacctct	aagtgtctca	agtcactggg	170018697
aacctgttcc	taataatagg	caaagcttca	gttgatggag	tgccatatatg	170018747
ggcccagccc	tgtgaacagc	ttcctctcag	ttttccaga	atgaagctca	170018797
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tgtttataga	attgocgggag	gggttaagag	aaagacaaga	gagtggtgaaa	170018947
tgccccagaa	ctagtagcag	gaagctacta	ccatccctga	gcctgaagga	170018997
cagaaccacag	agagacagac	ctgtgctgta	ggtcaggggcc	ccccagtgtg	170019047
agcctcagct	cccgtgcca	gtccccaact	caacaggaga	gagctggaca	170019097
ataaagaccc	tgtgagcacc	cacaacttcc	cattggctgc	atcctgttag	170019147
aatctagagg	tcatgggagc	ctgggagagg	ccacccatga	agatcagctt	170019197
ccaggggcag	agagcagagt	ggacatggag	gggcaaattg	ggaccgtcca	170019247
gcacagtccac	catctcatag	acattttcct	ccacctccta	cctcgagtag	170019297
ccagtaggg	tccagccgga	ctgtggagca	tcaccccaac	aactgcatgg	170019347
ctgcttccca	ctgtcccttt	aacagcgcac	atgggagggga	gccacagggtc	170019397
agcaaggccc	ttggctcccg	ctgtggccct	cacccatgcc	catccccacc	170019447
cgtcccatg	ctcagcacat	cagcttcaact	ctggctgacc	atgtgcacag	170019497
acatgactca	gtaagtctgt	cttttctttt	cttttttctt	tctttctttt	170019547
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ggccacgctg	gtcttgaact	cctgacctca	ggatgatctga	gcacctcgat	170019797
ctcccaaagt	cctgggatta	caggtgtgag	tcaccatgcc	cagccaaactc	170019847
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gccctgccac	ccattcccta	gggcaggcac	ccaccaccgc	cttggctcag	170019997
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gccctccagc	tctgtggctc	catgtcaaat	gccctgacc	acccttgaga	170020097
ttaacccttt	cccaaggata	gacagcttcc	cccatcatte	tagatccctc	170020147
acacttcccc	agctcctacg	gaaataacct	atcccatccc	ctaagatctg	170020197
caactgttga	gggtaagttt	ttggttaaaa	agagtggagac	agactttggc	170020247
gctagtgcaa	aacaagctgc	tgctgtaaga	gtgcatgtgt	gtacctgcag	170020297

FIG. 1.117

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actggtgcaa	tcagatgacc	ttcccaccag	gctgcacagc	actggatgtc	170020347
ctcacagtca	ctcagccact	cagcaaactt	tgactgcaca	gcaacccatg	170020397
ccagacctgc	tgctggactc	caggcatggt	gagaaatgaa	tataataccc	170020447
aggctatggc	ctcaaaacct	tcaaaaccca	gggcaggaca	cagacaggga	170020497
cacagatgtg	atacctgctg	ggatacagtc	ctcatgaggc	tctctaagag	170020547
gtatctaagc	agggacctag	agggaggagg	tattacctga	gttgaaccta	170020597
atggaaaggc	attgcaggca	gagggatcag	tataagcaaa	tactcagacc	170020647
aaaaacaatg	gcatggggga	ctccacccaa	gaagtaaaag	agaatagggt	170020697
gctacatggg	gtctcagtcc	cttttctgtt	gcttagaaca	ctgaaactag	170020747
gcaattttata	aagaaaagga	atttattttct	tatgggttatg	gaggcttgga	170020797
agtcccagggt	tgaggggagca	catctgggtga	gcccttcttg	ctggggggcag	170020847
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gctgagtgca	ctagctcagg	tttctcctaa	aaacccacca	gtcccactcc	170020947
ccaaataatc	cattaattca	ttcacccaca	aattttattaa	cctcttaaag	170020997
gtcctacctc	gcaatactgc	cacattggag	attgagtttc	aacatgagtt	170021047
tttgagggga	aaagtattca	aactatagct	cacagagatc	gcttttccta	170021097
gagatggcag	atgaattttg	gaggtagagg	gagaggggca	gatcacacag	170021147
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ggaagaagaa	atcaatggag	ccaaatgact	ccaccagatt	tgcatattgag	170021347
acgggtcactg	caagactgca	ccagtcacca	attcccaaga	cagcaatgtt	170021397
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tgctctcttt	gtggttaaaa	ttaccttcca	ttcgtgggtg	gtgtatgtca	170021847
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aaatttgggg	aaaaaagcaa	actagaaaga	agaaaaacca	cattgcctga	170022047
attcctactg	catggagaga	agcatcataa	acaccttttg	gaggagtctc	170022097
ttcttctctt	ctccctttct	ccttctttgt	atagagaggt	ctttcctgag	170022147
gacttcccag	aatcttgcag	atccaaaatc	ttaagaattt	gcagaggcag	170022197
tgaggagtta	acatgcacag	ctcagggaat	attctgcttt	ttatctggaa	170022247
ccaggctcgg	aacaagactc	cttgcttttc	tgctctgtgt	tttcatcttc	170022297
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gcaaaaagtaa	ttgtagtttt	tggcattatt	tttaatagaa	ctgcttctgt	170022397
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tattgcttat	tctggcctat	ttccttaggc	acattagccc	atctaaccgt	170022547
ttccatggcc	cacagagggt	ggaggagcat	gaagaaaaat	gcaaggaaat	170022597
aagctcatct	caaggatatc	ctggctccca	aagaacatag	gacattacca	170022647
acttgaagtt	agcttctcag	gaaactaaga	cccagctgct	tttcaaatac	170022697
tcaaaatatt	agtatgaatt	atagatatag	ttatagcctt	cagaacttct	170022747
ggcacagccc	aaaactgttg	gctgtaaaac	catgtttcct	aaattcaatc	170022797
atgtttctca	ttgattttcca	ttttgaaatt	ggaagtcttt	gccctcaaga	170022847
tataataaaa	accataccaa	agaaaatgga	aaacttttcc	cccttaatat	170022897

FIG. 1.118

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ttaaaggaga	atgatttttta	taaaaaaaaa	aaaaaacatt	catttgtcta	170022947
cttaaagtaa	atcacagtgc	agtgccagtc	tgggtttgga	gcataacact	170022997
ttttttgatt	tatggtttct	gccaggagac	acccagctaa	tgatatttgt	170023047
tcctatgtcc	ttctctgact	agctgggtgg	cagctaaaga	gctaggggtga	170023097
ggggagacca	gaactccagg	cctgtcccat	gttcctgtct	cacccatatg	170023147
tggatttcaa	ccctgggctt	agtgtctgcc	tctagcgaca	tgggaagaga	170023197
gggatgggtc	ctctccttct	tcttgtcaaa	tggcccccag	agtcccacca	170023247
aggtggagct	ccaggctcct	gaccagcggg	gctccccaac	cctcctgctg	170023297
tgcccagtct	atccctcctt	ccacgcccag	cagagctcag	cagacttgcc	170023347
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attaacaagt	cgaggtttgg	gatatatctt	agagatggag	ccaatggggc	170023497
ctgcagagga	tttccctggg	gactggaagg	gtgaggaagg	agaatgctct	170023547
cagatgacac	ctaggtggct	gatgtgatag	aatgggcatt	ttctggaaga	170023597
tctgttcagg	ggcattttgt	gagacagaaa	tcaagggttt	ggcttgggac	170023647
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gagttacaca	tttgagggca	tccatgatgt	gaagcacatg	ggggggccca	170023797
cacaggggtc	tgtgtgttcc	cctgtggtgt	gtgtggggac	acgtgagtat	170023847
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acaatttctt	gtctgacctt	ggctgaggta	tgtctgagtt	ttaatggcct	170023947
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acaattctag	gagttgggga	atcccaaaga	tgtgcccac	cctggtttgt	170024047
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atgcgagttc	tgcacctccc	ctggggcctt	cagcagctgc	attcctggcc	170024147
cagcagagga	cttgccctgat	ctccaggata	gcaaaggagc	tgaggccaaa	170024197
aagacacatg	ggctactgct	caccagccc	catattatac	ccttttcatc	170024247
gctgcaattc	aacataaaat	catatcatto	acacctaccc	actcatgcat	170024297
tcattcagca	catgtctatt	tttgaaccgg	caaatatata	ttagatatcg	170024347
atgctgtgct	gaatgccaca	gattgcaaca	ggaatcagac	gccaacctgt	170024397
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ataactgaac	ttgacttctt	tcttgggtcc	tcattctgct	gggcatggat	170024747
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cagtctaggt	aggggtgttct	ttcccttctc	ttcccactag	agaattttata	170024847
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aggctacatc	caggaagagg	caccaagccc	acttgtcctg	aatctcaaag	170025197
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tcctccactc	cctggagaaa	aacctatccc	acacaccctc	acataattctt	170025397
caagatctat	tgggttaaggc	atccaactta	ttgcttaagc	atttcaagga	170025447
ctggactttg	gaaagccaag	aatctgagtt	gcaaagtctt	ccttaaaact	170025497

FIG. 1.119

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caaaaactgg	gctcataggt	gctcttctct	ttttcttggc	atttgcctaa	170025547
aagccaccct	gaggacacct	aggagaggcc	acctcaccac	ttcttgaacc	170025597
aggcatgggg	gatggggaag	aagacactgg	ggaaaagctc	tgagtgggtac	170025647
ttcagatcat	cctgcctcag	gtgttggttc	tgatcctctc	aacgactccc	170025697
aagggaatat	gtcagctcca	ttttgcagac	tgaaacccga	gtctcggaat	170025747
gacttgtcca	tggtcacaca	gttgctaaac	atctgagcca	gagtgaact	170025797
ctgggggtatt	tgactttaaa	gtcccagcct	ttaaatcatc	ccacacttgc	170025847
ttattccaac	ttggacttgc	cggagtccca	tagacagagg	ctactctccc	170025897
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cctgggcttc	gtctccaccc	aggtgcctct	ccccagcag	ctgcaccagg	170025997
ccagctgagg	gggatttttag	cccgaatcca	gggtttctcc	tacagaagac	170026047
aaggagtttg	ggcactgcca	gaattagaag	aacagaaaga	aaatgttctg	170026097
gatttctcat	caaatgcccc	tagcctgaga	aatataacta	aattcaccct	170026147
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ggcctgtgcy	ttcactcctg	ccccctcctc	cagccctgtg	tacactccct	170026447
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aattctcact	gagcctcctc	cctagcatct	ccctctctgc	attataattc	170026947
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aaggggtttt	cagtttagtg	gggagcaaa	caaaaagaca	aacaaacagt	170027297
taaatataac	atctagtagt	gataaatact	ccaaagaaaa	ctaaagcagg	170027347
ggccagagag	catgggggca	ttgatgtttt	agacaagggtg	gtaaaggggag	170027397
gtctctctac	agaggtggta	tttcagcagc	agcccagagca	ctcagttaggt	170027447
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ttccaagtca	caagcatcag	gcttggaaga	cctgtgtggg	agagtaatta	170027597
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gatcatocca	agccttttga	atacgctgt	ctctcctgcc	atgctctgtt	170027997
cctatctagc	ttttcaaaac	aaactcttca	ttttagaata	gttttaaatt	170028047
atagtttagag	aaaaacttca	aagatagtaa	gagagttccc	atatcctgca	170028097

FIG. 1.120

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cacctggtga	gccccattgg	taacagctta	ggttaacact	gtcaccacta	170028147
atggacaaat	gttgcaatat	tattatttgc	tcaagtccat	acttaactca	170028197
gacttcctta	gtttttacct	gaagtccttt	ttctagttca	ggatcccaca	170028247
ttccatttcg	taggcatgtc	tccttagact	cttcttggct	gtgacagttt	170028297
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gaagggaagtc	actgtgtgca	actcacactg	aaggagtggtg	aagtttagaga	170028647
tcctccttga	gcgtgggcca	tcttcatgaa	ttattgggaa	ttattctgca	170028697
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tttgggttat	aatccaatag	tatttttactt	cttttcttgc	tcaaattact	170028797
ccacctttgg	gtactggggc	tcttgagttt	ggctcctatg	tccccgtcat	170028847
tgaggggttt	gggttttgtg	tgtgtttgctg	tgtgtgtgtg	tttgagcact	170028897
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gcccctggccc	tggagccact	ccaaggaacc	tccaagaacg	cctgattcct	170028997
tttattactg	gctcctatta	taattttcat	aatgggctgt	cattttgttt	170029047
tgtctggttt	tgtttataat	tataagggtg	agtcaagctca	ttgcataaaa	170029097
tatagcaaag	atataaaaaga	ataagaatga	aaataagtat	cccaaataat	170029147
ccaagcagca	aagaaatcca	gcgttaacat	tttgggggtat	tttcatctgg	170029197
tctttttgct	agttgctggc	tcttaagaag	tctgtgcttt	cattcttgat	170029247
ctctgccaga	ccaagggata	tcattggccc	tggtttacct	ccctgtccca	170029297
gcattctgtg	ttggagcagc	ttccattttg	ccatccctcag	gtgggtctgct	170029347
cgctgggccc	ctgcccactt	ctccctccag	cagaccgcag	gccaagaggc	170029397
caggagccag	ggtgtgtcct	ccagcagact	ctgaggaagt	gaatacatca	170029447
ctgttctgtg	acttccaacg	tgatagttgg	cctcattttc	ctcttcttta	170029497
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gaaacaggta	ttttaaaaag	taaaaactgt	cggctgggctg	tggtggctca	170029597
cgcctataat	cccaacactt	tgagaggccg	agggtgggctg	atcacgaggt	170029647
caggagtttg	aaaccggcct	gaccaatgtt	ggagaaaacc	cttctctatt	170029697
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gcagttagcc	aagatcgtgc	cattgcactc	cagcctgagc	aacaagagtg	170029847
aaactcgcgc	tcaaaaaaaa	aaaaaagtaa	aaactgtcat	tattataacc	170029897
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ggggatgcca	aataagttca	caaattggaag	aactttacac	agtacctagc	170030347
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aatcacagtg	actgagggat	tatccaagga	tcacactggc	cactttcaca	170030597
ggttttatcc	ctaaaggaaa	tcacaggtaa	tagatgtggg	gctgcagaaa	170030647
tgaacatgc	acttttccct	gaaactgcat	cccttttccc	tgaagatgaa	170030697

FIG. 1.121

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gcttgaaaga	actctaagag	gttaagcatg	gagctgatgg	gcaagccaca	170030747
ggcagaaaga	gtagctgtgc	agccaggctc	ctggccaggg	agggcagata	170030797
aggaggggag	gcaaagtttg	gtaaacagga	agctaatacta	tgggcaagaa	170030847
tcatttttctt	cagcatcctg	acctctccta	aaatgttctc	cactgggtccc	170030897
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gttctgctgt	atgacacagg	acaggtggct	tgcttgggtc	gggccacagc	170030997
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cttttccttc	aaataaagag	attggcatac	aggggaggag	cccagtacag	170031147
acggcatgct	tggctcaggt	tccagaaccc	agaaaccaga	caagagttgg	170031197
gaaacatga	tggtggagga	gggtgtgcc	ctccttacta	gtgcctaata	170031247
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agcccagatg	actaggggtca	gttattagca	tgcttctctg	aggtgggtcc	170031347
caggtgcagg	ctacctgcag	tctggctgga	tgggccctgc	accacacttg	170031397
cttctgggaa	gctgggtttg	gggttgccac	aatctctgaa	agaatcacta	170031447
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cactagtctt	accttcttgg	ggaacccttc	ctggattccc	aggctgggct	170031547
gggtgtccct	gcagcctagc	cccacagccc	tcctgcttct	ctttctcatc	170031597
acagtcttgt	tatctctacc	aactgtaggc	ctgccccact	gatggtgtga	170031647
ataaaggagc	tgggtctctc	tagcacctag	catagatctg	atacatagtg	170031697
ggtgatctct	attgaatgaa	cgatgaatga	atgaatgaat	gaatacattt	170031747
agataattca	gattactctt	tctagctcag	cagtgtaaag	caggaagaca	170031797
tgctgtcaat	atgatttagg	gcaagtttct	aaatctctct	ggacctcagt	170031847
tttacctctt	gaaaaataaa	tataataatt	tgctccttact	tcattgagact	170031897
attttgaaga	ttaaatgaga	taatgtatac	actactactc	actgtcctta	170031947
cttgaatatt	cctaggtcct	tggtgctaca	ttaggctaca	tagaatgtat	170031997
ttaaagtaat	agagtgggtat	ttataaata	ttcattttct	ttccccagaa	170032047
ctaccttaaa	ttaatattgt	gaaaggacag	atggatggat	ggttgatgga	170032097
agtagcaggc	ttccagcagc	aggggatgga	gtgagtgtgt	ggataccgct	170032147
ggatcagcag	aagggtatac	catttttagag	taactatctc	ggacttcgga	170032197
gagttcctgg	gtatgaagg	ttggctttta	ttaaagtctc	agcacagtgt	170032247
taaatgccat	tttatttttag	gtcataatta	acactaatga	gatgagtgga	170032297
ttacaaagag	cacacatttt	gagaaagtga	aaaacaacat	ctgagcttgg	170032347
tggtttccat	tttcgctttt	ccccctccca	tgctctgttc	aattaaaagt	170032397
tttgagaaaa	tattacaacc	atactccttg	tctttgtgg	aatgaagcat	170032447
attaatttga	atgtgatgaa	tacaatatcc	cactgacttt	tttattccct	170032497
tatctacaaa	agtttaaaat	aatggaccaa	ttaaaccagg	agagaagaat	170032547
gcagggtttg	cctggggatc	caattcagca	accagagaac	tgaaagaaca	170032597
aaattttttg	acggagtctg	ggccagactt	catcccttac	ctatagctga	170032647
caaacagtaa	gtcaaatttg	gcagatgtgg	accagcgcag	aacacatact	170032697
atattgagga	tcgaaaggcc	aggttccaga	ccgtcctcta	atattttctt	170032747
agtgaatatt	tgttggtatga	atgcattgat	gggtggatga	atagatggat	170032797
ggatggacag	atggacggag	agagagatgg	atgaatggat	tggtggatga	170032847
agttgaaaga	tgaaggtaga	tgacctccca	tggtctgatt	cttcctaagg	170032897
tagcaaatta	agcctaggat	gggttgacct	aacccttcca	aggacttaga	170032947
agtcagggca	agaacttaca	gggaagggtt	cagttctctg	acctcactac	170032997
cctagaggca	taaaactataa	attatagagt	tggtctgagc	tcagtttccc	170033047
tgggagctct	gctctaaagc	agagcccctt	gaccctgcac	caatttggtt	170033097
aaaccgagta	aggctgagct	tccccagca	ggagctcctg	ctttggaaga	170033147
gaacatcctg	ggccaggcgc	agtggctcac	gcctgtaate	ccagcacttt	170033197
gggaggctga	agcgggtgga	ccgcctgagc	tcaggagttc	aagaccaccc	170033247
tgggcaacat	ggtgaaaccc	catctctact	aaaatacaaa	aatttagcca	170033297

FIG. 1.122

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ggtgtggtga	tgcagcacac	ctgcagtccc	agctactcag	gagactgagg	170033347
caggagaatt	gcttgagcct	gggaggtgga	ggttgagctg	agctgagatc	170033397
acaccactgc	actccagcct	gggcgacaga	gtgagactct	gtctcaaaaa	170033447
acaaaaaaaa	aaataaaaaa	aaaagaagag	gacatctgga	gcaggcctgt	170033497
gaacctgaca	catggtccag	gtgtctccct	gaggacttct	ggaagtctcc	170033547
ccacctctct	gtggtccctt	aggcattaac	accaccttgt	cactgtgtct	170033597
tctgaggcag	tctggaagtt	catacccac	aatctctgtg	taccttgtcc	170033647
cccattctgt	tctctgcatt	gcagatgggt	taaaacacac	acacatacac	170033697
gcgcaaaatg	ttgttccttt	tcttaaaacc	catttgtggc	aggctagaca	170033747
aatccttaac	acggtctaca	atattctgca	tggcatggcc	cctgggtgcc	170033797
tcccaacctg	atctgtcaca	caccacctcc	acctttgcct	gttccctggg	170033847
ccctagcact	aacctttggt	tcattcctag	acaccttttc	agcacttagg	170033897
ccccacacgc	cctcagaacc	tttacacttg	ctgtctcttt	tgctttaaat	170033947
gttcttgccc	cacctaccac	ctagttaatg	ccttttcctc	cttcagctct	170033997
tagttgaagc	atcacttcct	caaggagggc	agccctgatg	aaactcatta	170034047
tgcaaaactcc	agcctggggt	gggccttatc	tttatgctgt	catggccctg	170034097
agtattcttc	ctttatggca	ccaatcacgg	cttatatgat	atacttatgc	170034147
tattatttga	gttatgtctg	tctccccag	tatgccacta	gtattagaat	170034197
cattgatatt	taatcattgt	atccctagt	cttagcacag	agcctggctc	170034247
ataatagatg	cttaataaat	atgtgttgaa	taaatgaatg	agtgaatgaa	170034297
taaatgcctc	attcaagagc	tttggctcct	tctgtactac	tacattactt	170034347
ctatttttta	gctcttaatt	ctcaaagcac	tttctttgtg	ctgggcttat	170034397
gctgggagct	tagacagtaa	agcttagatg	gtaaaactaca	gttgctctca	170034447
agcagttcac	aatgtaacaa	aaaagagaca	caaatacac	gtgacaatac	170034497
agtgtgtcga	gtgctacaat	agatggaggg	gtgcagtttt	atggatgtgg	170034547
agaagaaatc	cttctattcc	tactggagg	cttcactaag	gagatattcc	170034597
ctaagctgct	tctggaagga	aaaggatttg	gccaaagaaa	taagggtgga	170034647
ggcagaattt	caggtgaaa	gaccagcata	tgcaaaggct	cagagggcag	170034697
agcctggcac	tggaaacaaa	atgcaagtca	cttcgtggac	tgagacctgg	170034747
atgaggacat	ggggctatga	gagatgaggg	tggggaggga	gacagggggc	170034797
agatcacaga	ggcctttcaa	tgacagcaac	atatggcagc	tgacagagaca	170034847
gcatggaagg	gactggcatg	gtgagacctg	tgatattggag	aactccctct	170034897
cgaagggggt	cagaaaagag	atgtccatat	ttcaagtga	ggacttcctc	170034947
ccctggagaa	actgaggctc	tgccccagg	ctgtccatca	gactccttcc	170034997
cagaatccaa	acgcttccaa	aggatgttca	gtgtggctga	ccttgcttat	170035047
tcattgtggg	gagaattaat	ttcagggtgg	agaattttta	aaaaatataa	170035097
gattaagcag	tgtaatcagc	tgctgctgag	agttgcaaat	gcaataaata	170035147
ataatagcat	tgagagctgt	ttttaataac	tcaccagtgt	aatttagcct	170035197
cggcttctta	gagcatattt	aaaatatgtc	atagtgtgtc	taatggcaaa	170035247
tgccctcattg	ccagcctctg	aagacaaatg	tcttcccagg	agggaggggg	170035297
gcagaaaata	gaggagaaat	tggaggattt	gattgcaaac	aggggtgtagg	170035347
aaggcaagca	ttgttcattc	tgacaccact	aattcaaaat	ctgtgatctt	170035397
tgccataggca	ataggtttta	gttggtttgt	cttcaagggt	gaaacagatg	170035447
gatagcaata	atatggtaaa	ggagatattt	ataatttgta	agagaagagg	170035497
ttgttttcag	aatctataga	atcaccattt	tcatgcagtc	catattctaa	170035547
ttacagatca	tcttgacta	tctattatag	cagggtccca	ggcaactgat	170035597
atcttgacaa	catttgtttt	acttagttga	gttactaaat	attcatgata	170035647
ccatgaaaat	gtgttattta	aaagtgttcg	atgaattctg	agtttttagta	170035697
attcatatgt	gctgtccccg	cccaaccccc	attagtctaa	actggtgaga	170035747
tggggctagg	agtcctcccc	tcttgggtaa	cagacttgac	acagttaaag	170035797
tgagacaaac	tttggagtca	gacagacctg	agttcaaatt	ctagttctac	170035847
cacttactag	ctgtgacctt	ttgcagctta	aacactgagg	ctctattccc	170035897

FIG. 1.123

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gatctgttaa	gtgagagtgg	tgatgatgac	gaccatgaca	gctaataattt	170035947
atggatcgcc	tattgtgtta	tctccaacac	aacgatacag	tgacgtagggt	170035997
ctaccatggg	tcctgtttca	cagatgagga	aacttgaagc	ttagcgagct	170036047
caagtaactt	tcctgaggca	cagggctagt	gaataaccac	tctgggacct	170036097
agtatctgtt	ctagctgggt	tcaaagccta	tgctgttaag	tgggctctga	170036147
tactatcttg	tacagttggg	ggaagatttg	agaagacatg	tgtaagggtat	170036197
agttcctggg	atgtaattag	gactttataa	atatctctta	tatggaagga	170036247
ctgaatgtat	cttcctgggc	tgtgtcctcg	cagggagata	taacatctat	170036297
gtcactctca	acgctttatt	aatgtccctg	tcactctata	cccttgtcca	170036347
agttactcca	caccctccaa	agcctcaagt	ttttaatctg	taaaatgggtg	170036397
gtgggaggag	gtggggagtg	agcgtctcta	cacatactac	taggttgggg	170036447
gtaaattagt	aaaacaactt	tgggaaacaa	tttggcaaga	cttagtaaaa	170036497
ggtgcataga	tcctgtgaca	cagcagtttt	attcctggga	taaatgctaa	170036547
agcaggttgt	ctccatctct	gcactactga	catcctggga	cagatatttc	170036597
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ggcaatttat	tcccaagagg	aaagcaatga	ggaaggaagg	aaggaaggaa	170036697
ggaaggaagg	aaggaaggaa	ggaaggaagg	aagggaggga	gggaggagg	170036747
gagggaggga	aggaggga	tatttaataag	ttaagttaca	tccacagggt	170036797
tgattataaa	tgtgtgtatt	gaattggaat	ttctgttgaa	attctgatcc	170036847
cttctagaca	aagaaggtaa	aaattgaaac	atgtcaatgg	atatctaaat	170036897
atcattactc	actggcttta	tttgcaaattg	gctttccatt	gacaacagtt	170036947
acattttgtt	caaagcaaca	aatgattggc	gctgacaatc	cacaggaaca	170036997
tggtgcagtc	attaatgaat	gtgctcatta	ttcctccctg	ccgggaggga	170037047
tcgactcccg	ttctccagcc	tgtttttaagc	agacagacct	acatctgcac	170037097
ctgtcagctt	ggaaccctag	taggggagg	ggatgctgat	gtgatggaga	170037147
atgaagaatg	ggccctgcag	gctgacattt	tgggagagta	ggttctgaaa	170037197
tttatcccaa	aggacatgga	atcctggaag	cagggttcaa	gatcctccca	170037247
aaattgatct	cccaggatgc	ttggaatgat	tgttccgagg	gttttgtaaa	170037297
atgccagggg	aaaaccagga	agcttctctc	cagttgtctt	gcctccttcc	170037347
tctccagtct	ccatggagct	gactttgaga	attaactcct	gagggacaga	170037397
gaccctggga	tggagagcca	gccctgctgg	attccacaag	gtgctgctta	170037447
aagcacaaca	cctcttccca	atgacagggt	ctgaaagaag	gccttgtagc	170037497
tagatgcaca	gagggttttg	ttttgttttt	ttttttttaa	cctttcagca	170037547
tctgtctaaa	attgctctgg	gctgggtaca	gtggctccca	cctgtaatcc	170037597
caacactttg	agagctgagg	caggaggtac	gcttgagccc	aggcgttcta	170037647
gaccagcctg	ggcaatatag	tgagatctct	atgtctagaa	tgtttttttaa	170037697
ttagctgggc	ttgctgcctg	cacctgtaat	tccagctact	tgggaggcta	170037747
agggtggggg	atcactcgag	cccagggggc	tgaggctgca	gtgaaccatg	170037797
attacaccac	tgaactccag	cctgggcaac	agagtgagac	cctgtctcaa	170037847
aaaatatata	tatataaata	aataaataaa	aataaatggc	cagggtgcagt	170037897
agttcatgcc	tgtaatcctg	gcactttggg	aggccaaggc	aggcggatca	170037947
cgagggtcagg	agatcaagac	caccctggcc	aacacgggtg	aaccctgtct	170037997
ctoctaaaaa	atacaaaaat	attagccggg	catggtggca	cgcacctgta	170038047
gtoccagcta	ctcaggaggc	tgaggcaggg	gaatcacttg	aaccagggag	170038097
goggagggtg	cagtgcagccg	agattgtgcc	actgcactcc	agcctggcaa	170038147
cagagcaagc	ccccatctct	aaaataaaaat	aaattgctct	gtaagttgac	170038197
accactaaaa	acatcattag	tagttgtaat	aattaagata	aaggagaaaa	170038247
ctgtgcagag	cccagcacag	tgctgtctcc	atggaaaatc	ctaatagacat	170038297
ttagtttccc	tctctttgcc	cccattttct	tatctataaa	acagaaataa	170038347
tgctgtatcc	taactcaaaa	gttgattatg	gagagtggca	tagtattggt	170038397
tcaacaaata	tttattgaga	aactgcaaca	cgcaaataga	tgtaaaagggt	170038447
tgaacagaac	tttgcaaatt	aaaaatccta	aaggacattt	tagaccttat	170038497

FIG. 1.124

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gaacttccta	ataggttaaga	ctttttaatac	tatctgcagt	gtccaacagg	170038547
tgcaagagct	tgggcggact	gtgaatatct	aagaaaagag	agagagcaga	170038597
aaggagggag	gaagatgaaa	gaaggaaggg	aggaagatga	aagaagggaag	170038647
ggaggaagaa	gggagggagg	gagcgagggg	ggcgggggag	ggagagaagg	170038697
gggaggtagg	gagggaaaga	aggaaggaaa	ggaaaggaaa	ggaaaggaaa	170038747
ggaaaggaaa	ggaaaggaaa	ggattacagg	tgggagggag	ggaggaaggg	170038797
agatatcatt	attattgtgc	aattgttatc	attatataac	taattttaaac	170038847
aaacccatcc	tgtgcccaca	aaagggcacc	aagataaagg	ctaagataaa	170038897
gaacacacga	atcatttttc	cattttcgtc	agtgatggga	atggtaaatga	170038947
ttttctctct	gaaccataac	catcttgcag	ttaaataatt	gctttctgat	170038997
agaatcagga	gctctgagat	ggtgctctga	ggagttcttt	cattttctttc	170039047
gcacctttta	aagaaaagaa	aacttcaagt	gcaattattg	gcattatttt	170039097
aataccgact	gcagcagaac	attctggaaa	atgaggcccc	tatcaaatta	170039147
gtttttccaa	atgaggttta	gacagtacct	taccaggaga	accactcaga	170039197
aagcccccat	ggcagcagca	agccctgttg	agtcaagggc	acatggatgt	170039247
cacactgcac	atgtgttttc	agataactaa	gtgaactgct	ccgatcttgt	170039297
gggtcattgc	accacggggc	ctctccattt	acttcaggtt	acacagcaac	170039347
aagcaagctg	agagcagcag	aagtagctag	ctaaaattgc	atttgatttt	170039397
gtgactgcta	gaggccaata	ctcaagtga	gtttaagcaa	aaacaaatca	170039447
tactcagctg	aaaacatttg	cctggaagaa	agatctgtgg	ctggagaatt	170039497
ggagttcatg	cacccagcaa	tttccagagg	aagtctgatt	cccctacctg	170039547
aagtaacact	ccttcctctc	cccagatcca	gatctccaga	ctatacgtac	170039597
tcaatatatg	acttgtccat	ggggcccaga	tgagcattat	tgctcttagc	170039647
ttatggttaa	taataacagt	aataattata	ctaataattat	tctttctatg	170039697
cataattact	aattcatctt	aatctcacia	ctctatgaag	tacatactgt	170039747
gaatgtctct	gttttacagg	tgagaaaact	taggcacaga	gaagttaagt	170039797
aactcatcat	agtcacagag	ctaagtagga	ggcagagtta	agagtcaatg	170039847
taggcttctg	accagagat	tgtgctctgg	acctctgtgc	cacactccca	170039897
cttactgggt	atcagggact	gtgctgagca	gtttatggca	tcatctcatt	170039947
ttgttattgt	aacaacccta	tgctatgggt	atcagtatta	ttcccaggta	170039997
aggaaactgg	ctccttttgg	agcttgagtg	acttatcgtg	gtcacacatc	170040047
tagtaagtgg	cagagataaa	attgaaaccc	agagctaaaa	ttgtttggca	170040097
aaaacttggc	atttgtgatt	gtgaccatct	tggtttccaa	gacgcctggg	170040147
ggactctgca	gaccatggcc	agtattcatt	tgtcaagatg	caaggaccta	170040197
aactggaatc	cagtctttta	tgatgtctgg	atcataacaa	aagtcaggta	170040247
tctgtcccat	gaggccagct	aatcccccca	caacccca	tccccctgac	170040297
acacatcatc	ctcacctaga	gaaacctttt	cacaaataat	caaacctttg	170040347
tttctttaag	gcaaattggac	ctaaggggaa	aaaaaaatgc	ctgtcagtat	170040397
tgataaggaa	ttgaagagga	ccaacaatgt	gaagattctt	ggccaaaaaa	170040447
ataaaaatagt	aatttgggac	aaatttagta	agagaaatat	cagaatctat	170040497
gcaggctcac	atctccaata	caaacatatt	caccttacac	tctatatgga	170040547
aatagtaaag	agcaatttgt	gaaatagatt	ccatgagtg	cccaattagg	170040597
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caccatttct	aggaaatagt	aggtaagtct	ttctggttgc	cactgaggtg	170040947
actcacctga	gacacagttg	ctcctaaagt	tcaaggttag	gagacaatcc	170040997
agaaggggag	ctgtctgtga	agtcagaatt	cttggaagaa	tgtaagtctt	170041047
tacacagtaa	cagcaaagca	gacagtggga	accactactc	tgcttcttgc	170041097

FIG. 1.125

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catcattctt	tcctagaaat	accagaaagc	agtgagggat	taagtcta	170041147
tcctggcacc	tgaccttata	tctaacagat	gctcagtatt	acctgttgat	170041197
gggacctcac	tgggaatgtt	ttgtgtgcag	tacaaaaggg	caatagatga	170041247
aactttggga	cgggagccca	ggaaaatggc	tgagaggaga	gcttatgcct	170041297
agcttatgca	tgagcttgca	aaaagggaga	atacacggga	gggaagatca	170041347
gcaacagcat	gagttttata	aggcagagag	ttgttgggaa	ggaagcagca	170041397
gggagagggg	aaggagtaag	tagaaaccta	gaagagatac	agctaagata	170041447
agccaagaga	acaaagtatt	gacttaccag	aaacatggaa	gtcttcctgc	170041497
ttctaattta	gttccgcata	tctggatatg	tgaatgccta	aaatcccatt	170041547
aagoccagtg	ggttaattat	tacacttgct	agggccccag	aggagaggaa	170041597
acacagtaag	tcagaaaaac	ctctgggcag	gtgaatttct	cagggtttct	170041647
tctgggcaga	tgggatctgg	aatggtagcg	tggcatcctg	gtaattcaga	170041697
gacagtgggg	aggggtgaaga	aacactgatg	tgtagcattt	ctgtgggtgc	170041747
aacaccctac	catggctgat	ttcaagctga	caaagggttta	gcaactgcct	170041797
tgctgatttc	ctgaaaattt	aacaattagt	tttcatgaga	tgcagtgggc	170041847
tgaccccagg	acatcactgc	ctacacgcca	atgagaatgg	agattgacac	170041897
aaagaacaga	gtggagagac	acagagcagg	gaagacaaga	ttttcccag	170041947
tctcaatcca	atatgtagac	tatgtctccc	ttttcacaaa	gaagggaagg	170041997
gaggagagac	cagcattcac	attcagttat	tgttgtttta	aatccattac	170042047
gcacatacat	aggagaaaat	ttcagcaaca	gtcaccctct	gaaccagtt	170042097
cctcagttct	ctccagaggc	aactaaaatg	ctcaattatt	agtgtatcct	170042147
tttggaata	ttttatgtat	atgacagtgt	gtgtgtgtgt	gtgtgtgtgt	170042197
gtgtgtgtgt	gttcctttcc	aatattaaaa	taatattaac	attggtaata	170042247
gtggtactaa	acaacttagg	gtgttttttt	tttcatttaa	tagtatattt	170042297
ttagtatctt	tccaggaaaa	gatacatgga	tgtgccacat	tattttta	170042347
ggctcacatg	gtactccttt	tatgtatgca	ctataattta	tggaaaccagt	170042397
tttctcaccg	atgagcatgt	aagttctttc	agtcttttac	tgttataaac	170042447
gaatgatgca	atgaatatcc	ttgtacatat	atatttgtgc	gcatatgtag	170042497
gtatccttac	aagtgggaatt	tctgaataaa	tggatatata	caattttatt	170042547
atgaatttac	cttccctacaa	gtgattcaag	agagtgtctt	tgtctcacag	170042597
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aagcaccttt	ccccaccagg	ctcactgctg	acaatccagt	gtacgaagaa	170042847
gggaaattac	ccccacagag	cccaaaagtt	taggacatgc	cgacagcatc	170042897
actcttttgc	ctcctcattc	tctctttcat	ttccagaaca	tttgctcact	170042947
cagtgtctgcc	cagtgatact	tagccagcct	gattacccat	ctaataattt	170042997
ctgatactaa	tataaaacct	tcccaaagac	aaatataact	gagacgcact	170043047
ccagcttacc	atagctttcc	tgggtggtaca	gtttccaggg	acatttcact	170043097
gtgtcaaagc	agggaccaca	tatgttccag	accagcttgt	tgggtttttc	170043147
actgggaagt	gaagacaaat	tgttgtccct	ttgaaaaagc	atctttcatc	170043197
tctccatcta	tctgcgatct	aaagcaatgg	ggctctttct	gtatgtcttt	170043247
caaatggtct	acactgacac	acgttttctc	tgagctgccg	agagaatatg	170043297
ccatgagatg	ttgccagtga	tggttacact	cagctagcag	aagattaggg	170043347
actgggttaa	cctttggaga	aattgccttg	ggaaaagagg	aaataaaagc	170043397
aaatattact	atgaaacata	gagattacca	ggtaggagga	ggagagaggt	170043447
ggagggaggg	gtaggagtgg	aaggaaggga	gggaggcaga	aagaggaagg	170043497
cagactggtg	gaaaataaac	cgtgcacttt	agaacagcag	gaaggggaggc	170043547
ttggaagcct	ggttttctgg	ctttgaatga	ccgcctagcg	cttgccgggtg	170043597
cgccagggtg	ctgtgaggat	gtgggcagag	ggcgagtcgg	aagggtccca	170043647
gacactggga	atagtgggtg	tcgtgtgctc	ctccctgaaa	cttttgcact	170043697

FIG. 1.126

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acctcggact	gattgacttg	tcagacggta	agcgaaccct	ggagcttccc	170043747
cgttttctgt	gaatgtgttt	ttgtggcttc	ggttgctgtg	acagtcgttt	170043797
cgaaaatgca	cggaaatgag	ggcggagacc	cgagagattt	gaaaaagccg	170043847
ggctgaaaca	gcgtgggtatt	ggcccccgcc	tccccagtcg	cgccccagtg	170043897
ctgcgctgtc	cgtcgtgctg	aaatgtgggtg	cgccctgggga	gtgcggggagc	170043947
caggaagtta	gggtctcctg	ctccggccct	atgagcatgt	gagtcttgat	170043997
ggattattag	ctatgggtga	ggccagcaca	acacatcaca	attctctctg	170044047
aagctgtctg	gtaactacgt	atattgttga	tggaaagccag	tgactttttaa	170044097
aagccattat	gttgattaac	tttttttaaag	aagttagga	gattatatgg	170044147
aggtaaaaac	ctttgtaaaa	tgctaatacac	agtgtctgac	aattagaaca	170044197
catttaataa	atgtcagttt	ctttgctcaa	cccttataag	aacccttatt	170044247
ccaaagccac	ctcctcagct	ctgacttcag	ctccattcct	tagtgagaat	170044297
ggggttataa	atccagggtta	acccgattgt	ttaggattag	aaagtgattt	170044347
ggtttccaac	gttgaaggag	ttcaagaaac	aaagagtttt	atttttcctc	170044397
cttatgagat	attgttccaa	atagaacaca	gtttgtctag	atgatttttg	170044447
tcacttaaaa	ttaggtctca	ggaaagattc	caaatttcac	gagcaattgg	170044497
gctcataaaa	caagatcaaa	ctccaatagt	gtatatccaa	agtatgtata	170044547
atgtgtattc	ggtgtatatt	cttcaccac	tgcatgggtg	agacagaatt	170044597
tctcttccaa	ggggcaccac	atgacaaaac	cgtacataat	aatgaaatgc	170044647
attttagtag	aaaggactag	ctaaaatacc	aagtgaaggt	gggaagacca	170044697
gaaactgaag	tgtaagatga	ggtaagccct	ggagtaagag	tcaagaaatc	170044747
cactttctat	ccataatctg	tctcgggtta	atggttggtca	agtcattttt	170044797
taaaaaatte	taggtcttgg	tttccttatg	atgactttag	atctctgttc	170044847
cttggaatc	tagagtgate	caaagggttc	tttgaattca	gttttgtggg	170044897
ttgagacggg	cagccagact	gtgagtcctt	cagctctgct	tcaaccagaa	170044947
cagctccact	ttactgttca	gcatgttagc	cctgtatgta	aggatgtttt	170044997
ttagcttttag	ctaaaattta	gtgactctat	gaccctaagg	ccctgcttcc	170045047
ctgagatttt	gaaagctgaa	gcacattcgg	aaaacttttt	cttccttaaa	170045097
aatcacctga	aatctgacaa	tctggaagac	tagttctgtc	tgctccagcc	170045147
cttggtccct	tagatgtgct	tttctgaaga	tccaaactca	acctgccagt	170045197
caatatacca	actgagcaga	gcccctgttc	tccaccagat	ttcaagagaa	170045247
catgttccat	tcctgttcag	agcttcagag	cagcttccgc	taagattgca	170045297
cattaatgca	acagegtcct	attttctttg	tttctttttt	tttttttttt	170045347
tttttttttg	atgagacagg	gtttcaccat	gttggccagg	ctgggtctcaa	170045397
actcctgacc	tcaggtcatc	cacctgcctt	ggcctcccaa	agtgtctggga	170045447
ttacaggcgt	gagccaccgc	atctggccaa	gcttcctact	ttcttataag	170045497
gctaaagtgt	cagtagaaat	attccccctg	tcttcctttc	catatcataa	170045547
gtatccatct	tccttccctt	gctttaactt	ctcatgattg	cagtttttgt	170045597
tttattacaa	taaaggatat	caatcattca	tctaagtgtta	tagcaatgag	170045647
gggattttaag	gtgaaaggta	gagaacatat	gttgagaact	gtttctggaa	170045697
actctagggt	aagaaaaaga	agggaaattaa	cattttattca	acacctacaa	170045747
tgtgccagggt	acagtgtctaa	gtgcctttat	atacatgagt	taatataaac	170045797
ctcaaaaataa	tgctctaagg	aaaacatttt	aaataatgct	gaagttaaata	170045847
atcatgattc	cttttatata	aggaagaaga	cagatttaga	gaagttaaata	170045897
aaaatttcca	aaaatgcagc	aatagcaagg	tggagggtatt	tgtctctaaa	170045947
atttcaccct	ctgttctgta	caccaagtac	ctcagcaagt	aatccagttc	170045997
cagatgggat	ctgcagtctg	ccattaaagtc	tttaccacac	ataggctctt	170046047
atgctagagc	ccttaccata	tgggtccaaa	tgccattttt	aatgtgtatt	170046097
tgatatggag	actctgttca	caatttgagt	actaaagaga	gaataccacc	170046147
tcctagtaga	tacaccagga	ccaatgtaat	gctgtcattc	taaggagagc	170046197
agtggaaacat	ctccaaagaa	cccattctgta	gtcttccttc	ggcccttgat	170046247
cttattccta	ttttattttt	aagggttttt	tttttttctt	cgagactaaa	170046297

FIG. 1.127

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tctcactcta	tcacccaage	tggagtgacg	tggcatgata	tcagttcatt	170046347
gcaacctctg	cctcccggac	tcaagcgatt	ctcctcactc	agcatcccaa	170046397
gtatctggga	ctacaggcat	acaccactat	gccagctag	tgtatgtgtg	170046447
tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgttagta	gagacagggt	170046497
ttcaccatgt	tgcccagggt	ggtcctgaac	tccagagctc	aggcgatcca	170046547
cctgccgagg	cctcccaaag	tgctgggatt	acaggcatga	gccacagcgc	170046597
ctggccaatc	tttttagggat	aatttttagaa	cagtatacag	atattgagcc	170046647
aagagtcaaa	agagctgggt	tgcaattctg	gttgtgccat	ttatcagttg	170046697
tgtgaggtgg	gacaagtctc	tttttctccc	tagctttctc	tttcctcatt	170046747
tataaaataa	agaaatgaga	atgatagttg	tattaatttc	tgaggactgc	170046797
cagaacaaat	tactacaaac	tgggtggctt	aaaacaacaa	acattttattc	170046847
tcacatagtt	caggaggcta	gcagtttgaa	atcaagttct	tgacaaaactc	170046897
ccctagagtc	taaagtctct	agagaaggat	tccctccttg	ctcttccagc	170046947
ttttggtagc	tccagtgttc	tttggcttgt	ggcagcatca	ctccaatctc	170046997
agcctctagt	ttgtggtaat	gtattatgac	agtcttagga	aaataatata	170047047
tcagtatttg	gaaatgtttc	ttcatttgcc	acaatatgat	atcaaataaa	170047097
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ctagtgaatg	taaaggctta	ggtcaacttc	tctctgcagt	tccaaggagg	170047197
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tccctgggtca	ctggccacac	aaggacctgg	catctcccag	taaatgtgtt	170047297
cctctgcaac	ctgagccaca	aacctctctc	tcttttatct	ctttcctctt	170047347
tctaccttca	tatttggttg	gctattttta	gttcttctgc	agatatagtt	170047397
acactttaaa	tgacacacag	cctttaatta	cttacatgtt	gacttgaagc	170047447
aatgtctgtt	gctcaccttc	ttggaaatat	cagaagacaa	gaacactttt	170047497
acttctctct	ccttctccca	tccttctctc	tgtctactta	atctgtttat	170047547
catattctca	tttttacacc	atcaaggttt	ataatgctcc	cagaacatac	170047597
ctccttcaag	gtaaatggga	atggtaacct	ttggcctctc	cttgcccata	170047647
aggacaaccc	agtctcctgc	tctgcgtggg	ttcccaattt	ggccctaaga	170047697
cttttctgtt	tgtatgatca	gcaaaaggac	atcaaatact	ttccatcctc	170047747
caatgagcag	aacacattct	gtggtcagaa	gccttctcat	tacttctgat	170047797
ctcaaaggga	catccagagt	tgcccaaacc	caggccaacc	acccttccat	170047847
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cagatcccac	tctgccaaact	gcctaccta	taccagact	cttgagctg	170047947
agagagtctc	ttctaaaatc	cagcccaaaa	ggcacactag	atgtgaggac	170047997
cagaatatct	tgtattttgt	agtctattat	agcaagcata	ataaacttat	170048047
ttgtttgaga	ccgagtctca	ctctgtcgcc	caggctgaag	tacagtggca	170048097
cgatctcagc	tactgaaac	ctctgcctcc	cgggtttaag	cgattctact	170048147
gcctcagcct	cctgagtagc	tgggattaca	ggcatgtgcc	accgtgcctg	170048197
gctaattttt	gtatttttag	ttgagacatg	gcttccccat	gttgaccagg	170048247
ctagcctoga	actcctgacc	tcaggtgatc	caccacacctc	ggcctcccaa	170048297
agtgtctggga	ttacagggtg	gagccactgc	ccagccgata	aactttaaaa	170048347
ttactttttc	tattccatat	catagattct	gggaggaaac	aaggcccaat	170048397
ttgagtaaaa	gcaactgcat	ttagctggct	tgaacttctt	cagagaaaga	170048447
acaacataaa	atattcagct	catctgattt	tttaatgaca	tttccttttt	170048497
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gcattcagag	tgagcagatt	cctagtactg	acataaggag	gatcaccatc	170048697
taatttttaa	attttaaaaa	atgaacacaa	agtctattag	aggaatgaaa	170048747
tgaacctgct	ttgtaggtac	ataatatttc	tctctccaga	gagaaaggag	170048797
gagagcacac	ataagatagg	aagatgagag	ctacaataaa	tgagagaaga	170048847
gagaaactgt	cagaaatagc	agggcagaaa	gagggaaaga	ggtgagaatg	170048897

FIG. 1.128

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agagagaggg	ggaggggagga	acagaggaag	atgcgaacaa	ggagagtcac	170048947
tcagttctga	ggcaagcact	tgattctccg	tggttcattt	gggtatccaa	170048997
gtaagttatt	tcctataatc	attggccttt	aggagtctgc	ttagctaatt	170049047
aacagtttgc	aaattgccaa	ttgttttttg	ccccgcattc	tccagagact	170049097
ttacactgca	aaggcagacc	acagcagccc	accttacact	tgagttgtgg	170049147
ccaaagcacc	atccccacca	gacaaagcca	gccccacagc	tgaccccggc	170049197
ctgtgagtg	ctgaaaactg	gctgtaaaga	acattctgtc	tagttacttc	170049247
ctcagtaaac	tctggggctg	ggcactggag	gttttctgaa	aggaagtgtt	170049297
tggtgtctca	cacagccatg	tgcttagtat	attccatgca	gcactccact	170049347
gagccagtgc	ccttgaaatg	agcaagcact	gcagccatcc	tcctttattt	170049397
ccctcaaggc	aatatccaag	gattaaaaag	tcagagccgt	ctgcagattc	170049447
ctcctctcta	ccttgccctg	cactttttgt	gcccttcctc	ttccccctct	170049497
ccagccccaa	acctctctcc	tgatccacgg	tactcctcct	gggatgtcca	170049547
ctggggctga	tcctccccca	ttctccccct	gagttccctg	ctgttaatct	170049597
gtctccagca	aaattaacct	agcctatgtc	ccatgccttc	tggaactctgg	170049647
ctgctcgtca	atcactctta	aaaatccggg	ttctccttag	gcaatcattt	170049697
tgttttgatt	ttatgtgtaa	aaaaacctga	gtaaattttt	tttttttttg	170049747
agatggagtc	ttgctctgtt	gctcaggcta	gagtacagtg	gcatgatttc	170049797
tgctcactgc	aacctccgcc	ccccgggttc	aagcgattct	cctgcctcag	170049847
cctcttgagt	agctgggact	acaggtgccc	accaccatgc	ctggctaatt	170049897
tttgtatttt	tggtagagac	agggtttcat	catactggcc	aggctgggtc	170049947
caaactcctg	accttggtgat	ccacgcactt	cggcctccca	aagtaatcac	170049997
tgctgggatt	acagaagtga	gccaccgtgc	ctggccaaac	ctaagtaaat	170050047
gttttaaaat	tatactacta	acatagcata	caggctttag	actggttggtt	170050097
gcttttaagt	ttgcttactt	taaaagctag	agagaagatg	gttgagggtga	170050147
tcttgtctcc	ttcagtatcc	actctgagcc	atgcctcctg	aggaagtttg	170050197
cttttagggga	ggcattgcta	tggtatacac	tctacgatgc	accagccctt	170050247
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ccttaggaaa	tagattttat	ctccttaact	cactttttac	atttgcaaaa	170050347
tggtgtaaatt	gtgactacct	cacatggatg	tcattgagatg	aaatgtaaga	170050397
atgtgtgtcc	ctggcatata	gtaaccactt	tcgccaaaga	ctgagttatc	170050447
caactacaga	cagagaacag	ctgggtggcct	aatcaaaggg	agatacaaaa	170050497
taacaatgcc	aagactggaa	aaggaagtgc	atcttaggat	ttccaagaga	170050547
aaaagaaata	tgactgtatt	ataataggta	tatttattaa	gctcttacca	170050597
tgtgccaaagc	aaagtctctt	atatacatga	tatacttcat	atacattatt	170050647
tcatttagtc	ctcatggcta	ccaggtgagc	accattattt	ttccatttta	170050697
cagatgaggc	acagagaagt	taagccactt	acctaggaag	ggcagtccta	170050747
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tctattatga	gaagtaccta	aatagagatt	ggtttaacca	aagcctgagt	170050847
cccaactaag	ggcaagactg	tgacacagag	gtcactaatc	agaatgaaag	170050897
attgagccag	agttgagttg	ttggaatgta	ttttgggtaca	tttaggttgt	170050947
tttaagtata	tcaatctcca	ttccactcaa	tggttgagtt	cagtttcaag	170050997
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cacagctgca	attctcaaag	gatggactaa	gccatgtcac	ccctccagat	170051197
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atggaagcac	actacctgtg	ttgtgggtcat	atagatcatc	acctggcttc	170051447
tccagggcta	accagtttagc	atggaaatgg	gacacccaag	aacaagagga	170051497

FIG. 1.129

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tagaaagaag	ggaaggggtg	aaagaaggaa	ggaagaaagg	gtgggagggg	170051547
gggaagagt	gtagtttttg	aaggaaggag	ggaatcagag	ctaaagataa	170051597
tacatgat	gagtcagtgt	tcaatgtccc	tgaagattag	gggaatcaag	170051647
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ttaggaagtc	agaggagaca	ttctttcatt	cattcattcg	ttcattcatt	170051747
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cagaaagaga	gccttgcat	tggaatacaa	tatggagtaa	taatacctct	170051897
gtgttcagcc	tgacacaaat	actctgtatg	catgggtcata	tgtcccttga	170051947
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aaactgaggc	ttagggaggt	caaataactt	gcccagtaa	aacaactagt	170052047
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agagaagagg	aaaaaagtca	tttcaaacag	aaagaacagg	ttgtgcattc	170052247
aaaggtgaat	tgagaggaga	gaaaagcatg	ttcaggaaaa	gacaagacat	170052297
ttgtggccct	gggagctgag	atatgccctc	gggaaggctg	gagatgatgt	170052347
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tcaaatacagg	ccccctctt	attaaacatt	tcaaagggtt	tctgttctac	170052497
ttaaaaccta	aaacccttct	tttgtatgca	aggcctgaac	agcctgcctt	170052547
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gtgggttatgt	ctgctctact	cacacacatc	cctactgcc	cgacagggtgc	170052647
ccagcacata	gtaggtcctc	agtaggggtg	tgaatgaatg	aacaaatcac	170052697
tgatgaatga	cgcccttaag	cagggatttt	tctccaaagc	ttcctcacac	170052747
cttggaaatgc	atttgggggc	ccaacacaaa	ggtttccaac	ttcaacagca	170052797
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gggtttctgt	ctttctccac	agcctgactc	cttctcaaaa	tctctctatt	170052897
cccttccaaa	tatacattct	aaatattttac	agaagcttgt	tatttctctc	170052947
agagctggcc	tagagttctc	ctgatatttc	aaagaatttc	caagaatagg	170052997
gaaatctcct	gatatttcag	agaatatccc	agaatatagat	aaagttccat	170053047
ctgacaaata	gatgctcagt	aaaatctggg	gagtgaatgg	attaatgcaa	170053097
aaactaatta	tcatgctggt	catggcaagg	gatatgataa	ttttttcaag	170053147
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ccaggtggca	ttcagtagac	atagactaag	cctcaacccc	agccctcagg	170053247
cacatcagtg	ccctctctag	gctctctctc	accaacttta	gaattgaatt	170053297
acatcagttg	tttccagatg	gtgatctgca	gaattccttt	aaagaccacc	170053347
tgtgggattt	gagggaggaa	aactacactc	tcccaatctc	cctctttaac	170053397
ccaagcatct	gattgctttc	atctgtttta	catacttagc	ttctgtgcac	170053447
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agccttttatg	cttcataatt	ccactttatt	gatgtaggaa	gacaaatgat	170053597
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tcattctggg	caaagaccag	aatttagacc	ccagttctgc	catttgctga	170053997
ctaatagact	tgggcaaaat	acttaacttt	cctgagagtt	agtttcctca	170054047
tctataaagt	ggggtaatat	aaccacactt	gcaggatact	ggtaggatta	170054097

FIG. 1.130

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gttgaaataa	attgtaggag	aacatttggc	tcagtgctaa	gcctatataa	170054147
atactccaca	agggcacaga	gagggaaatga	cttgcctagg	atctcctcct	170054197
ggaaatcaca	caacaattcc	actagtatca	tgtggcccac	aggcagctgg	170054247
tgggcacaa	cacactgggt	cagcattgcc	atgggtccaag	aggcttctgg	170054297
tgcccaggga	accagcaggg	tcccctgagc	gttcctcctc	agctcccaac	170054347
acttccctcc	aggcaccagt	atgcaggggca	aggtcctgga	gggggcgccg	170054397
aaacaccact	cgagatcctc	actctcagga	attcaatata	gaaaacacat	170054447
taagacctgt	ttacatggaa	ctgctgttta	taattattgt	tccctatggg	170054497
atattcccca	ctgcttcctc	caatcctcct	ttaaactgct	caactaatag	170054547
agttttcctg	gcttccccag	ggagacattc	acagatgcta	atagagacat	170054597
aattcaaaaa	ttgcttgata	tacatgccct	caattttccc	caagaaccac	170054647
ctaagtaaag	agccccagac	atgcaacaca	ttcattggcc	agatgcaatt	170054697
taacatgcgt	gggattaaat	atacaggcta	ctacagccag	gttgtcatca	170054747
agcagcagca	ggcatggcat	tttatcctaa	ggtaccacca	cggccaaatg	170054797
caacaggaaa	gaagcaggct	gctgggtggg	acccctggaa	gatccccctc	170054847
tctgtaattt	ccactgcaag	cttttcccag	gccttttcag	gcaaagcggg	170054897
gagttttgaa	aataaatccc	ccaggcttgg	agaagcaaag	aatcaatgct	170054947
aagcagctcc	ggaaataata	gcttccatct	ctctgatata	taaagaggat	170054997
aaggaaggca	gaaagaaggg	gcatgatatt	atgagattgc	aacaatacat	170055047
tgcaacatta	cattaaagaa	ttacagaaag	caagatctag	cttcagatgc	170055097
cagttcatgc	acttactccc	tgtgtgaccc	tgggaatcac	ttaagctgtc	170055147
tgagacttag	cttgtcta	gacaaaactg	ggatacta	atcacctccc	170055197
aggattgttg	ggaaggtaaa	tggagattga	caaagtgtga	cacacttagt	170055247
atgtctttac	atagtaggta	ttcaataaac	cttctatat	atcttctcct	170055297
tctgaaaatc	tgaatatggg	gagcatggat	atgcttatat	gttggttaaa	170055347
caaatgcatg	aatgttgagc	aaatcagaaa	atactaaaat	tagaagacta	170055397
aaaggagtaa	actaggaccg	attaaaagaa	gtttgccttc	ccaaaactc	170055447
ataaaacttaa	tgaaacttgc	tatctccaga	ggaaattaat	ataaatttaa	170055497
aatagcatag	gtttgagatg	actttagcgg	agtttctgga	gaatagatcc	170055547
atcactgggt	aataaactaa	aaatatagag	agaactgccc	aaggttacac	170055597
gagtagaata	ttggtgtccc	caccactcct	ttttattgca	gaggggaattg	170055647
acattcaggg	aatggaaatg	cccagcccag	aattggggat	gtggtctggg	170055697
aaaccaggtc	tcccatccca	ctccctcgcc	ctctcacccc	ctcccgtctg	170055747
tcagtgttct	ttgtcctctg	ctggcatccc	tggggacggg	ccagccccc	170055797
tccccccgac	acacacacat	tgtcccttca	agatggagcc	aggctgacac	170055847
cacgtagaat	gacctggaag	ccccactca	gtctaccagt	cctccctcct	170055897
cacacaggaa	tagatgggag	ggaaatgaaa	taagctgcca	tctgctgtgc	170055947
atcctctgtg	tgccatgctc	tgggtaccca	tctaactcct	gtgaagaccc	170055997
tgagaagtga	gtgttcttca	cagactaggg	aacaccagaa	ggcagggtgaa	170056047
gaacgtacag	aagctacaga	gtgcacagg	gacaggatat	agagccaagc	170056097
cattcaaact	ccctgggtat	aggacccagc	tcttcccacg	tctctgcctt	170056147
taccgaatca	aacacctgag	cacggaagac	cctccatcaa	catgaactgc	170056197
tttgaattga	catgaacaag	cttcaatcaa	actataaatg	ctgaaatttt	170056247
tcaattatag	aaagtatttg	aaagatccca	taaattcccc	tgtcatatca	170056297
cgtgagctgc	atttactgca	gcagacactt	tttatctcgg	gcttggagga	170056347
aggattagca	agaagaaagt	ggaggggggtc	tgaggaagg	ctggcagcct	170056397
agaggaggac	agcagcaaga	agcaggctgg	aggcagttct	gtgctgccgg	170056447
ccttcatggg	tgtggccttt	ggacagcacc	ttagcaggaa	tgtggtggag	170056497
agcagcccca	ttcactccag	aggagagcct	caaactcttc	aggcagatct	170056547
agcctaggta	gaatcttggc	ctggcccttc	cgggatgaca	ggtgccattg	170056597
cccaagaatg	gggaaaaggc	tgaagtgtc	cagccaaaga	ccccaattta	170056647
tcttcaggac	aattttcact	ggaaaccttg	cctcaccact	gccactttt	170056697

FIG. 1.131

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tcagaagtaa	ttagaatgct	aatctataag	aaagatgact	attaaaaata	170056747
aattaataat	agataataca	ttttggctta	caattttgaa	taatatagcc	170056797
atcccatctt	aaagtaaaaa	ttcatatatt	tttaataagc	ctgagacatg	170056847
ttttccaatg	aaccacagat	ggttcatttt	tattatccta	taaagagaca	170056897
ttatgggcaa	gtgtttttta	aaatggtaaa	acagaacctt	agagcagctc	170056947
tcttttgaag	atctctaagc	actttctaag	catcaggacc	cccttctgtc	170056997
atcacagaga	ctgaaatgag	gagatggctc	ctgtcacccc	ctcactcacc	170057047
agtgaagccc	agaccttcac	ccctgatcag	atggaagcag	tgtggcatga	170057097
ttacagttca	tatttcaact	ctgccactca	atgactaata	gccaagcact	170057147
aataatgcag	aaaatgtaaa	tttaaaaaat	aatcttcctg	agattgggtta	170057197
tgaaatgcac	tcaacacagc	accatccaca	gagaggttct	ttttaattgc	170057247
tcttttcttt	cctctcgaca	cccagaatca	caaagcatgc	ctgaaagcgt	170057297
cacacatata	tgtctgtgac	cataacatgg	cattgcacat	gcaaaggaaa	170057347
taaatagggtg	ttacccatgt	gacaaagggtc	catgagctct	gtccgcaaaa	170057397
agctggttag	tttaaagaac	aaataattct	gaaaaatctt	ccaggagatg	170057447
aaattttag	aactcaaggg	cagtaaacta	gtgtctttcc	aaggacttgt	170057497
catagcttta	ttgacttaca	atagccaaag	ataagtcagt	attaatcaaa	170057547
ccattctct	agaaaaacct	catcatcact	ggggccagg	cagagaagtg	170057597
tgacacagct	ctctccagct	tcccacttc	acagcatgg	tccaccatcc	170057647
acccaattgc	taaagcctgg	atagtcttcc	ttgtcacctc	ccgatcccct	170057697
tctctaacac	ccatcccccg	gccacccaac	atcagcaagt	ctgggtggtt	170057747
ctctctgtca	cagagattca	agatcttccc	ctcatctgtc	tgtttcaaag	170057797
ttaacatcat	ctctcatcca	gacagttgca	acactctcct	agcaggctcct	170057847
tctgcatcta	ttttttaatt	aaatttttaa	agataaaaac	attcctctaa	170057897
atagaatctg	ctccagaacc	cagattaaaa	aagaacgaga	aggggggaaag	170057947
aagattaggg	catcccagaa	gctccctatt	tgccccattt	gattcattac	170057997
tccccaaggg	taactgctat	cctgacttct	agcaacactg	gttaatttcc	170058047
gttgattttg	cactgtatat	tcatccgtgc	tggttgacac	tgtcatactt	170058097
gattcattca	cattgctgtg	taacatttca	ttgtgtgact	attttaacat	170058147
ccattttact	gttgaacact	tgggtaaact	tctgctttga	ggctattata	170058197
aacttgacac	ttctgcttcc	cattgcttta	aagataagag	cccaagtcct	170058247
tgtcagacag	gtgaatgggtc	cacacagtta	gcatectagg	ctgggocgcg	170058297
tagctcacgc	ctgtaatccc	agcactttgg	gaggccaagg	cgggtggatc	170058347
atgaggtcag	gagatcgaga	ccatcctggc	caacatgatg	aaaccccgtc	170058397
tctactaaaa	atacaaaaat	tagccagggtg	tggtggcatg	cgcctgtaat	170058447
cccagctact	tggaaggctg	aggcaggaga	attgttcgaa	ccagggatcc	170058497
gaaggttgca	gtgagccgag	attgcaccac	tacactccag	cctgggacag	170058547
agcaagactc	tgtctcaaaa	aaaaaaaaaa	aagccaggct	ttttctcatc	170058597
tcataatctt	tgcgcatgct	gttccctctt	cctgaaactg	ctttcctacc	170058647
acttctcacc	tttatgcttc	acctcgtagt	gttcatagac	tctccttccct	170058697
tcctaactta	aaagaggctc	cttctgggtt	ttccttcata	cacttccctc	170058747
actcttttcc	ttcactgcac	taaagatgat	ttctaattgc	atagtcattg	170058797
atgccagtat	tgttttatgt	tgtcattcct	gctgaacaga	ggatgggcct	170058847
gacttatgtg	ggaccatggt	gctgatgcct	ggacctaagc	ctggcacaga	170058897
gtaggagctc	aacaaatttg	ttaaatgagt	ggctgaatgg	ccatactctc	170058947
aaaggaccca	cagtctagga	gagacagaag	aatctttgtc	tttttgtctt	170058997
gcagtgggat	ggaagctgca	gggaggggtc	ttgtcacatt	gatactgtct	170059047
ggggaagaca	gaaaaacttc	agtttcagag	gaggtagccc	ttgaaacgag	170059097
atgtgagaga	gggcagcaca	ttgtacaact	ccatgggcac	catgcacatt	170059147
gtagtccaga	taaacagagc	cccttgagga	tatgtgaggc	atgggataga	170059197
ctcagagaaa	cccaggaaat	aaccccttca	ggcatctgac	atgcaaagat	170059247
gtggaagtgt	caaccaggaa	gtcatgttgg	gggaacagca	agtatttaca	170059297

FIG. 1.132

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gaaagtgact	gtgtgtgtct	gtgtaggagg	gtgactttgt	ataggagaga	170059347
taaaacctgt	gagctaataca	aggagaagat	cataaaagac	cttcataaag	170059397
agcatggcct	ttttcctgca	agcagtgagg	agccattgaa	ggcttttagca	170059447
taaggacagt	cagatgtact	tccctagaat	gcacatttcc	ttctgctcca	170059497
gaacttctgc	acaggaggct	cctaaaagct	ctccccatcc	tcctgtaca	170059547
cgtagaatct	gcctctgtct	ctctttctct	ctcctcctcc	tcctccatct	170059597
cctcctcctc	ctcctctccc	tctctctcgc	tgtctcacac	acacatacac	170059647
acacactcct	tccttcctat	ctagtccagat	tcactcctt	gggatttcag	170059697
gcccaccgtc	actcctcagg	gaagcctgcc	ctgaatgcct	gcactacacc	170059747
agggccctt	tcccctgccc	ccatcccaga	gcaccaaata	gctttccctt	170059797
gcagcacttc	tcacagctgt	catttttatgt	ttgtgtctgt	gattcttagg	170059847
ttaagtccct	catgcaccaa	atcataagat	ctgggaacaa	ggaccacacc	170059897
tgtcctgttc	atcactgtaa	tcactcagact	gcctgccaaa	gtgccttgca	170059947
catattagat	acttagtagt	tatgtgttcc	atgaatgact	ctttaagaga	170059997
tcttctagct	gttcttgcaa	agaaccatt	ggtaagggtg	aacctacagg	170060047
ctgatacttt	gcactagtct	caggaagaga	tggtagtagt	atgaaattga	170060097
gtcccccaga	ggttaatgcc	cagtgcocca	gctaggaaac	gtccaaggag	170060147
gcaatttgaa	ccccatctgt	ctggctgcag	agcctagccc	tctaattgcat	170060197
tcaggggtcc	tagctcctcg	aggatgccac	tgtgccgtga	acttctttct	170060247
gaccctcatg	gctcccagca	cagcatccac	actcagaagt	gcaagatgaa	170060297
tgtttgcaga	taatgaacat	aaagctctca	ggaaccctca	tctcctgaga	170060347
atctgctttg	gccccacag	caggtctggg	tgtggacctt	ccccaatggc	170060397
cttgggaaat	tatcaacatc	tccccattag	ctgttgcaat	attaaattgt	170060447
gtgactggaa	atgaatgaat	aatcccatgg	gcaagtgagg	gagaccaagc	170060497
agcaggggatt	taataacaag	tcttgccctt	tctccaagca	gaaggtcttc	170060547
ctaattaaat	attaaaaatc	tatccataca	agcaagagcg	aaaaattgca	170060597
ttttcagcag	tgcagctttg	agatgctgcc	tcagaagacc	caagagctgt	170060647
gggaatgccc	tctccaggac	ctagaagagg	gggccagaaa	accgccatgt	170060697
ggtaagcact	gocgggtacc	cgggtatcac	aggccttgcc	acattcaatc	170060747
ctcatgggga	caatgagaca	ggggtagat	cacagccact	gtctaaatga	170060797
gcaaactgag	gcttagagag	ggtagtgac	ttaccaagg	ccaccaggta	170060847
tcaagtggca	aagttgggat	cttaaccag	ttctatgtgg	ctataaagtt	170060897
catggaatag	aatgctgcag	ttaagaacat	gggctttggc	atcaagcaga	170060947
cctgtatttg	agccccacct	ctgctgttta	ttactgtgg	ccctgggcag	170060997
atgaccttac	atccttaagt	ctctagttct	ttgtctttaa	aagggtggca	170061047
gaatgtacct	cactggtttt	aggaagggtca	catgagatag	tgcacatgaa	170061097
gccctaggca	tgggaaaatt	cttctaaaat	gtcagctgcc	attctgatca	170061147
ctgcaagacc	cccaccccca	atactcccaa	ttgtaccacc	ccacccact	170061197
caccagtgtc	tcagaaatgc	ctcctccaga	aggaaggcat	cctgtctaac	170061247
ccactgcttc	tagccaagct	gtctttcttc	agaaggtaga	aaaagattgt	170061297
tagtcattgt	ttaatcttta	ttgagtatat	accgccacac	caattgcact	170061347
gccattcatt	atctcattta	aatctgacaa	gagccttgta	aagtagggat	170061397
tattcccacc	atttcccaga	tgttgaaact	gaaattgata	aacacgacat	170061447
gttgccatgg	ctacatgaag	atctccaagc	cggaggatct	ccaccctcac	170061497
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agccctggcc	tctgggctcc	acccttcca	cattcatccc	agggccgctg	170061597
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ctttatgaat	ttcttcataat	acaaaaattg	tacttactca	ttgcagcaaa	170061697
tttagaaaat	acacataagc	aaaaaagaac	gtaacagcca	tcataaacc	170061747
taactctcag	agatcaccac	tattaaaatg	tttattatct	aagagagaga	170061797
tgatatagac	aaagatgaga	cagattgaca	cagagaagat	gggtacatga	170061847
tagatatattt	ctgttttata	acccttgctt	tttcttgcac	ttctaggaat	170061897

FIG. 1.133

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ttttctgaga	actaatctga	aatctgcaca	gggtccccac	gtctcggatc	170061947
ctcatcccat	tgctctccac	cttcttgaac	tttgcttcaa	taattatcac	170061997
acctcctttg	catgtttaat	cttccccctt	ttaatgacaa	ctaccaagac	170062047
ctgtttccta	gtgcagggtc	atgaggtaac	taaaataaga	attaaattgc	170062097
tctgtgaaaa	aaaaaaaaaa	aaaaaaaaag	tttacagtcc	caggagattt	170062147
tctccagcct	tatcatattg	ttgataccat	agggtcagtt	ctgaagctga	170062197
gcccactca	gccctaagct	ttctaaaggg	gaattgccag	gtccccctgt	170062247
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aaggagaaac	acacttcctt	ccccttccca	tgacttgtag	ggagtctagg	170062347
gtctcaggcc	tatgtcacag	gccctcgatt	gccatgagtc	agcaaggaga	170062397
ggaaggacac	gaagccagca	ggcagagagc	tggccccaca	gagccatcct	170062447
ccgtgaagcc	ccagcaaacg	ggagggacca	agtttgtttc	agttttccta	170062497
aaaataacaa	gactgtattt	tctttgctgt	tggctgtccc	taaaactgtt	170062547
aacatgggtt	cccagcctgg	cacaatgtgg	tccatgcctg	cctcccatat	170062597
acctgcctcc	cacccctctg	ggccttgttc	ccttcatccc	agcctccaga	170062647
cacacctgcc	tccgtgtcatc	tctagagcag	gcttatcttg	ttctcctgtg	170062697
ggctccttgt	agaggatgtt	ccctctgccc	agaacgctct	ccctcactca	170062747
tcacctgttg	gtcccccttc	cctccttcca	ggctctgtgt	caaggccacc	170062797
acagagaagc	cttgcggtta	tgtttagttc	ttcctgccta	agttcgcata	170062847
gtaaccata	cctttcctcc	atcataattt	gctcaactgt	aatcaaaccat	170062897
tattttttaa	aaatcattcc	agcctgggaa	acagtggaga	acccatctct	170062947
acaaaataaa	aaataaaaat	tagcttggca	ttgtggcata	tgcccgtggt	170062997
ccctgctact	caggaggctg	agatgaaagg	atcacttgag	cctgggaggt	170063047
tggggctgtg	gtaagccgtg	attgccccat	tgactcccat	tctaggcaac	170063097
agagtggagc	cctgtctcaa	aaaaaatatt	attcatttaa	tatctgttgc	170063147
caccacagga	ctgatccctc	tgtgaggggca	gagattgttc	atgcatggaa	170063197
ttgtgattta	taagcactgg	ctctggagcc	agggtgcctg	agcacggagc	170063247
cagctgtgcc	ctgcgggaca	cctgtggcac	acttcactcc	tgggacacct	170063297
gggacacgca	cacaatagaa	atgttcacat	tttactaggc	aatgccagtc	170063347
acatagtcc	acctaatttc	aaaagggtaa	aaggtaacac	caacacgcac	170063397
caggaaggag	gaggaccaga	aattgttggt	gacaagcaca	aatgaccacc	170063447
ccaataatat	attttgtttg	gaaggcattt	tattccacaa	aaacaacatt	170063497
acaataaaca	aaacaacaaa	acactgggtg	cagtagaacc	aactttccag	170063547
acctatctgc	acagcacaa	cattatccca	ctcaaatgt	catgttttta	170063597
ccaaaacat	taaaatttta	aaagcaattc	aaaccatag	cttaaaaaat	170063647
gttccaacca	gtaataaaag	gaaaagtgtg	cctcctcctc	ccaacttccc	170063697
tacccacaaa	tcgcaagata	ttatccttat	aggcgaaaag	ggtttcagga	170063747
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cttcaaactc	tttcttgtat	gtgagattta	attttcaaa	actcctctga	170063847
tccaacttaa	gctttatggt	aaatcacctt	gggacttaaa	tgatgagaag	170063897
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gagctctgat	ctggaaagtt	ccatcaaagc	gtcactccag	gcttagcggt	170063997
tgccacccac	cactcgtcag	actaaacagc	ctcagagccc	tgtgacctgc	170064047
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ctcaaactat	gcaagtcttc	cagctggccc	tccggcttgc	tgccctggct	170064147
aatggagtgt	tacgtggact	ctctgtaggt	tgcaccttac	tgcagccaa	170064197
gcaaaggcac	tcattaagaa	gctgagcccc	agggtcctcc	catgagtggg	170064247
gaggaaactc	atgagtgcct	tctatatgcc	agcgtcttat	ctgcaggggt	170064297
tcttttgata	gcagcagact	gagagatgat	gttactgtcc	cctttttcct	170064347
gttggttgga	actgagactc	agaggatgga	agtgacttgc	tcagggtccac	170064397
cacctcttca	gctgtggagc	tgcgacagga	gcctttgttt	gacttcaaag	170064447
ctcaccatca	ctcctctctc	actgatgctc	aagtgggcta	tcacctcgcc	170064497

FIG. 1.134

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tttcctgagc	cttccttcgc	tatcctaata	cagcgctcc	cgaaatcacc	170064547
actaaagaac	ttattcatgt	aaccaaacac	cagcggttcc	cctaaaaacc	170064597
tatggaaata	aaaattaaaa	ataaaaacag	tgccctcccat	gacccatgtc	170064647
tctccagtcc	cataactctg	ctctatttcc	attcacagct	ccatccccac	170064697
ctttatgtct	tttgttcact	gctttatccc	cagtgcctag	aagagtgtct	170064747
ggcacctagt	agacactcag	taagtatttg	tcgaatgagt	taataagggt	170064797
gtgaaaagaa	cgtagatta	ctggaaggat	tcatctgagt	ttaattctgc	170064847
tatgctggga	atccagtgtg	cggccttgga	tgaagccagt	tcctccctg	170064897
ggccccagta	gccacatctg	tacatttaga	gggcaggaga	aaagccacac	170064947
gctctgtgac	ttatacaact	tgttgcccag	agtggaggct	gctttgatgc	170064997
tcagaaaaaa	gaaacaaaca	tggaaatgct	aaatgggtgg	cagagagctt	170065047
gagggaggaa	ggagatgggg	aggggtactct	tgaaactgtt	tggtgtcttc	170065097
cctcctgccc	cctcagtacc	aattgtcaag	tacagaaagt	gaaggagact	170065147
tgtattagtg	gaatttggtc	cctgacttgt	tatagagaca	caattacaaa	170065197
gacacaagag	tgggcccagc	agagaccott	aggggtggtcc	cttgagggtc	170065247
caaagcatct	gcccatcaag	cagatgatgt	gattagtctc	tgtgaccca	170065297
aggatgctc	ctgaaattgc	tgattcaatt	tctcctaata	aaataggaac	170065347
aataattagc	taataagaaa	tcaacaatta	aagctatgag	agaattaagt	170065397
gagatcatgt	aagcaaagta	catgtcacag	tgctctgcaa	ataggcagtg	170065447
ctcagaagtg	tcaccttttc	tctttcttct	ctgagcctcc	gtcttctctt	170065497
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tgcttgggac	cccaaaaaat	gaagtctctg	catgtctcta	gaccaccacc	170065747
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gtgctctgca	aataggcagt	gtcagaagt	gtcacctttt	ctctttctct	170066947
tctgagcctc	cgtcttctct	tcggtaaaat	gagaataata	ttatgcatac	170066997
ctcacagggg	ttaagcaatg	tgaaagtact	ctgtaaagta	taaggctgaa	170067047
atgtactggg	ctcagaattg	gggaatcgtc	tggaaaggta	gaccagggcc	170067097

FIG. 1.135

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ctagcgtgga	ctcttcagcg	ccagcaggaa	aatctagget	ctgtcttgaa	170067147
ggttcctcag	caggaagggtg	gggggttggt	gtgggggtgaa	tctgatggaa	170067197
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tctcctgccca	tacaaccttc	ttttttattta	aaatagattt	aagcaggata	170067347
gagccccctc	ccccaccatc	aaggctggtt	ccttgtaggt	gggggggatgc	170067397
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ttggaaacag	gcagtatttc	ctctttttat	gatggtttca	ttttacattt	170067497
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gcgctgacat	ttatagaaat	caatacatta	ataaatcacg	aagttcataa	170067597
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gtctttcatc	cagagggttg	tgtttgctgg	tggccattac	ctttaacata	170068197
aaacgatcat	atttacttta	tcctattcat	gtccaacctc	aactgacaat	170068247
tgagttgtgt	ctctgacaat	aaatagcaga	aaaaggaaat	cttcctatac	170068297
tgaagagaaa	cacaattaat	taactagatc	catcaggaaa	ggtacaatca	170068347
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cgtgcttccc	aaagtatgat	cacttcattt	caacaacttc	acactaacag	170068947
cctgaactgg	gctgtgaagg	gaatatttag	accaaggaaa	ctggaaaact	170068997
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aaagagttgt	ctactgaaat	acactagctg	gtggcaggat	tgggacgtca	170069647
tttgactaat	tgccctcctag	agctgcagag	actgctggaa	ctacctaagt	170069697

FIG. 1.136

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aaatcatcaa	aaaaaaaaaa	aaaaaaaaatc	atcccagggc	actttttcca	170069747
gacaaaaagg	tccacttaaa	acatcctcta	gagatctgtg	cctgaagctg	170069797
agctgctgca	atgaaactga	catttctgcc	ttgcagcctg	gccatgggct	170069847
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caatcttgga	aaatatctgg	atgaatgtaa	cactgtcaca	cacaaacaga	170070047
attatgactt	acgtcacatt	ctatgtcgtg	attttgtgga	cttttaataa	170070097
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tctttgtgtt	tatcttgctt	gggttttgta	gtgctccttc	actctgtgac	170072247
ttgatataatt	tcactcattt	ttttaaaatg	ttcatttatt	agctcttttaa	170072297

FIG. 1.137

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atatacgttcc	attatcatta	tttatctctt	tcttttctga	gactccaatt	170072347
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gggtctctgg	tggaattatc	tagctttttg	tatatattct	tgaacaaatg	170072947
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cttttctttt	tctgcatctg	gttactaata	aagcttaatt	ggggaagaaa	170074847
gaatcaaaaa	ctttagtagt	gtaagctcca	agagaacaga	gaacagagct	170074897

FIG. 1.138

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gttttattca	ctgacttgta	cctagtagat	acttcattga	cagttattgg	170074947
gtggagtgag	caaacaaata	atcctacaag	atatgcagtt	tccaatcaca	170074997
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caagctcatg	ttttgtaatt	agtctttctca	tgaccagct	ttctgtgtcc	170075547
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ccttttacag	acatttgtaa	aaactcagag	cccatttgca	gctcaagtgt	170075697
agtaattgct	tcaaacaaat	ggcctggatt	tctgtgttct	ctttttctcc	170075747
atggtcttca	cctcctaata	taatcaacat	atactgaggg	agtttttctt	170075797
attactttat	ctctttttat	ttcatattta	tttctataaa	tcagcttcaa	170075847
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cagccggtgt	tcagctctag	caggctgctg	aagtgtctga	atttgagacc	170076097
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gtacatggat	ctctcatctt	ttaacatgga	caactaatte	caaaataatt	170076197
aagatacatt	ttacaggtca	aacaagacct	atctttgggc	cacactcaag	170076247
ccgaggatca	ctattttgta	acctcaaagc	tagacggatg	gccgggtgca	170076297
gtggctcatg	tctgtaattc	cagcactttg	gaaggccaag	gtgggcagat	170076347
cacctgaggt	cagaaacttg	agaccagcct	ggctaacgtg	gtgaaaaccc	170076397
gtttctacta	aaaataaaaa	aaaattagcc	gggcatggtg	gggcacacct	170076447
gtaatcccag	ctactcagga	ggctgaggca	ggagaattgc	ttgaaccogg	170076497
gaggtggagg	ttgcagtgag	ccgagatcac	accattgcac	tccagcttgg	170076547
gcaacaagag	caaaaatcca	tcttaaaaaa	aaaaaaaaagc	tagatgggta	170076597
agtataaagt	ccaaatcaga	gacaccatga	gggaggcact	attggccagt	170076647
ccagggagga	gatggtcatg	gtcacgggtc	tgagcctgac	agaggggtca	170076697
cctcactggc	gagaagaccc	aagggtgtgag	tcctcccact	gctcacagtc	170076747
caggtctaac	tggtacacaa	gcacacagct	tcgtaggagc	atgtgtgctg	170076797
caaggctggc	tacaagcgag	tttgcaattt	gtgcttgagg	aaagcagaat	170076847
ccactgtggg	gacatgtgga	aaccagatat	gatgaaaggg	gcctggactg	170076897
gctggattct	aggtccagat	atgtcaccca	ttgctcaacg	acttaggact	170076947
cagacaaagc	cagttagtga	gaaggtttag	aagagatctc	ctatgctaga	170076997
atagcttagc	attggctgga	tgtgtttaac	agatacagaa	accactgaa	170077047
agtacagtca	tgctctgcat	aatgacgttt	ccatcagcaa	cacaacatac	170077097
acaattgtgg	tcccataaga	ttataacaga	gctaaaaaat	tcctattgcc	170077147
cagtgcacttc	ttgaggttcc	tgaccctgtg	tgggctcagg	ctaactgtgtg	170077197
tggttgtgtc	ttcatttgta	attttaaaaa	aagggtttta	aaagaaaaga	170077247
aatgaaaata	aaaaatTTTT	aaatagagaa	aaagcttata	aaataagaaa	170077297
ataaagaaaa	atatttttgt	acagctaggc	agtgtgaatt	ttaagctaag	170077347
cgttatcaca	aaagagtcca	aaagtttgaa	aaaaaaccaa	atagtttgta	170077397
aaataaagtt	agagtaagct	aaggtttaatt	tcttattgaa	aaaaaaattt	170077447
attaatttag	tatagcccta	agcataaagt	atgtataaag	cctacctcat	170077497

FIG. 1.139

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gttttagtaat	atcccaggcc	ttcacactca	ctcaccatca	ctcactgact	170077547
cacccagagc	aacttccagt	cctgtaactt	ccattcatgg	taagtgcctt	170077597
aatagttgta	ccatttttta	ttttttacac	cttagtttta	ttgtaccttc	170077647
tctaaattta	gtatgtttgg	acacacaaat	acttaaaata	cttaccattg	170077697
tgttacaatt	gcctacagta	ttcagtacaa	taacacactg	tacaggttta	170077747
tagcctagga	gcaaaaaggcc	ataccataca	gcctaggtgt	gtagcagggc	170077797
taccccatct	aggtttgctg	gagtatactc	cacgatgttc	acacgatgac	170077847
aaaactgcct	aacaacacat	ttctcagagc	gtatccctgt	tggttaagcga	170077897
cacatgactg	aataagcaaa	tgtgcagtg	ttgtgcattt	tttttcctga	170077947
gagagtctaa	acccttcatt	ccacactcag	aagagtctat	gatcccaaaa	170077997
cattaaggat	cacttaatca	aaatcatcta	ctattcaatc	tgagaatttc	170078047
ctgtgtagca	tcctctagag	ttgggtgattc	catctctctt	tgccoctagt	170078097
gataggtatt	catcactgtg	tgaggcactc	acagttagaa	aatcacttct	170078147
taatatacaca	tgcgaggggc	aatgggtccc	tcactccctt	cacacgtaag	170078197
gttatggaac	aacaggcatg	agaacgctga	atggcttaaa	agtactttac	170078247
aaacaaaagg	tgctctaatt	tattcttggt	atgtcattat	tgccatagta	170078297
ttacatctca	agttaatttt	tatctcaacc	attcaaactt	aagtctgact	170078347
tagtaactag	ctcatcatta	ttttttataa	caaagtaatg	actagcaaca	170078397
tctggcatca	gactttgaac	aaacctcaga	aggaactgtc	aaggaggctc	170078447
cccacgggtt	cacgctcttc	tctcctcctg	cacacagggg	acagggccat	170078497
tctccttctt	ttactgggac	tacctgggct	tcattccagg	aatccccagg	170078547
tggaacacagg	agggtgggtga	aaaccgctgc	ccgtcacctg	taaagtttcc	170078597
tgtgaatgtg	tctacagcgg	ccagcaccac	aaggcataca	aagaaaggga	170078647
aggagagact	gatgtgagag	cggcagcgtg	ggcactcctg	tgagggtgcc	170078697
acagctgtag	acaagttaaa	tcagtgcagt	tcaatcaaaa	gtcatgacct	170078747
atgagcgtca	caaccagcac	gagtctacaa	aggaatacat	taaaactaag	170078797
accagagcac	agctcacatt	agtgaaggat	gggatcattt	catggagttt	170078847
ttgtttcaaa	atatttcatt	aacatttcac	ttatatatat	gtgtgtatat	170078897
tggggtgtga	tttaaattac	aattcttact	ataaaataca	gcaaaagaaa	170078947
gaagaaacaa	agagagggcc	actgggtttac	ctaacatcca	caggcaggct	170078997
acttcccagc	atcttgagcc	ccaaagaagt	aaatttctct	ccacaaccga	170079047
tggtaccaca	gcctgacact	tagccaatga	tgaaaacgaa	aaacaaaaca	170079097
aaagcttggc	agtcagtatc	caaatatgca	gatactacag	aatctgtttg	170079147
atgtagaagt	tgatcctgct	accagacag	caaacaactc	atattattaat	170079197
aaagtcaggt	tcctccttaa	tgaagtgggt	ttaatagttg	atatctcaat	170079247
aattacttag	tgcatTTTTT	atgaaggtga	tgggaaacaa	gtgctgtttc	170079297
ttgagtcgga	aagagtctct	caagctccca	caaagaaatt	tcccagagctt	170079347
gtgaggaatt	cagtcacagg	aagatcaagg	aattaagtgt	actgcaaaaa	170079397
acccttcatg	cttctggcta	agataaatct	aacagtgtac	tggtatgtctt	170079447
caagaatacc	tcatttactc	aaaaaataca	atattcccat	tttctttatt	170079497
tgcatTTTTA	tgtgattttt	gcttcatctc	ctttcttcac	tcaagccacc	170079547
tgggccgtac	ccaggggaatt	cctaaggggc	aaaaggaggg	atgtgaaaac	170079597
ctctgcagcc	ccttcggaag	tttcttgtga	atatatgcac	agataaacag	170079647
atgtgcattt	taaaaataaa	aatgctttta	gatctaattg	taggagattc	170079697
aaaccaacaa	ttaatttctc	tgttaaaatg	ggttaaaata	gatgtaaaat	170079747
attaatatgt	atataagcat	tctgaattag	acttatgtga	atTTTTctcc	170079797
TTTTctttct	ttctttttga	gaataagccc	tttcattttac	gtagaaatgc	170079847
ttcagcgttt	agataattgc	tacttatctt	gttagctaca	aacacaacca	170079897
taattaaagg	ctctgtaaga	attatgaatt	ctgggggaaat	tgggccacttg	170079947
tctctgtggc	gtaaacagta	tctaatttat	aacaaatcat	ctgccttagt	170079997
cccagcagga	taagggtgata	tgtattgccc	agcacatgag	aaagatggca	170080047
attaggaatt	gttaccaagt	tacggggagcc	tcacacgaac	atccatcacc	170080097

FIG. 1.140

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tttggggata	tgtacaagat	acaaacttaa	tttgatggat	tccttttcta	170080147
ttgggatcaa	agtctcaaaa	gggaaagtga	caatttcagg	gaaaatctgg	170080197
tgcaatgaga	ccaacactga	tgagagaaat	gcacacaatt	taatacacct	170080247
gctcacctga	tgtggcaact	cagcctgtgc	ttgctgtggg	ttgccacagg	170080297
atgagacatg	gtctgtgcat	attcccagca	gccacccatc	tcatacactat	170080347
tcttgccagc	ccagattttac	agttgttcaa	tagatggatt	tggtaaatatc	170080397
tgcatagaaa	caacaggcag	agaagggttag	atggcaattg	attcttgatt	170080447
ggtgtaagtt	tatagaacac	attctggcag	ggcccaaagg	aatcactca	170080497
cctacccctc	tgtgatggta	aaacggtgaa	aattccacgg	acttggacct	170080547
tgtgatcctt	cagtgggaaga	tgggcagatt	ccttgcttta	attgacagac	170080597
acttttctaaa	taactaatgc	aattcttatat	tacattatag	tccataaggg	170080647
agacatactt	aaactactac	ttacaacaac	tgtttttaga	gcctttctaaa	170080697
tggtttctac	aaagtagctc	ccattttaaga	tatttttcta	gtattttaagg	170080747
ctatctagta	gacattacaa	aacaatacgc	tgtaaatata	ttcagatttt	170080797
tatcagtaat	acttaacatg	ccgtaatttg	aactttctgc	taaatcatgc	170080847
tatccattcc	tagttggccc	caatgggtgag	agtttactgt	ttcttttaaat	170080897
aattttgttt	ccctttgctg	tctagaggtg	tttatcattc	tgccttacttg	170080947
cctgtgtctc	tgggaatattc	agaagggttcc	atgggaaaca	atttgaatat	170080997
gcaaagaagt	tattttttaa	gcaaggaaaa	tgttttcata	tggattttatt	170081047
ttgagcactt	ctgcctttgc	ctccactggg	aacatgtttc	tctccaacgc	170081097
cgaagccccc	tccctgtgtg	gtgtttgacg	cagaggtga	cagggcaggg	170081147
aagtgggggt	caagatagga	aggccattgg	cagtgtgacc	ccagcccaca	170081197
gtcctagatc	ccaggtcgtg	acaccactct	tttgacagcc	cagattgtta	170081247
cctaacaaga	atgactocca	agctcaacca	ttccaatgcc	atctcctctg	170081297
gttccAGATA	AGATTGAAGA	TGAGCTGGAG	ATGACCATGG	TTTGCCATCG	170081347
GCCCCGAGGGA	CTGGAGCAGC	TCGAGGCCCA	GACCAACTTC	ACCAAGAGGG	170081397
AGCTGCAGGT	CCTTTATCGA	GGCTTCAAAA	ATgtaagacc	cgtgcacgct	170081447
ctgaaggcct	gggggggggt	cccacgtgag	gctacactct	ccccaatgcc	170081497
aagggagctc	ataaggcggt	tcccatatgt	gaggctgtac	aaggaaggcc	170081547
agctctataa	agggggcatg	agagggagat	cacctggcta	gaaaggaagg	170081597
ctccaggcga	ggatggagca	acctcaggag	acagtaaacc	gccaactgcc	170081647
cagaaatttc	acaggggtggc	acatcctcaa	ggaattcacc	ctggcccagg	170081697
gtcaagcctt	agcccttaac	ataatcatac	cttccaacct	ggtgggtgcc	170081747
ccacaataat	gggatttggc	cctgtgtgact	tatgctaacc	aggctcaccg	170081797
agactgatgt	gtaagccgaa	tgtcggtgta	ttaatattacc	ttgggaaatg	170081847
gaactgacag	tggaaacaga	cactcctctc	ccttcgctgg	gacccgctct	170081897
ccttggaagc	cacatggaag	ccaggttaca	atcaaaagtg	gagtcagagg	170081947
acgggagttc	cttggttagt	tgttacttta	aatacattaa	tgtgttcctg	170081997
cagtctcagg	ccagtttgag	agctctcaga	tacaatcctg	gatattaatt	170082047
tatttttttaa	gtttaactct	cagagtgcga	tcttattccc	aatccttggg	170082097
gtggtgtgga	gtgggggtggg	ctacagcgac	atgcacctgg	tcacctctcc	170082147
tccaggtgca	gtctgtaggt	agagctgagc	tgggtcagtt	ccaaactgac	170082197
cacagcctca	atgttctcca	aactgctgac	ccacagggat	tccagccctt	170082247
cctgggagtt	atctgacagg	tgttgggatg	cctcttctct	ccacactagc	170082297
cttgactgca	catgccaaat	gccagtttc	ctaccattag	ggcttctttc	170082347
cttcgatggc	agcattagca	gtgggcagcc	gagttggaga	aggatcctgt	170082397
gggaaagttt	tccaggcagg	cactgggctc	agagggaaca	gcatccagaa	170082447
aagagaagaa	atctacactg	cttggcatct	accatggact	caataccacc	170082497
taacataggt	tcataagata	cccttgggga	agttattgtt	acccccattt	170082547
tacaggttaag	gatattgagg	atcagagact	ggcttggcca	aagtcacaaa	170082597
gcttagtatt	ggctgagcca	ggatttaaac	ccaggttttt	ctgatcttaa	170082647
agccccaat	ctctccacct	cacagtgcgc	attctctgac	aatgtctcat	170082697

FIG. 1.141

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cattttgcaa	agcagctcca	gtcctgagat	ggcactactt	gggagaagtg	170082747
gaaatgcaca	gggccctgtc	cctgggggatc	atgaggaacc	ccagacacca	170082797
aggctggggc	cagtcttctc	ctagtgtgtg	ccctcaaagt	cctcccgctg	170082847
actctctccc	cttcccacag	GAGTGCCCCA	GTGGTGTGGT	CAACGAAGAC	170082897
ACATTCAAGC	AGATCTATGC	TCAGTTTTTC	CCTCATGGAG	gtgagtctga	170082947
ccttgaaatc	tatcttgccc	agctccctct	ctggtaagca	gccttccctt	170082997
cctccaagtc	ctctcttcc	tgccatttgc	ttccttctcg	aggaagagac	170083047
aaactcaggg	caggacacct	ccctcatcgt	gagaggtggg	agtctccaaa	170083097
gcttttagcag	gaaagaactc	tgaaaatgaa	cccaccctgg	aagggggaaga	170083147
agggtctgata	atgcaacatc	acaacgtctc	agaacagctc	tagaaagcag	170083197
gtattataat	cccagatgga	gtaactgagt	ttcggggaag	ataagcagtg	170083247
tactcaagat	tgcacagctg	gtgagttagca	aaccaggatt	agattccata	170083297
agggtctgaa	acagggttttg	ccatgctggc	accaccattg	tgcagggcac	170083347
ttttgaatct	tttcccttaaa	atagctgaga	caagctggaa	ttttgtaaaa	170083397
gaacttcagt	aaataccgaa	gactataaaa	ataaactaat	tgaaaaagag	170083447
gcaggaaaca	taaagtgtgtg	cttattaagc	cagtttataa	gtgtgccagg	170083497
cccacaacag	ctgctctgtt	gccctgcccc	actcctgtgg	gaaccagctg	170083547
tgtccccatg	ggcctggggac	cacatcggtg	actcctcctg	tggcctccat	170083597
gtgtcacatg	ccacttttgca	tcctgtcacc	aagagctgtc	tcctgcaaga	170083647
catcttccct	ggatcctgac	aaaatgcaaa	tccaagtatt	ccaaacactt	170083697
cttggggccct	gtttctcatg	ggcctttttg	gcagcagaca	gatgccttcc	170083747
ttgggtgtgtg	gggcccctac	ccagatcagg	tgggggaggc	agttttgtcc	170083797
catgcaggcc	ccagaatttg	agtttgctga	gttccactga	gccactgttt	170083847
attgagttct	cactgtatgc	caggcacagc	tgtagttaa	aatacttttt	170083897
aaaaaatctc	aagagatagg	tcttgctaca	tccattgtga	gagaggtagg	170083947
aaagggaagc	tcagagaggt	cgtgcttgat	gcccacagtc	acatagctta	170083997
tgtagtacag	cggcattcaa	gttcagggtc	ctctactctg	gagtgagtgc	170084047
tcattcccagg	cattcatggc	cgttcagaag	aacattgtca	tgcagtcact	170084097
gtgccattca	tacaccaacg	actccattga	tagacaggca	ggagaatggg	170084147
tttctcatga	tggctagagg	gaggggcaag	ggctcatctc	actttttgct	170084197
agatctaact	tcacacccaa	acccaaagag	ttgagtcaat	gggccccact	170084247
ccataatctt	ctcctttcca	tcaccctagc	atcactctcc	tctctttctt	170084297
gtcgaagccc	tgccttggtt	ggaagggtct	ccctgtgtgg	aattcctgcc	170084347
cccatcacct	gccctccttt	tctgccttgt	agATGCCAGC	ACGTATGCCC	170084397
ATTACCTCTT	CAATGCCTTC	GACACCACTC	AGACAGGCTC	CGTGAAGTTC	170084447
GAGgtacgct	catctggggg	ccactctagg	ggctctctgg	ttctgcatca	170084497
cctccccctc	taaatctcaa	ggcattgggg	gaaggctctg	accatcaaaa	170084547
gctctcagtc	agaccaaaga	catgtttatc	catttgtaag	catttcctaa	170084597
agatggggaa	aagcagcagc	aactttccct	ggcctgcagg	aactcagggg	170084647
ctcagggggac	taataacaac	agtgtatgag	cttccgggca	cactgcttcc	170084697
cagtggcagc	ccctgtactt	agggccttgt	atgtattaat	tcatttactc	170084747
caattcccac	aataacccta	tagggtaggg	ttttattatt	gattaccttt	170084797
ttacagaaga	ggagagtaag	gcaaagagag	atagagtagt	tttcccaagg	170084847
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acagggctgg	ctgtgttgat	ctgtgtctct	cagagctcca	ttcttcctca	170085047
agggggcacc	ttgcaaaaaa	aaacaaaaaa	atgggggcagg	gtaggggaact	170085097
gaaggcagga	gctcttcaca	gagcatagcc	acatcctcca	ggcagacaag	170085147
aggacgcagg	aggcaccatt	ctgtgagagt	atcacagtct	gacccaaaga	170085197
cacagcttca	cactgtctga	tggcttgatg	gttaatgtca	ctctgccttt	170085247
tccccttctc	agGACTTTGT	AACCGCTCTG	TCGATTTTAT	TGAGAGGAAC	170085297

FIG. 1.142

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TGTCACGAG	AACTAAGGT	GGACATTTAA	TTTGTATGAC	ATCAACAAGG	170085347
ACGGATACAT	AAACAAAGAG	gtaagtgagc	tggggccagg	ggtgtgagag	170085397
ggctccagtg	aaggtaacta	acccaacaga	aaacagcccc	aggcatgagg	170085447
atagcactgt	ctgaatgagg	caggctctgc	tttggggcta	acagagctgg	170085497
tccctggcaa	aataaagaag	gcctccctca	ttgccctacc	ctgccctggt	170085547
cccaagcgcc	cagaaaggat	taaacagatt	cattctcact	gggtcaccta	170085597
gattcagtag	atattacaca	gtggataaaa	atgacttggt	tcagtgtgaa	170085647
gagttactct	tccctagggg	acctgcattt	gggaagggtta	ggagccacaa	170085697
gtcaaagcta	aaagttgaaa	tgggtggaatt	gtaggcagca	cctagaatag	170085747
aaaagaaaga	tttttaagga	agaggaacct	acaattgggt	catattggcc	170085797
ttaaactatt	ttgcctatta	atacaaccgc	caagggggta	atggaaggta	170085847
cagctgtctt	tacagaaatt	atcacaaata	atctctgaat	cttcactgct	170085897
ttgcactttt	agaacctcag	aggacatgtc	tctagccagt	gaaataccct	170085947
caggtctatc	tcaaaaactca	ctttgggtatc	cactgtatcc	tggtatctca	170085997
gtggaagctg	gaaattggca	tcctgtaaca	ctccacttgc	tgagctcctg	170086047
tgtgccaggc	acggtgcctg	gaggtataga	tatcagcacc	aatcttcacc	170086097
tcaaccgggc	aagcttctct	ctgtaagctc	agagagttta	tccaactttc	170086147
attcctcatt	catttagtca	tgtttttaat	taacacagat	ttgaaggctt	170086197
attagggtgt	ctaggtgctg	gaggtaaaga	ggtgaacaat	cagactaggc	170086247
cccacactgg	agcagcatag	agagatggac	aataaacagg	ccaaaaagga	170086297
atcagcaggt	agaagatatt	ttggcagggg	agggttagcaa	aggcctctcc	170086347
aaggaggtgt	cgtcatactg	gaaccagtta	tacaaaaagc	caggaaaagt	170086397
gttccaggca	gaaggaacag	ccactagaga	ggctttgagg	caagatagag	170086447
cttcattgtg	ttcaaaaaca	gaaaggcttc	agatggctgc	agatgaagg	170086497
atgaagctga	agactagtgc	aggatgagcc	tgacaggtca	gcagagtcag	170086547
atggtggagg	gctagggtaa	ggggcccatc	catattcccc	tgggaagctc	170086597
ttagatgaac	atgttttttg	aaagacacaa	aaggcaaaaa	cagacttaaa	170086647
aagaatcaga	aatcttgact	agctctgtat	tatttagaga	aatttatattc	170086697
acagttaaaa	accattccca	aataaaaatta	taggcccaga	tggtggactg	170086747
gtgaattcta	atatcaatcc	tacaaaaaaa	ttttagaaaa	tagaggagga	170086797
tggaacattt	cccagcttgt	tttataagtc	caatagtacc	ctgataccca	170086847
aaccaaagaa	aaaaagggtc	tatgaaagga	aacaactaca	aaacagtctc	170086897
cctcgtgagc	acagataaaa	aagctttcac	taaatattag	caaattgaat	170086947
tcagcaatat	ataaaaagga	tgatacaata	caactatgtg	agttttattc	170086997
taggaaggca	aggttgggtt	aacattcaaa	aaccaatcaa	tataattcac	170087047
tatatttaaa	gaaaccaaag	ggatatagac	tggaaaggaa	gaattaacac	170087097
tgtctttatt	tgtacatgg	ataattgtat	taatagaaaa	ccctaagagt	170087147
ctacaaataa	actgctaaaa	ataataagtg	aatttaacaa	agtgaagaca	170087197
tgagttctat	ttacaaaaat	cattttataat	tctacatcca	acaagcaacc	170087247
agaaaattaa	attaagaaaa	atagcatcaa	aaagcacaaa	atactttgag	170087297
aaaaattcaa	caaaacaggt	gcaagactca	tacactgaaa	actataaaat	170087347
attgctgaaa	taaagtaaag	aactaaataa	acacagagat	aaatcatgct	170087397
catgggttgg	aaggcccaat	atagttaaga	tgtggattct	ccaaatttga	170087447
tttatagatt	tagtgtgatc	tcaatcaaaa	tcccagcagg	tattttgtag	170087497
cagttgatat	gggaatgcaa	aaaacctaaa	ataaccaaaa	catctgaaaa	170087547
agaacaaagt	tgaaggacta	aacctacctt	acttcaagac	ttaatgaaaa	170087597
tgtgcagtag	tcaagatgg	agggaattgg	cataaggata	gacatataga	170087647
tcaatggatc	aaaatagaga	gtcaaaaaaa	ctaaaagtag	agctaccata	170087697
tgatccaaca	atcccactgc	tggctatata	ccccatgtaa	aggaaaccag	170087747
tatatcaaag	agatatctgc	actcccatgt	tttttgcaga	tctgttcata	170087797
atagccaaga	tttgggaagca	acctaagtgt	ccatcaacag	atgaatggat	170087847
aaagaaaatc	tggtacttat	acacaatgga	gtacttctgc	cataaaaatag	170087897

FIG. 1.143

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aatgagattt	aatcatctac	aacgtggatg	gaattggagg	tcattacatt	170087947
aagtgaatg	aaccaggcac	agaaagacaa	acatcccatg	ttctctctta	170087997
tttgttggat	ctaaaaatca	aaacaatatg	aagatagagg	gcagaaggac	170088047
ggttaccaga	ggctgggaag	gatagtaggg	gggctgtggg	ggaagttagg	170088097
atagtcaatg	ggtacaaaaa	aaatagaatg	aatgaataag	gcctggtatt	170088147
tggttagcaca	acaaggtgac	tgtagtcaat	aatttaattg	aacattttta	170088197
ctaaaagagt	gtaattgggt	tgtttgtaac	acaaaggata	aatgcttgaa	170088247
gggatggata	cccatttttc	atgatgtggg	tattacacat	tgtatgcctg	170088297
tatcaaaact	tgtcatgtac	cccataaata	tatacaccta	ctatgtgccc	170088347
acaaaaatta	aaaataaaaa	ataaatat	tttaaaaaata	gagatagacc	170088397
cacccatatg	tcaatgcaac	agatgccaaa	aagatcaaag	gggaaagaac	170088447
cgtgttttca	cagctgtata	tcattttgga	aacaaaaatg	gacattaacc	170088497
ttaacctcat	gccaaacata	aacatcaact	tggaaatggat	tatagactta	170088547
aatattaaaa	caaaagctgt	tttcttaagg	aatacatagg	agaaacattc	170088597
ttacaacttt	ggagttaggaa	aggataagga	atcattttctt	aaagtagata	170088647
aatttgactt	tatcaaagtt	aaaaattttg	tgcttttagaa	gacaccttta	170088697
agaaaatgga	aatgcaagcc	atgggacttg	aaaaaatgtt	tgcaaatatt	170088747
ataccagata	tataaagata	ccaggatacc	aaaccaatat	aaagactggc	170088797
atccaaaata	tataagggac	at ttataatt	taatacaaaag	ataaacaact	170088847
tcatataaaa	taggcaaaaag	at ttgatgag	atatttaaga	aaagaagata	170088897
tatgaatggc	cagtaaaacc	atgaaaggtt	gctctatatc	actggtcttc	170088947
aaagaaatgc	aaattataac	tataatgaaa	tacaattgca	cagaatggcc	170088997
acaattaaaa	agactgataa	taccaagcat	tggcaaagat	gtggagcaat	170089047
agaaactctc	atagatagct	ggcagaaatg	taaatgggtac	aaacacgttg	170089097
ggaaacattt	tggcatcttt	gataaagctc	agcacacact	taacatacaa	170089147
cccagaaatc	ccattccagt	caggcatggg	ggcttacgcc	tataatccca	170089197
gtactttggg	aggctgaggg	aggcggatca	cttgagctca	gggtgttcaa	170089247
accgagactgg	gcaacatggc	gagacactgt	ctctactaaa	aatacaaaaa	170089297
aaaaaaaaaa	aaaagccaga	catggttggt	agcacctgtg	gtcccagcta	170089347
ctagggaggg	tgaggtggga	gaattgctta	accctgggga	gtggaggttg	170089397
cagtgtgctg	agattgcacc	actgcactcc	agcctgggtg	acagagcaag	170089447
accctgtctc	aaaaaaagaa	aaaaagaaga	agaaaagaag	tcccactcct	170089497
ggatattttac	ccccaaaaga	aaaatatgta	attccataaa	gacttgtaca	170089547
aagatgtttca	tagcagcttt	at tcatagta	at tcaaaaac	ttaaatgacc	170089597
caaatgtctg	tcaacaggac	aatgggtaaa	tacatcatag	tctgttcatc	170089647
caatggaata	ttactcagca	gtaaaaagga	atgttatagt	tgcattgcagc	170089697
aatgtgtatg	aagctcataa	acctcatgct	gagtaaataa	agccagacgc	170089747
aaatgagttt	acactgtttt	actccattta	catgagattt	tagaaaatac	170089797
aaactaatct	atagtaacag	aaattagatc	tgtgggtgcc	tggtgtcaaa	170089847
gcttgagagg	cactcactgc	gaagaagtgt	gaagggatgt	cttttggttg	170089897
tgaaaatgtt	ctatatcttg	agtgtgggtg	aggttacatg	gggtggataca	170089947
tttgtcaaca	ttcatcaaac	agtacactta	aaatgggtga	atttggtata	170089997
agtaaaattat	gtcccaataa	at ttgattta	tttgttgaaa	aacttggtgt	170090047
aagggggaag	tgccctaacca	atagaagaca	ctcaaaaaat	gtgttggaagg	170090097
aaaaaaatcc	tgtgaaataa	agcaggtaag	agaaaataag	aactcaatat	170090147
catccaaaat	atagattaca	aatcctaata	gagataatag	gaaattaatc	170090197
ccagtgtctc	gtttaaaggc	tcatacctgt	aatcccaaca	ctttgggaga	170090247
ctgaggcagg	aggatgggtt	gagcccagga	gttcaagacc	agcctgggtca	170090297
acatagggag	agcctgtctc	ttcaaaaaca	aaatttaaaa	attacctggg	170090347
tgtagtggca	cgtgcctgtg	ctcccagcta	ctccagaggc	tgaggcagga	170090397
ggatagcttg	agcccaggag	ttcaagcctg	ccctgagcca	taatcactgc	170090447
accacactcc	agcctgggca	acagaacaag	acccttcctc	aaaaaagcaa	170090497

FIG. 1.144

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taaaataaaa	taaagaaatg	cacatgacta	acatagggtt	tattccagga	170090547
atgcaggaat	agcccagtag	cagagaaagc	ctattaaata	atztatcaca	170090597
ttaatatatc	aaaagatcaa	accattttgat	gctaaaatca	catttgatat	170090647
aattttaccat	ttattcataa	taatttttcag	gattcaatta	attaggaata	170090697
aaatacttct	tcagcataat	agaaaatacc	ccagcctggt	acacagcttc	170090747
atacttttatg	gtaacacgcg	gagattctca	ctgaagaaaa	gatgaggcaa	170090797
gaaaagatga	tgaagaaaag	atgaggcaag	aaaagatgat	gtctgcacac	170090847
tgtcagacat	caccactgtt	taacattttcc	tgaaagctct	tcaaacacag	170090897
tgaaacagaa	aaggaaatgc	gatctaaata	ggaaaaatta	caacattcct	170090947
tgtaaatgac	atgatttttct	atctgagaaa	aaagacagca	agaaaaatcaa	170090997
cttaaaaaca	ctagaacttt	taaaaagctg	gcaaagtgc	tggttaataaa	170091047
atacatatgc	aaaaagaaat	tgtgtagcca	atatatcagt	tgtgactagc	170091097
tagaaaattg	taatacaaat	attctcattg	tgatcacaat	aaaattttaa	170091147
gcacatgggc	attttttaaat	atccataatt	tagatgaaga	gaaagaaaat	170091197
tttgataagt	agagaaacat	accatcttct	gaaaggatgt	atattataaa	170091247
gatagcaata	ttataatgac	agcaattctt	ctctaattaa	atztatttta	170091297
ttttgaatca	aaatgggaag	gttattttggg	aaggaaattt	ggcacaattg	170091347
ttataaagtt	acattggaag	attaatcaga	tgaaaatagc	aaagataatt	170091397
ttcaaaaaga	agaaaaatgg	tgggatttgt	tctaccagat	actgaaatat	170091447
attataaagc	tgaaactatt	aaaatattat	aatatcagag	aagggaacagg	170091497
tagatcaatg	gaacaaaata	gaaatcccag	gtacaaatac	catcttggtt	170091547
cataataaag	ggagcatatt	gaatagagag	gtaatgaatc	attaaatgat	170091597
tcttggaata	ctgggttaact	atttttggcaa	taagtaagta	aatattctta	170091647
ctcggtacca	taaacacaaa	atcactatag	atatgtacag	ttgcttttta	170091697
actaaaaaag	aactaaaaat	catatgtgaa	tatctgatca	aagaatggaa	170091747
aaagcataaa	atcaaagtta	gaaacaattt	tttaaattat	tgatggcttt	170091797
acactgtaaa	tatttttaaaa	ttctgcatat	caaaaaatac	cataaacaaa	170091847
gttgaaaagt	aagtgacaaa	cttggttttta	aaaatctgca	atztatgatg	170091897
acagaaagga	ttgatattcc	tcagtagaca	ttcatcttaa	caaaggcaag	170091947
agtcatattc	atcgtgctta	tctttgtatt	tctttgacac	aatatctagc	170091997
acatggtaga	tgcgtaaaaa	taccttttaa	taaattaaaa	atctattaag	170092047
atatttttaac	aattttaataa	atctacacga	atatataaag	agctctcaca	170092097
atccagtcag	aaataggtga	acacaatgag	caaagcagat	gaaaaaatag	170092147
ttcatgggaa	aataaataaa	aatagtcaat	acatatatta	gagacctcac	170092197
taagaaagta	atgtatatct	ttaaaaacaa	tgaattatca	cttatctatt	170092247
aaattgcaaa	ggttttgtaa	agtcttttgt	gaaggttggt	ggaaagtggg	170092297
ttttcataca	tagttgctga	aagtgttctg	ataataaact	ttctaaaagg	170092347
tatttgagga	atatgtatca	aaagcattga	aagttatgca	tcccattctc	170092397
cttataaaaac	cacaccttgg	tatatgtccc	aaggaaataa	agaatagaca	170092447
caaagactta	aaagcaagaa	gagtcttcag	gtaatagtgc	cccagaatgt	170092497
gatagccatg	atatccacta	acagcagatt	tgtaaaatga	attacagtaa	170092547
atacatataa	tggaatagcc	agtggccact	taaaatcatg	aaagagtaat	170092597
ataaaaataaa	cattagtatg	atatattaaa	tttttaataa	tattacattt	170092647
taaattgata	aagtggatatg	tatgatattct	caattttata	aacaactaaa	170092697
tgcttatata	cacatgcaaa	tatatgatac	tctaaaatat	tcaaatacta	170092747
ccttgcaaaa	catataaaga	aaaaaatata	gaaataggat	ttagttgggc	170092797
ttcaactttg	gttcactcat	tattccatca	ctgaataaac	ttactagtgc	170092847
ctactccctt	tttgtaattt	gcaaactagg	cagaattctc	cccattaatc	170092897
tatcagacct	ctctggaggg	cagagttaat	aaagtacccc	ttaaaagaaa	170092947
aagaaagtgt	ggataagtag	cttctcagaa	aagatagcag	gatcttcccc	170092997
tggcaatcat	ttggagataa	cctcatccaa	gttgtaggct	atgaaaatcc	170093047
tgagagagca	acaaaattgc	tctttctgtg	attaaaaaaa	aatatcagac	170093097

FIG. 1.145

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aggaaaagca	tcaatggcca	tgtagatgtg	aagggttgt	aaagcacaca	170093147
tttaaaaata	aacacatgga	tagagacatc	tatttcctcg	ttctatctgt	170093197
tgagggcacc	tcagagcaat	gacatccctg	tagcagttag	catactagta	170093247
cctagacttt	gatttctaaa	taccattctt	cgataaacag	aaccagtctt	170093297
cttgaagaat	agttgattct	aagattggga	aagagaaaat	acaagatgag	170093347
cctggagtag	tttattatgc	tgaagggtata	aaagtgttta	aaaaaaaaaa	170093397
actgcaggag	tcaacctgaa	ggagttccca	atagtcagaa	tgaaagcaat	170093447
ttgagcaaaa	ttaaaaatta	ttaagtactg	gattataacc	tgtaaaatat	170093497
ggtaaatgcc	cacaagtcca	tgctaattgta	aataaacaac	tgaatacata	170093547
aataaatgca	ggagagaagg	tagctcttcc	ttacagaaga	attgtaatta	170093597
ataagtatag	aaggaataaa	ggaaatacaa	aattaccatc	aggcaaacac	170093647
tacagtaata	atttttgcag	gcaagatcca	ctgaaagata	ctaaatcagt	170093697
aaggaaactt	gacagacacc	accttaatca	agtgatcaag	gttaacatta	170093747
tcagtaataa	gacatctcaa	cactatgtaa	ctccctgata	tgacgcactg	170093797
agaaggttat	accatcactt	ctgtggtatt	cttgccagaa	atgcataact	170093847
tcaatctaata	cataactaaa	ccagggatta	actcaaattg	agagacattc	170093897
tacaaaacaa	ctgacctgta	ctcatatcaa	aagtgtgagg	tcctgaaaga	170093947
caaggaaaca	aagaaactca	ggctgggcat	gggtggctcat	gcctataatc	170093997
ccagcacttt	gggaggcaga	ggcaggaaga	tcacttgagt	ccaagagttt	170094047
gagaccagcc	tgggcaacat	ggcaaaaacc	catctctaca	aaaaattagc	170094097
caggtgtggt	ggcacttgcc	tgtagtccca	gctacttgag	aggctgaggc	170094147
gggaggatca	cttgaacccg	ggaggtcgag	gctgcagtga	cggggattgt	170094197
gccactgcac	tcagcctgg	gtgacagagc	aagaacctgt	ctcaaaaaaa	170094247
aaaaaaaaaga	aaaaagaaaa	aaagaatgag	aaactcatat	agattagaag	170094297
agactaagga	gacacaacaa	ataaatgcaa	tgtagaatca	ttgaagggaa	170094347
aaaaatatta	gttgaaaagc	tgagatcccg	ccactgcact	ccagcctggg	170094397
ccacagagcg	agactccgtc	tcaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	170094447
aagaaaagct	gataaaaatt	gaataagccc	tgtagtttag	ttaataatag	170094497
tgaagccatg	ttaatttcct	gggtttgggt	attgtgctct	ggttatgcaa	170094547
gttggttaaca	ttagaggaga	ctgagtgaag	ggtagcatg	aactctctgt	170094597
actaattttg	taaattttct	gtaagtctaa	aattattcat	aatatgcaaa	170094647
aattaaacaa	aaaataaaaat	aaaataagca	catggaatga	gactgtcccc	170094697
tgggtctctg	tagaaaccag	gtcaaacatc	ccaaatgctc	ttttaccccc	170094747
attctgagtt	gggccagaat	ggtcagaata	atgggtccca	atgtaccttg	170094797
ataaacacgg	aaactctcag	gaccgagtc	taagggtctc	tgattcaata	170094847
ggtttgaggt	ggacttgaga	actgatcttt	ttaataaggg	cctcagtctg	170094897
tggaaactatt	ggcctcatgt	gccctgtgga	taatcttggc	tgttggttca	170094947
tttttcttaa	ctgaaaacag	tggcagaaac	tatggggatt	tttaaatctc	170094997
taggctagaa	cattaacttt	ttaaaaattc	agaatagtat	tttatttgcc	170095047
tcaagcctgt	gaatggggat	cccacaaatc	acccccact	gaagacaatg	170095097
cccataacaa	ggtaacctac	ccatgagctt	ctgagggatt	taggaattgt	170095147
ctaccatctc	ctctctaaga	agggtcccca	caatatatcc	ccttctgctt	170095197
gcttctaact	ccctatcacc	tgctaaagaa	ggacctcacc	ttttaatcac	170095247
tttcattgco	aaggggcaca	aggagcccca	aactctgtca	cctaggaaga	170095297
gcttgacctc	atggtttcca	cactgtgtgc	ttttatgtcc	ctgctccagG	170095347
AGATGATGGA	CATTGTCAAA	GCCATCTATG	ACATGATGGG	GAAATACACA	170095397
TATCCTGTGC	TCAAAGAGGA	CACTCCAAGG	CAGCATGTGG	ACGTCTTCTT	170095447
CCAGGtaagt	gcacacaccc	tgacacatgag	ctgtaagccc	agcctagatc	170095497
aagtcaaccc	acgagcatct	gagcaaatga	tttgtgtcca	accctgtact	170095547
aagcatgggt	ggtaacagaa	aagaattata	agatacattg	tcctcaagaa	170095597
acagatgata	tccttaagct	gcaagtgtac	atgacagaag	agaacaagaa	170095647
agtatattat	taaacgctag	tggtatagta	tgaactctaa	atccataaaa	170095697

FIG. 1.146

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at tt t g g g g a t	c a g g g t a a a c	a c g a a a g a c t	t c a t t a a t t a	c a a c t g t g g a	170095747
g g t g t t a a g c	a t t t g t g t c t	g g g a a g t a a g	g g g a a a t a a g	a t t g g a a a c t	170095797
a g g a t a g g g c	c a g a t t a t g a	g a c c t t t t a a a	t g g a a g a g t t	t g g c c t t g c t	170095847
c t g g t a c a g g	a t g g g c a g c t	a g t g c t g a t c	c t t g a c t a a g	g g a g t g g t a t	170095897
a a t c a t t g g g	g c a t t t t t a g g	a a a a a a t t a a	t c t a g c g g t g	g a g t a t c a g a	170095947
g a a t a t c a a g	a g t t c a c t c t	a g t t c a a c c t	c c c a c t t t g c	a g a t g g g a a a	170095997
a g a g a g t c c t	c t c t g g c c t t	g t g c a a g t t t	g t a c a g c a a g	t a a c a g g c c a	170096047
g a a t c a g a a c	c t c t t t t t g c c	c a g t g t t c t g	c c a g a t g g a c	a g g g t a g c a g	170096097
g g a g t c t a c a	g a a g a a g c a g	a a t a a g c c a g	c a g t g a g g t g	a t g a g t g t c c	170096147
a g a g c a a g t c	t t t t g a t t t a	a g g a a g c t c a	t g g g g c t c a a	a g t g t t g t a a	170096197
t c a g g a c c t a	a t t g g a g t t g	t c t g g c c a g t	g a a a g a c a a c	t c t c a t t c t c	170096247
a g g g c a a a g t	t g g t t a a t g a	a a t g a a t g a a	a t g a g c t c c a	g c t c g t t a c t	170096297
c t g a g c t c c a	g c a a g a a a g c	a g g g g a g t a a	g c t t t g g a a t	g g a g a t c a c c	170096347
a g a t t c t g t a	a a g t g c t t t c	t g t t a t g t c t	t t c a g A A A A T	G G A C A A A A A T	170096397
A A A G A T G G C A	T C G T A A C T T T	A G A T G A A T T T	C T T G A A T C A T	G T C A G G A G g t	170096447
a a g g a g a g a t	c t c a g g g c a c	a a t a a c t c t a	c a t c t g g g a a	a g g a a a c c t g	170096497
g g g c c t g g g g	a c c t g c a g a a	g g a a g g t g a t	g a g a a a c c t g	c a c a t a c c t g	170096547
c a a c c c c t c c	c a t c a g a g c c	a a c a a c a c c a	g c a a c a a c t g	t g a a g t c c a c	170096597
a g t t c c a c t c	c t c a a c c t g a	c c t g c a g t t g	g t c t t g g c t a	a g c a c a a g a c	170096647
t g a a c a g a g a	g c c t a a g t a g	g g g t c t g g g g	g c a t g t g a a a	a c t c a g a g g g	170096697
g g t c t c t g t g	a a a a t a g a c t	t c c c g a g a g g	g c a a c a c c a t	t a t t t t t t a g	170096747
c c t g c c t c t g	g c t t g a t g a c	c c a t t t c c c a	g a c t a c a a g g	a a g c a g c t g g	170096797
g g g g a a a a a a	a c c t a c a a t t	g t g t g a t t c t	c a a a c c a c a g	t g t g c a t a a a	170096847
a a t t g c c t g g	a a t g a t t c t g	a a a a t g c a t a	t t t c c a g g c c	t c a a t c c c a g	170096897
a g a c t c t a g a	t c t g g g t c a c	t t t a a c a c a a	a t g t c c t g g a	c c a a t g c t t c	170096947
t a a c a c t t t a	a t g t g t g a a a	c a a t a t c c t t	g a t g a t t t t g	t t a a a a t g c a	170096997
g a t t c t a a t t	c c a t a g g t c t	g g g g t a g g g c	c t g a g a t g t t	a c t t t t t c t c a	170097047
c a t t c t c c c c	a g t c a c a c t g	g t g a t g c t g a	t c c t g g g a a c	a c a a c t t t c a	170097097
t t a a g t c t a a	c c a a t a g a c c	a g c c c c a g a g	t c c a c c a g a g	a c t g a a c t g g	170097147
a a a t a a t t g c	t t c a t c t a c t	t t t g a g a a a t	c c a t t t g t a c	c c c c a c a t t a	170097197
t t t t a g a a a t	g t t c a g a g t t	a c t c t g a g c t	c c a g c c a a g a	a g a a t a g c a a	170097247
a t g t a a g a a a	g c c g g g g a g a	a g t t c c t a g c	a g a t a c t g a g	c c c c c a t c a a	170097297
g t t t c a a g c a	c a t a c a t a a a	c a t c a c a g c c	a c c c t g t t a t	g t a g a t g t c c	170097347
t a t g t g c a g g	g t g a t a t c c a	a g a t a t t t a a	c a a c t a g a a t	g g a a t g a a c a	170097397
c t g a c c c c c t	t g g g g g t g a g	t t c t c a c t g t	t a a t t c c c t t	g a g a g c t g g t	170097447
t g t a a a a c a g	c c t g g c a c c t	t c c c c a c c t c	c a a c c t t g a t	t c c t c t c c c a	170097497
c c a t g g g a t c	t c t g c a c a c c	c a g c t t c c c t	t c a c a t t c c a	c t g t g a g t g g	170097547
a a g c a g c c t g	a a a c c c t c a c	c a g a t g c a g a	t g c c c a g c t g	a a c t t t c c a g	170097597
c t g c c a g a a t	a a t g a g c c a a	a t a a g c c t a t	a c t g a c a t t a	a c c t t t t c a t	170097647
t t c t g a t a t t	g a t a a t t t g a	a a a g c a g t c t	t a a t a a g c a t	t t a t c t a c t t	170097697
t a t t g a t t t t	t t t g a a a g a g	a g c g c t t t g g	g g g g t t t t c t	t a c t g t a t g t	170097747
c t c t a t t g c a	t g t t c t g t a t	t t t a c a t t t t	t c t a t t a t t t	c t t c t c t g a g	170097797
g t a t a g t a t t	g a a t g t a g a a	a a a t c c t c a a	a t g t t c g g t a	t t a a g c a a t a	170097847
c a c t t c t a a t	t c a t g g t t c a	g a g a a g a a a a	t a t c t c g a a t	a a a a a t a a a a	170097897
t a a a a a t a t g	a c t t a t c a a a	a t t t g t a g g a	t c t a a a g c a g	t a t t c c a g g a	170097947
a t g c a a g g t t	g g t t t a a c a t	t c a a t a a t t g	g t c a g t g t a a	t t a a t c a c a t	170097997
t a a t a g a a t a	a a a a g a g a a a	a a a t a t a a t c	a t t t c a g t g g	a t g t a a t t g t	170098047
t c a g a g c t t c	t t a a a a g a a g	c a a c t c a c t a	t t t t a c t a g a	t g a t t t g t t t	170098097
c t t c t g a a t t	c c t c t t t a a g	g c t a c a g g t g	g t g c t t c t t a	c t t t g a a c t g	170098147
a t c a c t t t c t	a g g t c c c c a c	c c t t a c t t c t	t g t t t t t c a t	a c c c t t g t a g	170098197
a g t t t t c t c c	a t a t a g g a a a	c c c a t g c t t g	a c a t t t g c t c	a c c a g a g t t a	170098247
c a g a g c t c t c	a g g g a g g a g a	c t c a g a g t t c	t a a c c c t c t t	g c c c t c c t t t	170098297

FIG. 1.147

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```
tttcccagGA CGACAACATC ATGAGGTCTC TCCAGCTGTT TCAAAATGTC 170098347
ATGTAAActgg tgacactcag ccattcagct ctcagagaca ttgtactaaa 170098397
caaccacctt aacaccctga tctgcccttg ttctgatttt acacaccaac 170098447
tcttgg
```

FIG. 1.148

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Amino acid sequence of KChIP1

MGAVMGTFSSLQTKQRRPSKDKIEDELEMTMVCHRPEGLEQLE
AQTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYA
HYLFNAFDTTQTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKD
GYINKEEMMDIVKAIYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKN
KDGIVTLDEFLESCQEDDNIMRSLQLFQNVN (SEQ ID NO: 2)

FIG. 2

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Nucleic acid sequence encoding the amino acid sequence of KChIP1

ATGGGGGCGCGTCATGGGCGACCTTCTCATCTCTGCAAACCAAA
CAAAGGCGACCCCTCGAAAGATAAGATTGAAGATGAGCTGGA
GATGACCATGGTTTGCCATCGGCCCCGAGGGACTGGAGCAGC
TCGAGGCCCAGACCAACTTCACCAAGAGGGAGCTGCAGGTC
CTTTATCGAGGCTTCAAAAATGAGTGCCCCAGTGGTGTGGTC
AACGAAGACACATTCAAGCAGATCTATGCTCAGTTTTTCCCT
CATGGAGATGCCAGCACGTATGCCCATACCTCTTCAATGCC
TTCGACACCACTCAGACAGGCTCCGTGAAGTTCGAGGACTTT
GTAACCGCTCTGTTCGATTTTATTGAGAGGAACTGTCCACGAG
AAACTAAGGTGGACATTTAATTTGTATGACATCAACAAGGA
CGGATACATAAACAAAGAGGAGATGATGGACATTGTCAAAG
CCATCTATGACATGATGGGGAAATACACATATCCTGTGCTCA
AAGAGGACACTCCAAGGCAGCATGTGGACGTCTTCTTCCAG
AAAATGGACAAAAATAAAGATGGCATCGTAACTTTAGATGA
ATTTCTTGAATCATGTCAGGAGGACGACAACATCATGAGGT
CTCTCCAGCTGTTTCAAAATGTCATG
(SEQ ID NO:3)

FIG. 3

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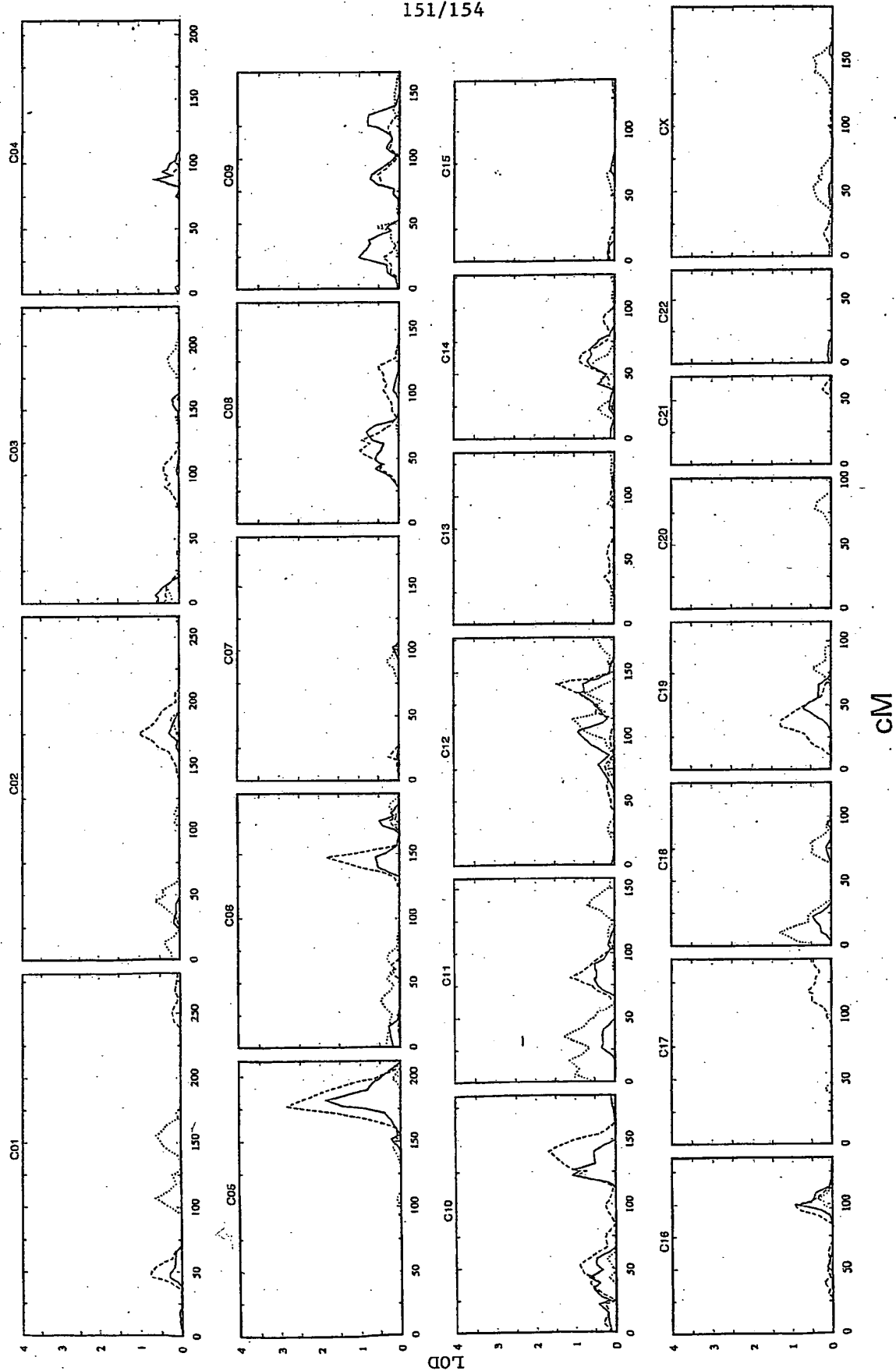


FIG. 4

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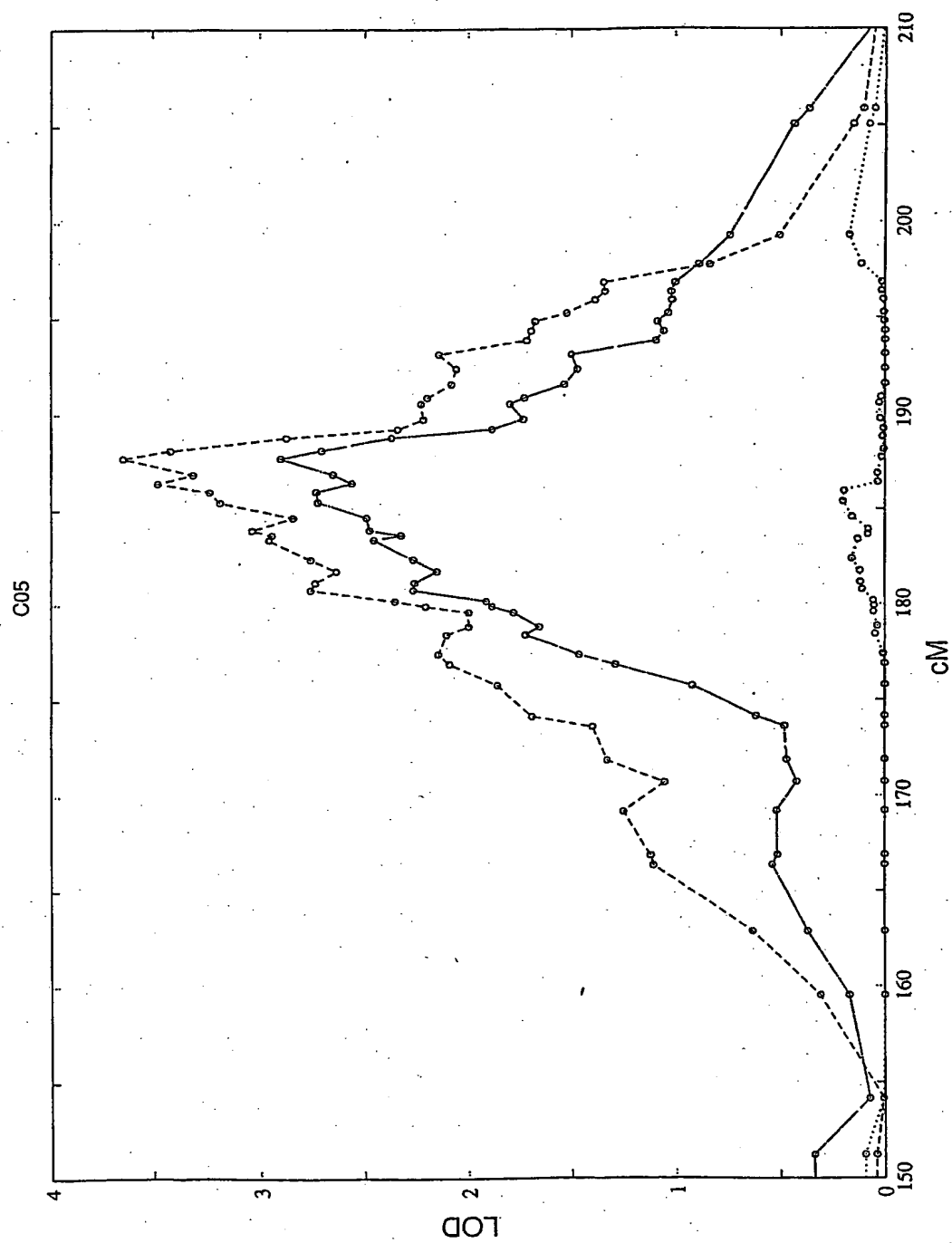


FIG. 5

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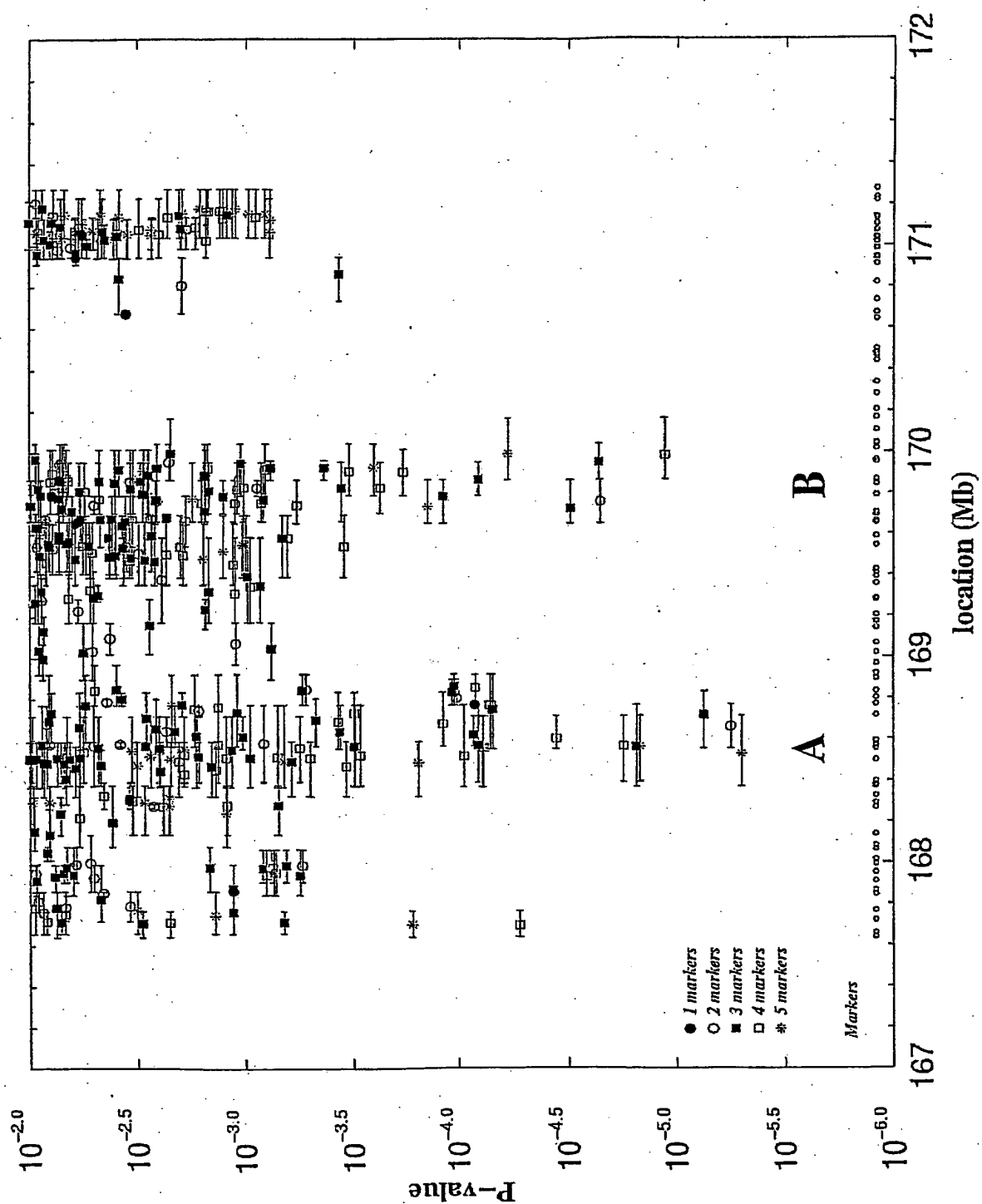


FIG. 6

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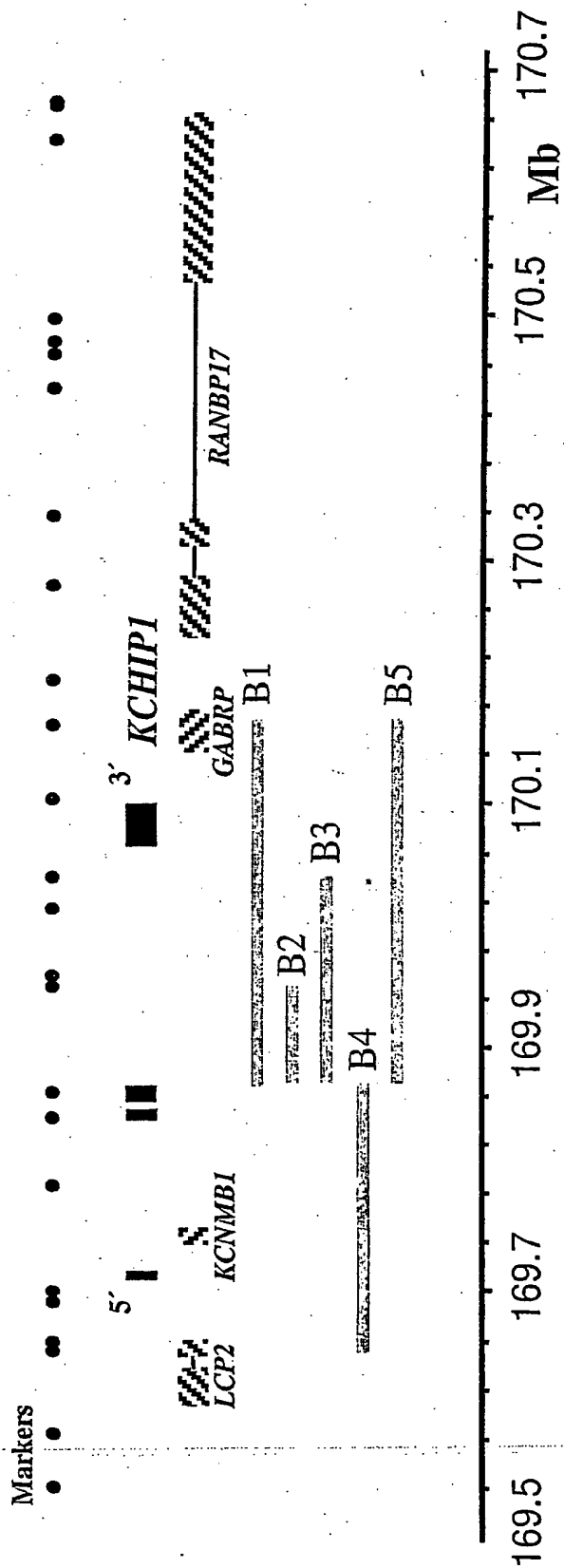


FIG. 7

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(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
21 May 2004 (21.05.2004)

PCT

(10) International Publication Number
WO 2004/041193 A3

(51) International Patent Classification⁷: **C07H 21/04**,
C12Q 1/70, C12P 19/34

(74) Agents: CARROLL, Alice, O. et al.; Hamilton, Brook,
Smith & Reynolds, P.C., 530 Virginia Road, P.O. Box 9133,
Concord, MA 01742-9133 (US).

(21) International Application Number:
PCT/US2003/034681

(22) International Filing Date: 31 October 2003 (31.10.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/423,545 1 November 2002 (01.11.2002) US
60/449,945 25 February 2003 (25.02.2003) US
60/477,111 9 June 2003 (09.06.2003) US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR,
CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR,
KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,
MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT,
RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR,
TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (BW, GH,
GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE,
SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA,
GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): DECODE
GENETICS EHF. [IS/IS]; Sturlugotu 8, IS-101 Reykjavik
(IS).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): REYNISDOTTIR,
Inga [IS/IS]; Gunnarsbraut 26 1R, IS-105 Reykjavik (IS).
GULCHER, Jeffrey, R. [US/US]; 25663 Countryside,
Lake Barrington, IL 60010 (US). GRANT, Struan, F.
[GB/IS]; Sorlajkov 1, IS-107 Reykjavik (IS). THOR-
LEIFSSON, Gudmar [IS/IS]; Vesturberg 10, IS-111
Reykjavik (IS).

Published:

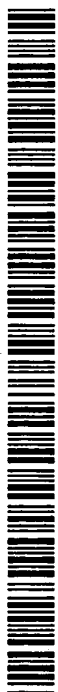
- with international search report
- before the expiration of the time limit for amending the
claims and to be republished in the event of receipt of
amendments

(88) Date of publication of the international search report:
6 October 2005

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: HUMAN TYPE II DIABETES GENE-Kv CHANNEL-INTERACTING PROTEIN (KChIP1) LOCATED ON CHRO-
MOSOME 5

(57) Abstract: Association of Type II diabetes and a locus on chromosome 5 is disclosed. In particular, the gene KChIP 1 within
this locus is shown by linkage analysis to be a susceptibility gene for Type II diabetes. Pathway targeting for drug delivery and
diagnosis applications in identifying those who have Type II diabetes or are at risk of developing Type II diabetes, in particular those
that are non-obese are described.



WO 2004/041193 A3

INTERNATIONAL SEARCH REPORT

International application

PCT/US03/4681

A. CLASSIFICATION OF SUBJECT MATTERIPC(7) : C07H 21/04; C12Q 1/70; C12P 19/34
US CL : 435/6, 91.1; 536/23.4, 24.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1; 536/23.4, 24.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN, East**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, T	KROESE, M. Genetic Tests and Their Evaluation: Can We Answer the Key Questions? Genetics in Medicine. Nov/Dec 2004, vol. 6, pp475-480	
A, T	LUCENTINI, J. Gene Association Studies Typically Wrong. The Scientist; Dec. 2004, Vol. 18, page 20	1-3
A, T	PAGE G. P. Are We There Yet? Deciding When One Has Demonstrated Specific Genetic Causation in Complex Diseases and Quantitative Traits. Am. J. Hum. Genet., 2003, vol. 73, pp. 711-719	1-3
A	US 6,361,971 B1 (RHODES et al.) 26 March 2002 (26.03.2002)	1-3
Y, P	VAN HOORICK, D. Differential Modulation of Kv4 Kinetics by KChI P1 Splice Variants. Molecular and Cellular Neuroscience, 2003, vol. 24, pp. 357-66.	1-3
Y, P	REYNISDOTTIR, I. Localization of a Susceptibility Gene for Type 2 Diabetes to Chromosome 5q34-q35.2 Am. J. Hum. Gen. 2003 vol. 73, pages 323-335	1-3
A, P	MARTIN L.J. A Quantitative Trait Locus Influencing Type 2 Diabetes Susceptibility Maps to a Region on 5q in an Extended French Family. Diabetes, Dec. 2002, vol. 51, pages 3568-	1-3
A	LINDGREN C.M. Contribution of Known and Unknown Susceptibility Genes to Early-Onset Diabetes in Scandinavia. Diabetes, May 2002, vol. 51, pages 1609-1617	1-3

☒ Further documents are listed in the continuation of Box C.☐ See patent family annex.

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"&"

document member of the same patent family

Date of the actual completion of the international search

21 March 2005 (21.03.2005)

Date of mailing of the international search report

11 AUG 2005

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US
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P.O. Box 1450
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Facsimile No. (703) 305-3230

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PRIMARY EXAMINER

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

PCT/US03/34681

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, T	PEZZOLESI M.G. Examination of Candidate Chromosomal Regions for Type 2 Diabetes Reveals a Susceptibility Locus on Human Chromosome 8p23.1	1-3
A	TAKIMOTO K. Palmitoylation of KChIP Splicing Variants Is Required for Efficient Cell Surface Expression of Kv4.3 Channels. J. Biol. Chemistry, July 2002, Vol. 277, pp. 26904-26911	1-3
A	AN, W.F. Modulation of A-type Potassium Channels by a Family of Calcuim Sensors. Nautre, 3 February 2000, Vol. 403, pages 553-556	1-3

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/34681

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1-3, species SG05S96, DG00AAJIB, DG00AAJHF
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/US03/34681

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Group 1, claims 1-3 a method of diagnosing susceptibility to Type II diabetes by detecting polymorphism in KChIP1.

Group 2, claims 4-5, a nucleic acid molecule comprising KChIP1.

Group 3, claim 6, a method for assaying for presence of nucleic acid molecule in a sample.

Group 4, claims 7-8, a vector and host cell comprising a nucleic acid molecule.

Group 5, claim 9, a method of producing a polypeptide.

Group 6, claim 10, a method of assaying for a polypeptide.

Group 7, claims 11, 13-14, a method of identifying an agent that alters expression of KChIP1 nucleic acid.

Group 8, claims 12, 15-16, an agent that alters expression of KChIP1 nucleic acid.

Group 9, claim 17, a method of altering expression of KChIP1.

Group 10, claim 18, a method of identifying a polypeptide that interacts with KChIP1 polypeptide.

Group 11, claims 19-22, a therapeutic agent.

Group 12, claims 23-25, a method of treating a disease associated with KChIP1.

Group 13, claim 26, a transgenic animal comprising KChIP1.

Group 14, claims 27-30, a method for assaying a sample for the presence of KChIP1.

Group 15, claims 31-35, a reagent for assaying a sample for KChIP1.

Group 16, claims 36-38, the use of a nucleic acid.

Group 17, claims 39-48, a method of diagnosing susceptibility of Type II diabetes by a haplotype of one or more markers.

Group 18, claims 49-51, the use of a therapeutic agent for treatment of Type II diabetes.

Further species election:

For group 1 and 17, the species are each SNP recited in Table 13.

For group 2-6, 14-16, the species are each sequence recited in Table 10.

For group 17, the species are each sequence recited in Table 2, 5, or 13.

The first named invention which will be searched is Group 1, species rs1895301, claims 1-3.

The inventions listed as Groups 1-18 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the common technical features that joins all the inventions is gene KChIP1.

INTERNATIONAL SEARCH REPORT

PCT/US03/34681

An et al (Nature, vol 403, ppp.553-556) teach the KchIP1,2, and 3 cDNA, gene expression and protein localization (see 2nd column, 3rd paragraph, page 553 and 1st column, 1st paragraph, page 554). Thus, the technical feature linking the recited groups 1-2 does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art. Thus, there is no special technical feature that joins the methods.

The species listed above do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the species do not share a significant structural element and each element does not belong to a recognized class of chemical compounds (see AI Annex B, part 1(f)). Further, these are known special technical feature in view of the prior art.